

STIC-Biotech/ChemLib

88836

From: Yaen, Christopher
Sent: Wednesday, March 12, 2003 9:12 AM
To: STIC-Biotech/ChemLib
Subject: 09822698

could you please run a seq search on seq id 5, 24 and 26

thanks

Christopher Yaen
Patent Examiner
US PTO
Art Unit 1642
CM1-Rm 8E18
Mail Box 8E12
703-305-3586

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MAR 12 2003
(STIC)

Mary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155

Searcher: Ruhl
Phone: _____
Location: _____
Date Picked Up: 3/12/03
Date Completed: 3/14/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

STIC-Biotech/ChemLib

88803

From: Yaen, Christopher
Sent: Tuesday, March 11, 2003 6:58 PM
To: STIC-Biotech/ChemLib
Subject: 09822698

could you please run a seq search on
seq id no 3 regular search
amino acids 97-110 of seq id no 3 regular and oligo search
amino acids 99-110 of seq id no 3 regular and oligo search
seq id no 1 regular search

thanks

Christopher Yaen
Patent Examiner
US PTO
Art Unit 1642
CM1-Rm 8E18
Mail Box 8E12
703-305-3586

Edward Han
Technical Info. Specialist
STIC/Biotech
CMI 6802 Tel: 305-9203

RECEIVED
MAR 12 2003
(STIC)

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 3/13/03
Date Completed: 3/14/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 6
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Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
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Sequence Sys.: EUIP
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:30:39 ; Search time 12.3846 Seconds
(without alignments)
33.261 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_l10
Perfect score: 14
Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents.AA.*
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3: /cgn2.6/prodata/2/iaa/6A_COMB.pep.*
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5: /cgn2.6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2.6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	6	42.9	95	4 US-08-928-383B-18	Sequence 18, Appl
2	5	35.7	8	4 US-08-637-732A-34	Sequence 34, Appl
3	5	35.7	8	4 US-08-637-732A-36	Sequence 36, Appl
4	5	35.7	14	4 US-08-973-131-75	Sequence 75, Appl
5	5	35.7	20	1 US-08-103-742-12	Sequence 12, Appl
6	5	35.7	20	1 US-08-199-508-5	Sequence 5, Appl
7	5	35.7	22	1 US-07-791-930C-9	Sequence 9, Appl
8	5	35.7	22	1 US-08-173-515B-12	Sequence 12, Appl
9	5	35.7	22	3 US-08-329-793-40	Sequence 40, Appl
10	5	35.7	33	2 US-08-415-788-28	Sequence 28, Appl
11	5	35.7	34	2 US-08-415-788-11	Sequence 11, Appl
12	5	35.7	34	2 US-08-415-788-14	Sequence 14, Appl
13	5	35.7	34	2 US-08-415-788-18	Sequence 18, Appl
14	5	35.7	34	2 US-08-415-788-24	Sequence 24, Appl
15	5	35.7	41	2 US-08-415-788-5	Sequence 5, Appl
16	5	35.7	41	2 US-08-415-788-41	Sequence 41, Appl
17	5	35.7	56	4 US-07-741-453A-47	Sequence 47, Appl
18	5	35.7	58	4 US-09-605-785-553	Sequence 55, App
19	5	35.7	116	2 US-08-428-197-10	Sequence 10, Appl
20	5	35.7	116	5 PCT-US93-10555-10	Sequence 10, Appl
21	5	35.7	187	4 US-09-117-257-23	Sequence 23, Appl
22	5	35.7	187	4 US-08-945-476-23	Sequence 23, Appl
23	5	35.7	187	4 US-09-489-352-23	Sequence 23, Appl
24	5	35.7	188	4 US-09-117-257-44	Sequence 44, Appl
25	5	35.7	188	4 US-09-489-352-44	Sequence 44, Appl
26	5	35.7	264	4 US-08-856-841-14	Sequence 14, Appl
27	5	35.7	325	1 US-08-118-270-30	Sequence 30, Appl

28	5	35.7	325	5 PCT-US93-08528-30	Sequence 30, Appl
29	5	35.7	329	1 US-08-348-792-12	Sequence 12, Appl
30	5	35.7	329	2 US-08-462-738-12	Sequence 12, Appl
31	5	35.7	329	4 US-09-199-955-12	Sequence 12, Appl
32	5	35.7	329	4 US-08-880-875-12	Sequence 12, Appl
33	5	35.7	343	1 US-08-348-792-10	Sequence 10, Appl
34	5	35.7	343	2 US-08-462-738-10	Sequence 10, Appl
35	5	35.7	343	4 US-09-199-955-10	Sequence 10, Appl
36	5	35.7	343	4 US-08-880-875-10	Sequence 10, Appl
37	5	35.7	356	4 US-08-259-451-17	Sequence 17, Appl
38	5	35.7	359	1 US-08-181-271A-98	Sequence 98, Appl
39	5	35.7	359	1 US-08-449-315-98	Sequence 98, Appl
40	5	35.7	359	1 US-08-444-803-98	Sequence 98, Appl
41	5	35.7	359	1 US-08-047-413-15	Sequence 15, Appl
42	5	35.7	359	1 US-08-449-043-98	Sequence 98, Appl
43	5	35.7	359	1 US-08-456-265A-98	Sequence 98, Appl
44	5	35.7	359	1 US-08-455-416-98	Sequence 98, Appl
45	5	35.7	359	1 US-08-455-244-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-08-928-383B-18
; Sequence 18, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cossackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-928-383B-18

Query Match 42.9%; Score 6; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 HTGGGV 8

Db 88 HTGGGV 93
|||||
US-08-637-732A-34
RESULT 2
; Sequence 34, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant pILC Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-732A-34
Query Match 35.7%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 HTGGG 7
Db 1 HTGGG 5
RESULT 3
US-08-637-732A-36
; Sequence 36, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant pILC Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia

; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-732A-36
Query Match 35.7%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 HTGGG 7
Db 1 HTGGG 5
RESULT 4
US-08-973-131-75
; Sequence 75, Application US/08973131
; Patent No. 6326166
; GENERAL INFORMATION:
; APPLICANT: Pomerantz, Joel L.
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Pabo, Carl O.
; TITLE OF INVENTION: Chimeric DNA-binding proteins
; FILE REFERENCE: APV-022.02
; CURRENT APPLICATION NUMBER: US/08/973,131
; CURRENT FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: PCT/US95/16982
; EARLIER FILING DATE: 1995-12-29
; EARLIER APPLICATION NUMBER: 08/366,083
; EARLIER FILING DATE: 1994-12-29
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chimeric motif
US-08-973-131-75
Query Match 35.7%; Score 5; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 HTGGG 7
Db 3 HTGGG 7
RESULT 5
US-08-103-742-12
; Sequence 12, Application 08/103742

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; Patent No. 5420244
; GENERAL INFORMATION:
; APPLICANT: RUDOLPH, DONNA L.
; APPLICANT: LAL, RENU B.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; DIAGNOSING HTLV-I ASSOCIATED MYELOPATHY AND ADULT T-CELL LEUKEMIA
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/103,742
; FILING DATE: 06 AUG 1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: SPRATT, GWENDOLYN D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-103-742-12

Query Match 35.7%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 WDPID 13
Db 11 WDPID 15

RESULT 6
US-08-199-508-5
; Sequence 5, Application US/08199508
; Patent No. 5717058
; GENERAL INFORMATION:
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Stetler, Gary L.
; APPLICANT: Anthony-Cahill, Spencer J.
; APPLICANT: Anderson, David C.
; TITLE OF INVENTION: Modulators of Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,508
; FILING DATE: February 18, 1994

; Patent No. 5420244
; GENERAL INFORMATION:
; APPLICANT: RUDOLPH, DONNA L.
; APPLICANT: LAL, RENU B.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; DIAGNOSING HTLV-I ASSOCIATED MYELOPATHY AND ADULT T-CELL LEUKEMIA
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/103,742
; FILING DATE: 06 AUG 1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: SPRATT, GWENDOLYN D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-103-742-12

Query Match 35.7%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 WDPID 13
Db 11 WDPID 15

RESULT 7
US-07-791-930C-9
; Sequence 9, Application US/07791930C
; Patent No. 5360726
; GENERAL INFORMATION:
; APPLICANT: Natasha V. Raikhel
; TITLE OF INVENTION: Polypeptides Enabling Sorting
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,930C
; FILING DATE: 1991 No. 5360726member 12
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/612,200
; FILING DATE: No. 5360726member 13, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5360726e
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION: Peptide
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Tobacco -1,3-glucanase
; ORIGINAL SOURCE:
; ORGANISM: N. tabacum
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: -glucanase peptide
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
; US-07-791-930C-9

Query Match 35.7%; Score 5; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWVD 10
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Db 3 GGWVD 7

RESULT 8

US-08-173-515B-12
; Sequence 12, Application US/08173515B
; Patent No. 5525713
; GENERAL INFORMATION:
; APPLICANT: Natasha V. Raikhel
; TITLE OF INVENTION: DNA Encoding Polypeptides
; TITLE OF INVENTION: Enabling Sorting of proteins to
; TITLE OF INVENTION: vacuoles of plants.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,515B
; FILING DATE: 1993 December 23
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/791,930
; FILING DATE: 1991 No. 5525713member 12
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5525713e
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22

;
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Tobacco -1,3-glucanase
; ORIGINAL SOURCE:
; ORGANISM: N. tabacum
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
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; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: -glucanase peptide
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
; US-08-173-515B-12

Query Match 35.7%; Score 5; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWVD 10
| | | | |
Db 3 GGWVD 7

RESULT 9

US-08-329-799-40
; Sequence 40, Application US/08329799
; Patent No. 6054637
; GENERAL INFORMATION:
; APPLICANT: Boller, Thomas
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Ryals, John
; TITLE OF INVENTION: No. 6054637el Signal Sequences
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,799
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,521
; FILING DATE: 13-JUN-1991
; APPLICATION NUMBER: CH 2007/90-9
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: GA/5-18123/A
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-329-799-40

Query Match 35.7%; Score 5; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGVD 10
DB 3 GGVD 7

RESULT 10
US-08-415-788-28
; Sequence 28, Application US/08415788
; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-415-788-28

Query Match 35.7%; Score 5; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGG 7
DB 13 HTGGG 17

RESULT 11
US-08-415-788-11
; Sequence 11, Application US/08415788
; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-415-788-11

Query Match 35.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGG 7
DB 13 HTGGG 17

RESULT 12
US-08-415-788-14
; Sequence 14, Application US/08415788
; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-415-788-14

Query Match 35.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGG 7
Db 13 HTGGG 17

RESULT 14
US-08-415-788-24
; Sequence 24, Application US/08415788
; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-415-788-24

Query Match 35.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGG 7
Db 13 HTGGG 17

RESULT 15
US-08-415-788-5
; Sequence 5, Application US/08415788
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; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-415-788-5

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Query Match      35.7%; Score 5; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 HTGGG 7

Db 24 HTGGG 28

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Job time : 13.3846 secs

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:59 ; Search time 33.9231 seconds
(without alignments)
54.992 Million cell updates/sec

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Perfect score: 14
Sequence: 1 AKHTGGGWDPIDY 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	121	AAE12706	Human PH1 Fab anti
2	14	100.0	381	AAE12707	Human b1vPH1-IL-2
3	14	100.0	451	AAE12715	Human recombinant
4	13	92.9	14	AAE12740	Human PH1 Fab anti
5	13	92.9	14	AAE12762	Human PH1 Fab anti
6	13	92.9	14	AAE12770	Human PH1 Fab anti
7	12	85.7	14	AAE12718	Human PH1 Fab anti
8	12	85.7	14	AAE12719	Human PH1 Fab anti
9	12	85.7	14	AAE12741	Human PH1 Fab anti
10	12	85.7	14	AAE12744	Human PH1 Fab anti

11	12	85.7	14	22	AAE12748	Human PH1 Fab anti
12	12	85.7	14	22	AAE12751	Human PH1 Fab anti
13	12	85.7	14	22	AAE12754	Human PH1 Fab anti
14	12	85.7	14	22	AAE12755	Human PH1 Fab anti
15	12	85.7	14	22	AAE12759	Human PH1 Fab anti
16	12	85.7	14	22	AAE12761	Human PH1 Fab anti
17	12	85.7	14	22	AAE12765	Human PH1 Fab anti
18	12	85.7	14	22	AAE12767	Human PH1 Fab anti
19	12	85.7	14	22	AAE12774	Human PH1 Fab anti
20	11	78.6	14	22	AAE12743	Human PH1 Fab anti
21	11	78.6	14	22	AAE12746	Human PH1 Fab anti
22	11	78.6	14	22	AAE12747	Human PH1 Fab anti
23	11	78.6	14	22	AAE12753	Human PH1 Fab anti
24	11	78.6	14	22	AAE12756	Human PH1 Fab anti
25	11	78.6	14	22	AAE12757	Human PH1 Fab anti
26	11	78.6	14	22	AAE12758	Human PH1 Fab anti
27	11	78.6	14	22	AAE12763	Human PH1 Fab anti
28	11	78.6	14	22	AAE12764	Human PH1 Fab anti
29	11	78.6	14	22	AAE12766	Human PH1 Fab anti
30	11	78.6	14	22	AAE12768	Human PH1 Fab anti
31	11	78.6	14	22	AAE12734	Human PH1 Fab anti
32	10	71.4	14	22	AAE12720	Human PH1 Fab anti
33	10	71.4	14	22	AAE12742	Human PH1 Fab anti
34	10	71.4	14	22	AAE12749	Human PH1 Fab anti
35	10	71.4	14	22	AAE12772	Human PH1 Fab anti
36	10	71.4	16	22	AAE12735	Human PH1 Fab anti
37	9	64.3	14	22	AAE12745	Human PH1 Fab anti
38	9	64.3	14	22	AAE12769	Human PH1 Fab anti
39	8	57.1	14	22	AAE12771	Human PH1 Fab anti
40	8	57.1	14	22	AAE12773	Human PH1 Fab anti
41	7	50.0	16	22	AAE12722	Human PH1 Fab anti
42	7	50.0	16	22	AAE12723	Human PH1 Fab anti
43	7	50.0	16	22	AAE12724	Human PH1 Fab anti
44	7	50.0	16	22	AAE12725	Human PH1 Fab anti
45	7	50.0	16	22	AAE12726	Human PH1 Fab anti

ALIGNMENTS

RESULT 1
AAE12706
ID AAE12706 standard; Protein; 121 AA.
XX AC AAE12706;
XX DT 04-JAN-2002 (first entry)
XX DE Human PH1 Fab antibody variable heavy chain region (VH).
XX KW Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody.
XX OS Homo sapiens.
XX FH Key
XX FT Region
XX FT Location/Qualifiers
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 97..99
FT /label= FR3
FT /note= "Framework region 3"
FT 97..112
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FT 99..110
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT 111..112
FT /label= FR4

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FT      /note= "Framework region 4"
PN      WO200175110-A2.
XX
XX      11-OCT-2001.
PD
XX
XX      30-MAR-2001; 2001WO-US10589.
XX
XX      30-MAR-2000; 2000US-0538913.
PR      (DYAX-) DYAX CORP.
XX
XX      Hoogenboom HRJM, Henderikx MPG;
PI
XX      WPI: 2001-626437/72.
XX      N-PSDB; AAD20731.
DR
XX
XX      Novel isolated tumor-associated antigen mucin-1-specific binding member
PT      for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT      its portion for binding to an epitope of the protein core of mucin-1 -
PT
XX
XX      Claim 2; Page 94-95; 126pp; English.
PS
XX      The invention relates to an isolated tumour-associated antigen mucin-1
CC      (MUC-1)-specific binding member comprising an antigen binding domain
CC      region having an antibody variable light (VL) or heavy (VH) region,
CC      or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC      binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC      The binding of MUC1-specific binding member to MUC1 is detected by a
CC      detection method selected from enzyme-linked immunosorbent assay,
CC      magnetic resonance imaging, scintillation counting, and X-ray film.
CC      MUC1-specific binding member is useful for treating cancer, preferably
CC      adenocarcinoma, in an individual, where the cancer is present in tissue
CC      of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC      binding member is useful for diagnosing and imaging MUC1-expressing
CC      cancer cells and tissues, for purifying or isolating non-glycosylated,
CC      underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC      containing molecules, and for therapeutically or prophylactically
CC      treating cancer. The present sequence is anti-MUC1 human PH1 Fab
CC      antibody VH region.
XX
XX      Sequence 121 AA;
SQ
Query: Match 100.0%; Score 14; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKHTGGGVWDPIDY 14
      |||||
DB      97 AKHTGGGVWDPIDY 110

RESULT 2
AAE12707
ID      AAE12707 standard; Protein; 381 AA.
XX
XX      AAE12707;
AC
XX
XX      04-JAN-2002 (first entry)
DT
XX
XX      Human b1vPH1-IL-2 immunocytokine protein.
DE
XX
XX      Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
KW      breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
XX
XX      Homo sapiens.
OS
XX      WO200175110-A2.
PN
XX      11-OCT-2001.
PD
XX      30-MAR-2001; 2001WO-US10589.
PF
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PR      30-MAR-2000; 2000US-0538913.
XX
XX      (DYAX-) DYAX CORP.
XX
XX      Hoogenboom HRJM, Henderikx MPG;
PI
XX      WPI: 2001-626437/72.
XX      N-PSDB; AAD20732.
DR
XX
XX      Novel isolated tumor-associated antigen mucin-1-specific binding member
PT      for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT      its portion for binding to an epitope of the protein core of mucin-1 -
PT
XX
XX      Claim 9; Page 95-97; 126pp; English.
PS
XX      The invention relates to an isolated tumour-associated antigen mucin-1
CC      (MUC-1)-specific binding member comprising an antigen binding domain
CC      region having an antibody variable light (VL) or heavy (VH) region,
CC      or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC      binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC      The binding of MUC1-specific binding member to MUC1 is detected by a
CC      detection method selected from enzyme-linked immunosorbent assay,
CC      magnetic resonance imaging, scintillation counting, and X-ray film.
CC      MUC1-specific binding member is useful for treating cancer, preferably
CC      adenocarcinoma, in an individual, where the cancer is present in tissue
CC      of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC      binding member is useful for diagnosing and imaging MUC1-expressing
CC      cancer cells and tissues, for purifying or isolating non-glycosylated,
CC      underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC      containing molecules, and for therapeutically or prophylactically
CC      treating cancer. The present sequence is human b1vPH1-IL-2
CC      immunocytokine protein. b1vPH1 is mucin specific binding portion.
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XX      Sequence 381 AA;
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Query: Match 100.0%; Score 14; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKHTGGGVWDPIDY 14
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DB      97 AKHTGGGVWDPIDY 110

RESULT 3
AAE12715
ID      AAE12715 standard; Protein; 451 AA.
XX
XX      AAE12715;
AC
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XX      04-JAN-2002 (first entry)
DT
XX
XX      Human recombinant immunoglobulin (Ig) heavy chain region.
DE
XX
XX      Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
KW      heavy chain region; cancer; breast; ovary; lung; bladder;
KW      cytostatic; therapy; immunoglobulin; Ig.
XX
XX      Homo sapiens.
OS
XX      WO200175110-A2.
PN
XX      11-OCT-2001.
PD
XX      30-MAR-2001; 2001WO-US10589.
PF
XX
XX      30-MAR-2000; 2000US-0538913.
PR
XX      (DYAX-) DYAX CORP.
XX
XX      Hoogenboom HRJM, Henderikx MPG;
PI
XX      WPI: 2001-626437/72.
DR

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DR N-PSDB; AAD20745.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Claim 12; Page 106-108; 126pp; English.

XX

CC The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human recombinant immunoglobulin

CC (Ig) heavy chain region (variable VH and CH constant heavy chain).

XX

SQ Sequence 451 AA;

Query Match 100.0%; Score 14; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 4.3e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIY 14

Db 97 AKHTGGVWDPIY 110

|||||

RESULT 4

AAE12740

ID AAE12740 standard; peptide; 14 AA.

XX

AC AAE12740;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #7.

XX

KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

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PN WO200175110-A2.

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PD 11-OCT-2001.

XX

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PF 30-MAR-2001; 2001WO-US10589.

XX

PR 30-MAR-2000; 2000US-0538913.

XX

XX (DYAX-) DYAX CORP.

XX

XX Hoogenboom HRJM, Henderikx MPG;

PI

XX WPI; 2001-626437/72.

XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 119; 126pp; English.

XX

CC The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX

SQ Sequence 14 AA;

Query Match 92.9%; Score 13; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.5e-07;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPID 13

Db 1 AKHTGGVWDPID 13

|||||

RESULT 5

AAE12762

ID AAE12762 standard; peptide; 14 AA.

XX

AC AAE12762;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #29.

XX

KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

XX

PN WO200175110-A2.

XX

PD 11-OCT-2001.

XX

XX

PF 30-MAR-2001; 2001WO-US10589.

XX

PR 30-MAR-2000; 2000US-0538913.

XX

XX (DYAX-) DYAX CORP.

XX

XX Hoogenboom HRJM, Henderikx MPG;

PI

XX WPI; 2001-626437/72.

XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 123; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 13; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVDPID 13
 . | | | | | | | | | |
 Db 1 AKHTGGGVDPID 13

RESULT 6
 AAEL2770
 ID AAEL2770 standard; peptide; 14 AA.

XX AAEL2770;
 AC
 XX 04-JAN-2002 (first entry)
 DT Human PH1 Fab antibody VH region FR3-CDR3 variant #37.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

FT WO200175110-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 125; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

SQ Query Match 92.9%; Score 13; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KHTGGGVDPIDY 14
 . | | | | | | | | | |
 Db 2 KHTGGGVDPIDY 14

RESULT 7
 AAEL2718
 ID AAEL2718 standard; peptide; 14 AA.

XX AAEL2718;

XX 04-JAN-2002 (first entry)

DT Human PH1 Fab antibody VH region FR3-CDR3 variant #2.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

FT WO200175110-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Claim 2; Page 75; 126pp; English.

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 | | | | | | | | | |
 Db 1 AKHTGGGVWDPI 12

RESULT 8
 AAEL12719
 ID AAEL12719 standard; peptide; 14 AA.
 XX
 AC AAEL12719;

04-JAN-2002 (first entry)
 Human PH1 Fab antibody VH region FR3-CDR3 variant #3.
 DE
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 XX variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 KW
 OS Homo sapiens.

Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 PD 11-OCT-2001.
 XX
 PD 30-MAR-2001; 2001WO-US10589.
 PF
 XX 30-MAR-2000; 2000US-0538913.
 PR
 XX (DYAX-) DYAX CORP.
 PA
 PI Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.

Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Claim 2; Page 75; 126pp; English.
 XX

The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 XX region FR (framework region)3-CDR3 variant.
 SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 | | | | | | | | | |
 Db 1 AKHTGGGVWDPI 12

RESULT 9
 AAEL12741
 ID AAEL12741 standard; peptide; 14 AA.
 XX
 AC AAEL12741;

04-JAN-2002 (first entry)
 Human PH1 Fab antibody VH region FR3-CDR3 variant #8.
 DE
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 XX variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 KW
 OS Homo sapiens.

Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 PD 11-OCT-2001.
 XX
 PD 30-MAR-2001; 2001WO-US10589.
 PF
 XX 30-MAR-2000; 2000US-0538913.
 PR
 XX (DYAX-) DYAX CORP.
 PA
 PI Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.

Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 119; 126pp; English.
 XX

The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.8e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPI 12

Db 1 AKHTGGGVWDPI 12

RESULT 10

AAE12744

ID AAE12744 standard; peptide; 14 AA.

XX

AC AAE12744;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #11.

XX

KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

XX

PN WO200175110-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US10589.

XX

PR 30-MAR-2000; 2000US-0538913.

XX

PA (DYAX-) DYAX CORP.

XX

PI Hoogenboom HRJM, Henderikx MPG;

XX

DR WPI; 2001-626437/72.

XX

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 119; 126pp; English.

XX

CC The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.8e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPI 12

Db 1 AKHTGGGVWDPI 12

RESULT 11

AAE12748

ID AAE12748 standard; peptide; 14 AA.

XX

AC AAE12748;

XX

DT 04-JAN-2002 (first entry)

XX

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #15.

XX

KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

XX

PN WO200175110-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US10589.

XX

PR 30-MAR-2000; 2000US-0538913.

XX

PA (DYAX-) DYAX CORP.

XX

PI Hoogenboom HRJM, Henderikx MPG;

XX

DR WPI; 2001-626437/72.

XX

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 120; 126pp; English.

XX

CC The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX

SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 | | | | | | | | | |
 Db 1 AKHTGGGVWDPI 12

RESULT 12

AAE12751
 ID AAE12751 standard; peptide; 14 AA.

XX
 AC AAE12751;

XX
 DT 04-JAN-2002 (first entry)

XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #18.

XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotstatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key

FT Region Location/Qualifiers

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPT; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or
 its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 121; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 (MUC-1)-specific binding member comprising an antigen binding domain
 region having an antibody variable light (VL) or heavy (VH) region,
 or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX

SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 | | | | | | | | | |
 Db 1 AKHTGGGVWDPI 12

RESULT 13

AAE12754
 ID AAE12754 standard; peptide; 14 AA.

XX
 AC AAE12754;

XX
 DT 04-JAN-2002 (first entry)

XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #21.

XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotstatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key

FT Region Location/Qualifiers

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPT; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or
 its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 121; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 (MUC-1)-specific binding member comprising an antigen binding domain
 region having an antibody variable light (VL) or heavy (VH) region,
 or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 |||||
 Db 1 AKHTGGGVWDPI 12

RESULT 14
 AAEL2755
 ID AAEL2755 standard; peptide; 14 AA.
 XX
 AC AAEL2755;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #22.
 XX
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 DR for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 122; 126pp; English.

XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 SQ Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
 |||||
 Db 1 AKHTGGGVWDPI 12

RESULT 15
 AAEL2759
 ID AAEL2759 standard; peptide; 14 AA.
 XX
 AC AAEL2759;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #26.
 XX
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 DR for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 122; 126pp; English.

XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX
SQ

Sequence 14 AA;

Query Match 85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12

Db 1 AKHTGGGVWDPI 12

Search completed: March 13, 2003, 15:31:41
Job time : 33.9231 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:05:54 ; Search time 51.7192 Seconds
(without alignments)
291.136 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
Sequence: 1 EIVLTQSLPLPVTGPEPAS.....MQGLOSPTFGPTKVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	592	100.0	113	22	AAE12705 Human PH1 Fab anti
2	592	100.0	220	22	AAE12714 Human recombinant
3	592	100.0	381	22	AAE12707 Human blyPH1-IL-2
4	540	91.2	239	21	AAE12705 Human PTHrp monocl
5	537	90.7	239	21	AAE12705 Human PTHrp monocl
6	534	90.2	262	23	ABP46070 Human BLYS binding
7	528	89.2	239	21	AAE12705 Human PTHrp monocl
8	528	89.2	239	21	AAE12705 Human PTHrp monocl
9	527	89.0	239	21	AAE12705 Human PTHrp monocl
10	524	88.5	112	19	AAW53586 Light chain of a h

11	523.5	88.4	114	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
12	523.5	88.4	131	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
13	522	88.2	112	17	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
14	521	88.0	239	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
15	520	87.8	239	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
16	519.5	87.8	113	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
17	518.5	87.6	113	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
18	517.5	87.4	112	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
19	517.5	87.4	222	22	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
20	517.5	87.4	222	22	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
21	517.5	87.4	248	22	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
22	512.5	86.6	111	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
23	512.5	86.6	222	22	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
24	511	86.3	109	20	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
25	510	86.1	114	18	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
26	510	86.1	281	18	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
27	507	85.6	112	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
28	506	85.5	114	23	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
29	505	85.3	112	22	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
30	504	85.1	239	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
31	502	84.8	113	15	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
32	501	84.6	112	19	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
33	501	84.6	139	22	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
34	497	84.0	239	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
35	497	84.0	239	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
36	488	82.4	143	20	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
37	487	82.3	148	20	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
38	486.5	82.2	260	23	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
39	484.5	81.8	113	17	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
40	483	81.6	112	23	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
41	483	81.6	116	19	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
42	483	81.6	116	19	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
43	483	81.6	116	20	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
44	483	81.6	116	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).
45	483	81.6	116	21	AAE12705	Human PH1 Fab antibody variable light chain region (VL).

ALIGNMENTS

RESULT 1	
AAE12705	
ID	AAE12705 standard; Protein; 113 AA.
XX	
AC	AAE12705;
XX	
DT	04-JAN-2002 (first entry)
XX	
DE	Human PH1 Fab antibody variable light chain region (VL).
XX	
KW	Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;
KW	variable light chain region; cancer; breast; ovary; lung; bladder;
KW	cytostatic; therapy; PH1 antibody.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Region
FT	Location/Qualifiers
FT	24...39
FT	/label= CDR1
FT	/note= "Complementarity determining region 1"
FT	55...61
FT	/label= CDR2
FT	/note= "Complementarity determining region 2"
FT	94...102
FT	/label= CDR3
FT	/note= "Complementarity determining region 3"
WO200175110-A2.	
11-OCT-2001.	
30-MAR-2001; 2001WO-US10589.	

Anti-platelet glyc
Anti-platelet glyc
Human IGM GM607 va
Human PTHrp monocl
Human PTHrp monocl
Anti-platelet glyc
Anti-platelet glyc
Anti-platelet glyc
Synthetic antibody
Synthetic antibody
Anti-hEDRF antibod
Anti-platelet glyc
Synthetic antibody
Tf1.6 antibody lig
Human AB light cha
Consensus single c
Amino acid sequenc
HLA-DR-specific pr
Human anti-Rh(D) c
Human PTHrp monocl
Anti-CMV monoclon
Human Anti-CD4 ant
Human protein SEQ
Human PTHrp monocl
Human PTHrp monocl
IgM antibody CEM 1
IgM antibody CEM 1
Human Blys binding
Vlkappa for antibo
Mouse monoclonal a
Human ICR-8.1 V-K
Humanised murine a
Humanised antibody
Protein sequence o
Humanised ICR-8.1

PR 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 PA Hoogenboom HRJM, Henderikx MPG;
 PI WPI; 2001-626437/72.
 XX N-PSDB; AAD20730.
 DR Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Claim 3; Page 93; 126pp; English.
 PS The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
 CC antibody VL region.
 XX SQ Sequence 113 AA;
 Query Match 100.0%; Score 592; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 9.2e-42;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVLTQSPVLSPLVPTGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHRA 60
 DB 1 EIVLTQSPVLSPLVPTGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHRA 60
 QY 61 SGVPRFSGSVSGTDFTLIRSRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
 DB 61 SGVPRFSGSVSGTDFTLIRSRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
 RESULT 2
 AAE12714
 ID AAE12714 standard; Protein; 220 AA.
 XX AAE12714;
 AC AAE12714;
 XX 04-JAN-2002 (first entry)
 DT Human recombinant immunoglobulin (Ig) light chain region.
 XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
 KW light chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; immunoglobulin; Ig.
 XX Homo sapiens.
 OS WO200175110-A2.
 XX 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US10589.
 PF 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 PA Hoogenboom HRJM, Henderikx MPG;
 WPI; 2001-626437/72.

XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.
 DR N-PSDB; AAD20744.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Claim 12; Page 103; 126pp; English.
 PS The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human recombinant immunoglobulin
 CC (Ig) light chain region (variable VL and CL constant kappa light chain).
 XX SQ Sequence 220 AA;
 Query Match 100.0%; Score 592; DB 22; Length 220;
 Best Local Similarity 100.0%; Pred. No. 1.8e-41;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVLTQSPVLSPLVPTGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHRA 60
 DB 1 EIVLTQSPVLSPLVPTGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHRA 60
 QY 61 SGVPRFSGSVSGTDFTLIRSRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
 DB 61 SGVPRFSGSVSGTDFTLIRSRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
 RESULT 3
 AAE12707
 ID AAE12707 standard; Protein; 381 AA.
 XX AAE12707;
 AC AAE12707;
 XX 04-JAN-2002 (first entry)
 DT Human bivPHI-IL-2 immunocytokine protein.
 XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
 KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
 XX Homo sapiens.
 OS WO200175110-A2.
 XX 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US10589.
 PF 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 PA Hoogenboom HRJM, Henderikx MPG;
 WPI; 2001-626437/72.

DR N-PSDB; AAD20732.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Claim 9; Page 95-97; 126pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human bivPH1-IL-2
 CC immunocytokine protein. bivPH1 is mucin specific binding portion.
 XX
 SQ Sequence 361 AA;

Query Match 100.0%; Score 592; DB 22; Length 381;
 Best Local Similarity 100.0%; Pred. No. 3.2e-41;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLVPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
 DB 127 EIVLTQSLPLVPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPOLLIYSGSHRA 186
 QY 61 SGVPRFSGSVSGTDFTLIRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKR 113
 DB 187 SGVPRFSGSVSGTDFTLIRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKR 239

RESULT 4
 AAY82615
 ID AAY82615 standard; Protein; 239 AA.
 XX
 AC AAY82615;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 155
 FT /label= "possible Ala"
 FT /note= "possible Ala"
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX
 PF 12-OCT-1998; 98JP-0304793.
 XX
 PR 17-JUN-1998; 98JP-0188196.
 PR 26-JUN-1998; 98JP-0196729.
 XX
 PA (N1SB) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.
 DR N-PSDB; AAA13925.
 XX A human monoclonal antibody to parathyroid hormone related protein. -
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX
 PS Claim 31; Page 45-46; 88pp; Japanese.
 XX
 CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone protein sequence from the
 CC present invention.
 XX
 SQ Sequence 239 AA;

Query Match 91.2%; Score 540; DB 21; Length 239;
 Best Local Similarity 90.3%; Pred. No. 3.9e-37;
 Matches 102; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLVPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
 DB 21 DIVMTQSLPLVPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPOLLIYSGSHRA 80
 QY 61 SGVPRFSGSVSGTDFTLIRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKR 113
 DB 81 SGVPRFSGSVSGTDFTLIRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKR 133

RESULT 5
 AAY82616
 ID AAY82616 standard; Protein; 239 AA.
 XX
 AC AAY82616;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 2G4-12-20 protein SEQ ID NO:16.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 5
 FT /label= Val, Ala, Asp, Gly
 FT Misc-difference 13
 FT /note= "possibly Leu"
 FT Misc-difference 25
 FT /label= Ile, Thr, Asn, Ser
 FT Misc-difference 27
 FT /label= Phe, Ser, Tyr, Cys
 FT Misc-difference 216
 FT /note= "possible Val"
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX

PF 12-OCT-1998; 98JP-0304793.
 XX
 PR 17-JUN-1998; 98JP-0188196.
 PR 26-JUN-1998; 98JP-0196729.
 XX
 PA (NISB) JAPAN TOBACCO INC.
 XX
 XX WPI; 2000-286723/25.
 DR N-PSDB; AAA13926.
 XX
 PT A human monoclonal antibody to parathyroid hormone related protein. -
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX
 PS Claim 31; Page 48-49; 88pp; Japanese.
 CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone protein sequence from the
 CC present invention.
 XX
 SQ Sequence 239 AA;
 Query Match 90.7%; Score 537; DB 21; Length 239;
 Best Local Similarity 89.4%; Pred. No. 6, 9e-37;
 Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EIVLTQSLPLVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 DB 21 DIVMXQXPLSLVTPGEPASISCRSSQSLHNSGYNYLDFWFLQKPGQSPQLLIYLSNRA 80
 QY 61 SGVDPFRFSGSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGCTKVDIKR 113
 DB 81 SGVDPFRFSGSGTDFTLIRSRVEADGVVYCMQALQTPFTFGCTKVDIKR 133
 RESULT 6
 ABP46070
 ID ABP46070 standard; Protein; 262 AA.
 XX
 AC ABP46070;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 2081.
 XX
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR
 XX
 PT Antibodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 1; Page 2880-2881; 3148pp; English.
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 262 AA;
 Query Match 90.2%; Score 534; DB 23; Length 262;
 Best Local Similarity 90.3%; Pred. No. 1, 3e-36;
 Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EIVLTQSLPLVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 DB 150 EIVMTQSLPLVTPGEPASISCRSSQSLHNSGYNYLDFWYLOKPGQSPQLLIYLSNRA 209
 QY 61 SGVDPFRFSGSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGCTKVDIKR 113
 DB 210 SGVDPFRFSGSGTDFTLIRSRVEADGVVYCMQALQTPFTFGCTKVEIKR 262
 RESULT 7
 AAY82617
 ID AAY82617 standard; Protein; 239 AA.
 XX
 AC AAY82617;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.
 XX
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN
 XX
 PD Key Location/Qualifiers
 FT Misc-difference 3 /label= Phe, Leu, Ile, Val
 FT Misc-difference 4 /label= Phe, Leu, His, Arg
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys

KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX Homo sapiens.
XX OS
XX Location/Qualifiers
FH Key
FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 156
FT Misc-difference 156 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 164
FT Misc-difference 164 /label= Phe, Leu
XX JP2000080100-A.
XX 21-MAR-2000.
XX 12-OCT-1998; 98JP-0304793.
XX 17-JUN-1998; 98JP-0188196.
XX 26-JUN-1998; 98JP-0196729.
XX (NISB) JAPAN TOBACCO INC.
XX PA
XX WPI; 2000-286723/25.
XX N-PSDB; AAA13920.
XX A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX Claim 31; Page 33; 88pp; Japanese.
XX The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX Sequence 239 AA;
Query Match 89.0%; Score 527; DB 21; Length 239;
Best Local Similarity 88.5%; Pred. No. 4.6e-36;
Matches 100; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQQLIYSGSHRA 60
DB 21 DIVMTQXPPLSLPVTGPEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQQLIYLSNRA 80
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPTKVDIKR 113
DB 81 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQALQTPFTFGPTKVDIKR 133
RESULT 10
AAW53586
ID AAW53586 standard; Protein; 112 AA.
XX AC AAW53586;
XX AC AAW53586;
XX 23-JUL-1998 (first entry)
XX Light chain of a human antibody.

XX Light chain; human; humanised immunoglobulin; NOK2; Fas ligand;
KW inhibition; apoptosis; Fas expression; treatment; AIDS; rejection;
KW transplant surgery; autoimmune disease; SLE; RA; diabetes.
XX Homo sapiens.
XX OS
XX WO9810070-A1.
XX 12-MAR-1998.
XX 27-AUG-1997; 97WO-JP02983.
XX 20-SEP-1996; 96JP-0271546.
XX 02-SEP-1996; 96JP-0231742.
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX Eda Y, Higuchi H, Maeda H, Nakata M, Okumura K;
XX Ushio Y;
XX WPI; 1998-193620/17.
XX Human immunoglobulin or its active fragment specific for Fas ligand
PT - for treatment of AIDS, organ rejection, autoimmune diseases e.g.
PT systemic lupus erythematosus and diabetes
XX Disclosure; Page 261; 348pp; Japanese.
XX The present sequence represents the light chain of a human antibody, and
CC can be used in the humanised immunoglobulin of the invention. The
CC humanised immunoglobulin reacts specifically with a region of a Fas
CC ligand that is important in inhibiting apoptosis induced by cells with
CC Fas expression. The immunoglobulin of the invention can inhibit
CC physiological reactions between a Fas ligand and Fas, typlified by
CC apoptosis. The humanised immunoglobulin is used for treatment of AIDS,
CC rejection following transplant surgery, autoimmune diseases such as
CC SLE or RA, and diabetes.
XX Sequence 112 AA;
Query Match 88.5%; Score 524; DB 19; Length 112;
Best Local Similarity 87.5%; Pred. No. 3.8e-36;
Matches 98; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQQLIYSGSHRA 60
DB 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQQLIYLSNRA 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPTKVDIKR 112
DB 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQALQTPFTFGPTKLEIKR 112
RESULT 11
AAAY95186
ID AAY95186 standard; Protein; 114 AA.
XX AC AAY95186;
XX 29-AUG-2000 (first entry)
XX Anti-platelet glycoprotein Ib human H1b-5 VL.
XX Variable light chain; single chain antibody; scFv; human; H1b-5;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic.
XX Homo sapiens.
XX OS
XX Key
FH Location/Qualifiers
FT Region 1..23
FT /note= "framework region 1"

```
FT Region 24..39 "complementarity determining region 1"
FT Region 40..54 /note= "framework region 2"
FT Region 55..61 /note= "complementarity determining region 2"
FT Region 62..93 /note= "framework region 3"
FT Region 94..101 /note= "complementarity determining region 3"
FT Region 102..114 /note= "framework region 4"
PN WO200026667-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US25495.
XX 30-OCT-1998; 98US-0106275.
PA (MILL/) MILLER J L.
XX Miller JL;
XX WPI: 2000-365744/31.
XX N-PSDB; AAA27664.
XX Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX Claim 11; Page 77; 89pp; English.
XX The present sequence is that of the light chain variable region
CC (VL) of human single chain antibody (scFv) Hb-5, which is directed
CC against platelet glycoprotein Ib (GPb). The Hb series of scFv
CC was isolated from a human synthetic VH and VL scFv library by 3
CC rounds of phagemid selection against transfected CHO cells
CC expressing the GPb alpha component of the GPb/IX/V complex
CC on their surface, followed by a 4th round of selection against
CC washed human platelets, and 2 final rounds in which attempts were
CC made to displace scFv from washed platelets by flooding with
CC murine monoclonal antibody or mimotope peptide (see AAY95229).
CC Whether displayed as surface proteins on a phagemid or secreted
CC as free scFv by Escherichia coli, the Hb scFv clones are capable
CC of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombi in
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GPb alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.
XX SQ Sequence 114 AA;
Query Match 88.4%; Score 523.5; DB 21; Length 114;
Best Local Similarity 87.7%; Pred. No. 4.2e-36;
Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;
QY 1 EIVLTQSPISLPTVTPGEPASISCRSSQLHNSGYITLDWYLOKQPSQLLIYGSNRA 60
:::|||||
Db 1 DVVMTQSPISLPTVTPGEPASISCRSSQLHNSGYINLWYLOKQPSQLLIYGSNRA 60
:::|||||
QY 61 SGVPDRFSGSGTDTFTLISRVEADGVGYCMQGLQS-PFTFGQTKVDIKR 113
|||||
Db 61 SGVPDRFSGSGTDTFTLISRVEADGVGYCMQALQTPPTFGQTKLEIKR 114
|||||
RESULT 12
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AAY95226
.. ID AAY95226 standard; Protein; 131 AA.
XX AC AAY95226;
XX DT 29-AUG-2000 (first entry)
XX DE Anti-platelet glycoprotein Ib human Hb-5 VL region and linker.
XX KW Variable light chain; single chain antibody; scFv; human; Hb-5;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic.
XX OS Chimeric - Synthetic.
XX OS Chimeric - Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..17
FT Region /note= "vector-derived linker"
FT Region 18..131
FT Region /note= "light chain variable region"
FT Region 18..40
FT Region /note= "framework region 1"
FT Region 41..56
FT Region /note= "complementarity determining region 1"
FT Region 57..71
FT Region /note= "framework region 2"
FT Region 72..78
FT Region /note= "complementarity determining region 2"
FT Region 79..110
FT Region /note= "framework region 3"
FT Region 111..119
FT Region /note= "complementarity determining region 3"
FT Region 120..131
FT Region /note= "framework region 4"
XX WO200026667-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US25495.
XX 30-OCT-1998; 98US-0106275.
XX (MILL/) MILLER J L.
XX Miller JL;
XX WPI: 2000-365744/31.
XX Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX Disclosure; Fig 8; 89pp; English.
XX The present sequence is that of the light chain variable region
CC (VL) plus linker peptide of human single chain antibody (scFv)
CC Hb-5, which is directed against platelet glycoprotein Ib (GPb).
CC Hb-5 is composed of a heavy chain variable region and light chain
CC variable region joined via a vector-derived peptide linker. The
CC Hb series of scFv was isolated from a human synthetic VH and VL
CC scFv library by 3 rounds of phagemid selection against transfected
CC CHO cells expressing the GPb alpha component of the GPb/IX/V
CC complex on their surface, followed by a 4th round of selection
CC against washed human platelets, and 2 final rounds in which
CC attempts were made to displace scFv from washed platelets by
CC flooding with murine monoclonal antibody or mimotope peptide (see
CC AAY95229). Whether displayed as surface proteins on a phagemid or
CC secreted as free scFv by Escherichia coli, the Hb scFv clones are
CC capable of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
```

CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombi in
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GPIb alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.

XX
SQ Sequence 131 AA;

Query Match 88.4%; Score 523.5; DB 21; Length 131;
Best Local Similarity 87.7%; Pred. No. 4.9e-36;
Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 18 DVVMTQSPVLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 77
QY 61 SGVPDRFSGSVSGTDFTLRISVEAEADVGVVYCMQGLQS-PFTFGPGTKVDIKR 113
DB 78 SGVPDRFSGSVSGTDFTLRISVEAEADVGVVYCMQALQTPPTFGGQTKLEIKR 131

RESULT 13
AAR95218
ID AAR95218 standard; protein; 112 AA.
XX AAR95218;
DT 16-DEC-1996 (first entry)
XX Human IgM CM607 variable light chain.
DE
XX
XX Antibody; fusion protein; single chain; inhibition; tumour;
KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
KW immunoassay; Lewis(Y) carbohydrate antigen.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Domain 24..39
FT /label= CDR 1.
FT Domain 55..61
FT /label= CDR 2.
FT Domain 89..97
FT /label= CDR 3.
XX
PN W09613594-A1.
XX
XX
PD 09-MAY-1996.
XX
XX 26-OCT-1995; 95WO-US13811.
XX
XX 28-OCT-1994; 94US-0331398.
XX 28-OCT-1994; 94US-0331396.
XX 28-OCT-1994; 94US-0331397.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;
PI Padlan EA, Pai L, Pastan I, Willingham M;
XX WPI; 1996-251462/25.
XX
XX Single chain fusion proteins and antibodies - useful to diagnose and
PT treat cancer, specifically bind Lewis(Y) related carbohydrate
PT antigen
XX
XX Example 13; Figure 11b; 116pp; English.
PS
XX A novel recombinant DNA molecule which encodes a single chain fusion
CC protein or antibody comprising the Fv region of both the light and
CC heavy chains of an antibody (Ab) fused together, and an effector

CC molecule, where the fusion protein or Ab has the binding specificity
CC of monoclonal Ab (MAB) B1, B3 or B5, can be used for the production
CC of such fusion proteins or antibodies. The fusion proteins can be
CC used in compositions as an immunotoxin to inhibit tumour cell growth.
CC The single chain antibody can be used to detect the presence or
CC absence of cells bearing a Lewis(Y) carbohydrate antigen in a
CC patient. The antibodies are also useful as multiple targeting
CC moieties, providing at least 2 kinds of biological activity. They
CC can also be used in diagnostic assays and for the imaging of tumours
CC when attached to a radiolabel and for the pathological diagnosis of
CC tumours. Humanised antibodies are less immunogenic than the mouse
CC MABs B1, B3 and B5, making them more suitable for long term
CC treatment.

XX
SQ Sequence 112 AA;

Query Match 88.2%; Score 522; DB 17; Length 112;
Best Local Similarity 89.3%; Pred. No. 5.5e-36;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQSPVLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
QY 61 SGVPDRFSGSVSGTDFTLRISVEAEADVGVVYCMQGLQS-PFTFGPGTKVDIKR 112
DB 61 SGVPDRFSGSVSGTDFTLRISVEAEADVGVVYCMQGLQTPQTGQGTKEIKR 112

RESULT 14
AAY82611
ID AAY82611 standard; protein; 239 AA.
XX AAY82611;
XX
DT 02-AUG-2000 (first entry)
XX
XX Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
XX hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
XX Homo sapiens.
XX
PN JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISB) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX N-PSDB; AAA13921.
XX
XX A human monoclonal antibody to parathyroid hormone related protein, -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Claim 31; Page 34-35; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment

CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX
SQ Sequence 239 AA;
Query Match 88.0%; Score 521; DB 21; Length 239;
Best Local Similarity 86.7%; Pred. No. 1.4e-35;
Matches 98; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPVLPVTPGEPATISCRSSQSLHNRNNYLDWFLQKPGQSPQLLIYLSNRA 80
Qy 61 SGVPDRFSGVSGTDFTLRIISRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 81 SGVPDRFSGVSGTDFTLKLSRVEADVGYYCMQALQIPFTFGPGTKVDIKR 133
RESULT 15
AAY82614
ID AAY82614 standard; Protein; 239 AA.
XX
AC AAY82614;
XX
DT 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 2F8-10-3 protein SEQ ID NO:12.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 25 /label= Ile, Thr, Asn, Ser
FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 117 /label= Leu, Ile, Val
FT Misc-difference 146 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 216 /note= "possible Val"
FT
XX JP2000080100-A.
XX
PN
XX
PD 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
PR 26-JUN-1998; 98JP-0196729.
XX
XX (NISR) JAPAN TOBACCO INC.
PA
XX
XX WPI; 2000-286723/25.
DR N-PSDB; AAA13924.
XX
PT A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
PS Claim 31; Page 43; 88pp; Japanese.
XX

CC The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX
SQ Sequence 239 AA;
Query Match 87.8%; Score 520; DB 21; Length 239;
Best Local Similarity 87.6%; Pred. No. 1.8e-35;
Matches 99; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DIVMXQSPVLPVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGQSPQLLIYLSNRA 80
Qy 61 SGVPDRFSGVSGTDFTLRIISRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 81 SGVPDRFSGVSGTDFTLKISRVEADVGYYCMQAXQIPFTFGPGTKVDIKR 133
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:44 ; Search time 17.3846 Seconds
(without alignments)
191.249 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	532	89.9	113	4	US-09-025-769B-15
2	522	88.2	112	1	US-08-331-398A-49
3	522	88.2	112	2	US-08-331-397B-49
4	522	88.2	112	2	US-08-759-804A-49
5	522	88.2	112	4	US-09-227-693-49
6	510	86.1	114	4	US-09-025-769B-29
7	510	86.1	114	4	US-09-025-769B-45
8	510	86.1	281	4	US-09-025-769B-178
9	505	85.3	112	4	US-09-240-274-30
10	502	84.8	113	1	US-08-082-623-4
11	501	84.6	112	1	US-08-478-039-88
12	501	84.6	112	1	US-08-476-349A-88
13	499	84.3	112	1	US-08-053-171-16
14	484.5	81.8	113	1	US-08-264-093-10
15	484	81.8	112	1	US-08-331-398A-50
16	484	81.8	112	2	US-08-331-397B-50
17	484	81.8	112	2	US-08-759-804A-50
18	484	81.8	112	4	US-09-227-693-50
19	483	81.6	116	1	US-08-482-882-66
20	483	81.6	116	2	US-08-483-389-66
21	483	81.6	116	2	US-08-487-113D-66
22	483	81.6	116	2	US-08-473-503-66
23	483	81.6	116	2	US-08-483-932-66
24	483	81.6	116	2	US-08-720-420A-66
25	483	81.6	116	3	US-08-714-017-66
26	483	81.6	116	3	US-08-475-680-66
27	482	81.4	112	1	US-08-053-171-15

28	482	81.4	112	3	US-08-815-190A-14	Sequence 14, Appl
29	475	80.2	131	4	US-09-000-088-2	Sequence 2, Appli
30	475	80.2	131	1	US-08-129-930B-95	Sequence 95, Appl
31	475	80.2	131	4	US-08-134-346A-50	Sequence 50, Appl
32	475	80.2	131	4	US-08-976-288A-95	Sequence 95, Appl
33	474	80.1	108	1	US-08-488-113B-151	Sequence 151, App
34	474	80.1	108	1	US-08-477-484B-151	Sequence 151, App
35	474	80.1	108	1	US-08-107-669D-15	Sequence 15, Appl
36	474	80.1	108	2	US-08-472-788A-15	Sequence 15, Appl
37	474	80.1	108	2	US-08-477-531B-15	Sequence 15, Appl
38	474	80.1	108	2	US-08-646-360-151	Sequence 151, App
39	474	80.1	108	2	US-08-082-842A-15	Sequence 15, Appl
40	474	80.1	108	4	US-08-839-765-151	Sequence 151, App
41	474	80.1	108	4	US-09-136-389-151	Sequence 151, App
42	474	80.1	108	4	US-09-610-838-151	Sequence 151, App
43	473	79.9	112	1	US-08-478-039-89	Sequence 89, Appl
44	473	79.9	112	1	US-08-476-349A-89	Sequence 89, Appl
45	459	77.5	125	1	US-08-331-398A-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-15
; Sequence 15, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-15

Query Match 89.9%; Score 532; DB 4; Length 113;
Best Local Similarity 88.5%; Pred. No. 4.9e-43;
Matches 100; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy	1	EYVLTQSP	LSLVPTG	PEPASTIS	CRSSQS	LLHSGNY	YVLDWY	LQKPG	QSPQLLI	YSGSHRA	60
		:	:	:	:	:	:	:	:	:	
Db	1	DIWVTQSP	LSLVPTG	PEPASTIS	CRSSQS	LLHSGNY	YVLDWY	LQKPG	QSPQLLI	YLSGNRA	60
		:	:	:	:	:	:	:	:	:	
Qy	61	SGVPDR	FGSGV	SGTDF	TLIRSR	VAEDV	GVVYCM	QGLSP	FTFG	PKVDIKR	113
		:	:	:	:	:	:	:	:	:	
Db	61	SGVPDR	FGSGSG	TDFTLK	IRSRVA	EDVGVVY	CMALQ	PTPTFG	QGTGLEIKR	113	

Query Match 88.2%; Score 522; DB 1; Length 112;
Best Local Similarity 89.3%; Pred. No. 4.2e-42;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

	61	SGVPDPSGVSCTDFTLRISVEAEDGVVYCMQGLQPSTFEGPGTKVDIK	112
Qy		: :	
	61	SGVPDPSGGSCGTDLTISRVEADPVGYCYMQLPOTFGOGTVKEIK	112
Pb		: :	

Query Match 88.2%; Score 522; DB 2; Length 112;
Best Local Similarity 89.3%; Pred. NO. 4.2e-42;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0

QY 61 SGVPDRFSGVSGTDFTLRISRVEAEDG VYYCMQGLQSPTFGPGTKVDIK 112
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
pb 61 SGVPDRFSGSGSDTFLKISRVEAEDG VYYCMOGLTPOTFGGTKEIK 112
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||


```

; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-29

Query Match 86.1%; Score 510; DB 4; Length 114;
Best Local Similarity 86.7%; Pred. No. 5.6e-41;
Matches 98; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSLPVTGPGEASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSLPVTGPGEASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLSNRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPCTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYCCQHQHYTPTTFGGQTKVEIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
US-09-025-769B-45
; Sequence 45, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York

```

```

; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-45

Query Match 86.1%; Score 510; DB 4; Length 114;
Best Local Similarity 86.7%; Pred. No. 5.6e-41;
Matches 98; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSLPVTGPGEASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSLPVTGPGEASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLSNRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPCTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYCCQHQHYTPTTFGGQTKVEIKR 113
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RESULT 8
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-178

Query Match      86.1%; Score 510; DB 4; Length 281;
Best Local Similarity 86.7%; Pred. No. 1.5e-40;
Matches 98; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLRKPGSQPLLIIYSGSHRA 60
DB 166 DIVMTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLRKPGSQPLLIIYSGNRA 225

QY 61 SGVDPFRSGSVSGTDTFLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 226 SGVDPFRSGSVSGTDTFLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 278

RESULT 9
US-09-240-274-30
; Sequence 30, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match      85.3%; Score 505; DB 4; Length 112;
Best Local Similarity 87.3%; Pred. No. 1.6e-40;
Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLRKPGSQPLLIIYSGSHRASGV 63
DB 3 LTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLRKPGSQPLLIIYSGSHRASGV 62

QY 64 PDRFSGSVSGTDTFLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 63 PDRFSGSVSGTDTFLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 112

RESULT 10
US-08-082-623-4
; Sequence 4, Application US/08082623
; Patent No. 5750106
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO

```

```

; TITLE OF INVENTION: CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,623
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,228
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-055-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..113
; OTHER INFORMATION: /note= "The peptide sequence of the
; OTHER INFORMATION: V-1 region of SD2 MSL 109"
US-08-082-623-4

Query Match      84.8%; Score 502; DB 1; Length 113;
Best Local Similarity 85.0%; Pred. No. 3.1e-40;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

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DB 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLRKPGSQPLLIIYSGNRA 60

QY 61 SGVDPFRSGSVSGTDTFLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVDPFRSGSVSGTDTFLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 11
US-08-478-039-88
; Sequence 88, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

```


RESULT 14
US-08-264-093-10
; Sequence 10, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: NO. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:

CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
ATTN: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331.398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Humanized B3 Variable Light
; OTHER INFORMATION: chain (V-L) (Humb3V-L)"
US-08-331-398A-50

Query Match      81.8%; Score 484; DB 1; Length 112;
Best Local Similarity 81.2%; Pred. No. 1.5e-38;
Matches 91; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHSHNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
   :::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DVLMTQSPVLPVTPGEPASISCRSSQIIIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNR 60
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 SGVPDRFSGSVSGTDTLTIRISRVEAEDGVVYVCMQGLQSPFTFGPGTKVDIK 112
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYVCFQGSHPVPTFGGQTKVEIK 112
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Job time : 18.3846 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:09 ; Search time 16.0808 Seconds
(without alignments)
323.890 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
Sequence: 1 EIVLTQSPVTPGPEPAS.....MQGLQSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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4	513	86.7	239	9	US-09-924-340-8
5	513	86.7	239	9	US-09-922-600A-8
6	510	86.1	113	12	US-10-025-687-9
7	505	85.3	112	9	US-09-848-798-30
8	492	83.1	112	10	US-09-850-165-96
9	483	81.6	116	10	US-09-753-436-66
10	481	81.2	157	10	US-09-864-761-48255
11	480	81.1	100	9	US-10-194-975-79
12	480	81.1	100	9	US-10-194-975-80
13	480	81.1	100	10	US-09-822-698A-19
14	480	81.1	100	12	US-10-025-687-24
15	480	81.1	138	10	US-09-748-960-8
16	476.5	80.5	113	10	US-09-840-459-65
17	475.5	80.3	113	10	US-09-840-459-64
18	474	80.1	222	9	US-09-479-614-26
19	474	80.1	242	9	US-09-479-614-20

20	464	78.4	112	10	US-09-850-165-97
21	462.5	78.1	113	10	US-09-840-459-68
22	455	76.9	239	9	US-10-124-905-6
23	455	76.9	239	9	US-09-948-429B-6
24	448	75.7	149	10	US-09-990-205-2
25	447	75.5	111	10	US-09-835-087-2
26	447	75.5	111	10	US-09-809-739-13
27	447	75.5	111	10	US-09-840-459-59
28	446	75.3	140	9	US-09-341-894-4
29	444	75.0	132	12	US-10-006-773-15
30	441	74.5	111	10	US-09-840-459-11
31	440	74.3	112	10	US-09-840-459-55
32	440	74.3	112	10	US-09-840-459-60
33	439	74.2	112	10	US-09-840-459-56
34	438	74.0	112	10	US-09-840-459-58
35	437	73.8	112	10	US-09-840-459-70
36	436.5	73.7	228	9	US-09-909-567B-50
37	436	73.6	112	10	US-09-840-459-62
38	436	73.6	112	10	US-09-840-459-66
39	436	73.6	298	10	US-09-883-758-2
40	435.5	73.6	110	10	US-09-864-761-48276
41	435	73.5	112	10	US-09-840-459-69
42	435	73.5	135	10	US-09-925-301-1527
43	434	73.3	113	10	US-09-971-543-4
44	434	73.3	253	10	US-09-971-543-2
45	433	73.1	114	10	US-09-217-268B-27

ALIGNMENTS

RESULT 1
US-09-822-698A-1
; Sequence 1, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of PH1 Fab antibody
US-09-822-698A-1

Query Match	100.0%;	Score 592;	DB 10;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 1.4e-37;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EIVLTQSPVTPGPEPASISCRSSQLHNSGYTYLDWYLOKPGQSPQLLIYSGSRA 60		
Db	1	EIVLTQSPVTPGPEPASISCRSSQLHNSGYTYLDWYLOKPGQSPQLLIYSGSRA 60		
QY	61	SGVPDRFSGVSGTDFLTRISRYEAEADVGYVYCMQGLQSPFTFGPTKVDIKR 113		
Db	61	SGVPDRFSGVSGTDFLTRISRYEAEADVGYVYCMQGLQSPFTFGPTKVDIKR 113		
RESULT 2				
US-09-822-698A-24				
; Sequence 24, Application US/09822698A				
; Patent No. US20020146750A1				
; GENERAL INFORMATION:				


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Matches 98; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
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[illegible]

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RESULT 6
US-10-025-687-9
; Sequence 9, Application US/10025687
; Patent No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody light chain variable region
US-10-025-687-9

```

Query Match	86.1%;	Score 510;	DB 12;	Length 113;
Best Local Similarity	86.7%;	Pred. No. 1.7e-31;		
Matches 98;	Conservative 6;	Mismatches 9;	Indels 0;	Gaps 0;

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1  EIVLTQSPLESLPVPTGPASISCRSSQSLHLSNGITYYLDWYLOKPGQSPQLLIYSGSHRA 60
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1  DIVMTQSPLESLPVPTGPASISCRSSQSLHLSNGYNYLDWYLOKPGQSPQLLIYLSGNRA 60

61  SGVPRDSGSGVSGDFTLRISREAEDGVYVYCMQGLQSPFTFGSGTKVDIKR 113
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
61  SGVPRDSGSGSGDFTLTKISREAEDGVYVYCCQHVTPTPTFGGKTVEIKR 113
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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```

RESULT 7
US-09-848-798-30
; Sequence 30, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-848-798-30

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Query Match	85.3%	Score 505;	DB 9;	Length 112;
Best Local Similarity	87.3%;	Pred. No. 3.9e-31;		
Matches	96; Conservative	7; Mismatches	7; Indels	0; Gaps 0;

QY	4	LTQSPSLPVTGPEPASTICRSQSLLHNSGYTYLDWYLPKGQSPQLLIYSGSHRASGV	63
Db	3	LTQSPSLPVTGPEPASTICRSQSLLHSSGFNFDWYLPKGQSPQLLIYMGSNRASGV	62
QY	64	PDRFGSGVSGTDFTLRISRVRAEDGVYCYCMQGLQSPFTFGPGTKVDIKR	113
Db	63	PDRFGSGSGTDFTLTKINRVRAEDGVYCYCMQALQFPLTFGGGTKVEIKR	112

RESULT 8
US-09-850-165-96
; Sequence 96, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIORITY APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIORITY APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIORITY APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIORITY APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIORITY APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIORITY APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1

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: LENGTH: 112
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: MOD_RES
: LOCATION: (44)
: OTHER INFORMATION: Arg or Lys
: FEATURE:
: NAME/KEY: MOD_RES
: LOCATION: (103)
: OTHER INFORMATION: Val, Leu or Asn
: FEATURE:
: NAME/KEY: MOD_RES
: LOCATION: (112)
: OTHER INFORMATION: Arg or Lys
: US-09-850-165-96

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Query Match 83.1%; Score 492; DB 10; Length 112;
Best Local Similarity 84.7%; Pred. No. 3.5e-30;
Matches 94; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSLPVTGPCEPASISCRSSQSLHSHNGVITYLDWYLKPGSQPOLLIYSGSHRA 60
 ::::||||| | ||||| ::||| |::: ||| |::| |::| |::| |::| |::| |::| |::|
Dd 1 DIVMTQSPISLPVTGPCEPASISCRSSQSLVHSNNTYLNMYLQXPGGSQPOLLIIYKVSNRF 60

Qy	61	SGVPDRFSGSVGDTFLRISRVEADGVYYCMQGLSPFTFGPGTKVDI	111
		: : : : : :	
Db	61	SGVPDRFSGSGTDTLKRISRVEADGVYYCMQALSPYTFGGGTKEI	111

RESULT 9
US-09-753-436-66
; Sequence 66, Application US/09753436
; Patent No. US2001029293A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay

```

: TITLE OF INVENTION: ICAM-Related Materials and Methods
: NUMBER OF SEQUENCES: 120
: CORRESPONDENCE ADDRESSES:
: ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/753,436
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/382,289
: FILING DATE:
: APPLICATION NUMBER: US 08/487,113
: FILING DATE: 07-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/286,754
: FILING DATE: 05-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/102,852
: FILING DATE: 05-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/009,266
: FILING DATE: 22-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/894,061
: FILING DATE: 05-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/889,724
: FILING DATE: 26-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/827,689
: FILING DATE: 27-JAN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams, Joseph A., Jr.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 33282
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 66:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 116 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: DS-09-753-436-66

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Query Match      81.6%; Score 483; DB 10; Length 116;
Best Local Similarity 83.0%; Pred. No. 1.7e-29;
Matches 93; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
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QY    1 EIVLTQSPLSLPVTGCEPASISCRSSQSLHSHNCYTYYLDWYLKPGQSPOLLIIYSGSHPA 60
       :|:||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     5 DIVMTQSPLSLPVTGCEPASISCRSSQSLVHSNGDTYLLHWYLKPGQSPOLLIIYKVSNRF 64

QY    61 SGVPDRFGSSVSGTDFTLIRSRVAEDGVVYICMQGLSQSFPTGPGTKVDIK 112
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     65 SGVPDRFGSGSGTDFTLIRSRVAEDGVVYICSQSTHVPTFGQGTKVEIK 116
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RESULT 10
US-09-864-761-48255
Sequence 48255, Application US/09864761
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; Patent No. US20020048763A1
;
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
;
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
;
; FILE REFERENCE: Aecomica-x-1
;
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
;
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
;
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
;
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
;
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
;
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
;
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
;
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
;
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
;
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
;
; NUMBER OF SEQ ID NOS: 49117
;
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48255
; LENGTH: 157
; TYPE: prt
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; OTHER INFORMATION: MAP TO AP001224.1
;
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 18
;
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 14
;
; OTHER INFORMATION: SWISSPROT HIT: P06309, EVALU8 8.00e-55
;
; OTHER INFORMATION: EST_HUMAN HIT: AW406883.1, EVALU8 3.00e-54
;
; SW-09-864-761-48255

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	Query Match	81.2%	Score 481;	DB 10;	Length 157;
	Best Local Similarity	90.2%;	Pred. No.	3.le-29;	
Matches	92;	Conservative	5;	Mismatches	Indels 0; Gaps 0;
Qy	1	EIVTQSPLSLPVTPGEPASISCRSSQLLSHNGVYILDWYLKPKCSPQLLIYSGSURA	60	:	: :
Dd	4	DIVMTQSPLSLPVTPGEPASISCRSSQLLSHNGVNYLDWYLKPKCSPQLLIYLSNRRA	63	:	: :
Qy	61	SGVPDRFSGSVSGTDFTLRIRVEAEADVGVYYCMOGLQSPPT	102	:	: :
Dd	64	SGVPDRFSGSVSGTDFTLTKRVEAEADVGVYYCMALQTPTT	105	:	: :

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RESULT 11
US-10-194-975-79
; Sequence 79, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-79

Query Match      81.1%; Score 480; DB 9; Length 100;
Best Local Similarity 91.0%; Pred. No. 2.5e-29;
Matches 91; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60
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Db 1 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMQGLQSP 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 SGVPDRFSGSGGTDTFLKISRVEAEDGVYYCMQALQTP 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 12
US-10-194-975-80
; Sequence 80, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-80

Query Match      81.1%; Score 480; DB 9; Length 100;
Best Local Similarity 91.0%; Pred. No. 2.5e-29;
Matches 91; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60
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Db 1 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMQGLQSP 100
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Db 61 SGVPDRFSGSGGTDTFLKISRVEAEDGVYYCMQALQTP 100
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RESULT 13
US-09-822-698A-19
; Sequence 19, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-698A-19

Query Match      81.1%; Score 480; DB 10; Length 100;
Best Local Similarity 91.0%; Pred. No. 2.5e-29;
Matches 91; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMQGLQSP 100
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Db 61 SGVPDRFSGSGGTDTFLKISRVEAEDGVYYCMQALQTP 100
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RESULT 14
US-10-025-687-24
; Sequence 24, Application US/10025687
; Patent No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-687-24

Query Match      81.1%; Score 480; DB 12; Length 100;
Best Local Similarity 91.0%; Pred. No. 2.5e-29;
Matches 91; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMQGLQSP 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 SGVPDRFSGSGGTDTFLKISRVEAEDGVYYCMQALQTP 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

US-09-822-698A-19
; Sequence 8, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Allison, David Edward
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855.2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
```

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; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Portion of the light chain of LDP-02 with a light
; OTHER INFORMATION: chain signal peptide
; NAME/KEY: SITE
; LOCATION: (20)...(21)
; OTHER INFORMATION: signal peptide cleavage site
US-09-748-960-8

Query Match      81.1%; Score 480; DB 10; Length 138;
Best Local Similarity 81.4%; Pred. NO. 3.3e-29;
Matches 92; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60
DB 21 DVVMTQSPVLPVTPGEPASISCRSSQSLAKSYGNTYLSWYLOKPGQSPQLLIYGISNRF 80
QY 61 SGVPDRFGSGSGTDFTLRISRVEADGVYVCMQGLQSPFTFGPGTKVDIKR 113
DB 81 SGVPDRFGSGSGTDFTLRISRVEADGVYVCMQGLQSPFTFGPGTKVDIKR 133

```

Search completed: March 13, 2003, 15:30:30
Job time : 17.0808 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:14:49 ; Search time 240.777 Seconds
(without alignments)
302.582 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 592

Sequence: 1 EIVLTQSPSLPVTPGPAS.....MQGLQSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
- 17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
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- 19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	100.0	113	19	US-09-538-913-1
2	592	100.0	113	22	US-09-822-698A-1
3	592	100.0	220	22	US-09-822-698A-24
4	592	100.0	381	19	US-09-538-913-5
5	592	100.0	381	22	US-09-822-698A-5
6	540	91.2	114	21	US-09-791-537-86326

7	534	90.2	262	1	PCT-US01-19110-2081	Sequence 2081, Ap
8	534	90.2	262	22	US-09-880-748-2081	Sequence 2081, Ap
9	533	90.0	136	21	US-09-791-537-71827	Sequence 71827, A
10	533	90.0	137	21	US-09-791-537-56427	Sequence 56427, A
11	532	89.9	113	18	US-09-490-070-15	Sequence 15, Appl
12	531	89.7	114	21	US-09-791-537-86001	Sequence 86001, A
13	529	89.4	116	21	US-09-791-537-43479	Sequence 43479, A
14	529	89.4	117	21	US-09-791-537-48291	Sequence 48291, A
15	529	89.4	118	21	US-09-791-537-129360	Sequence 129360, A
16	529	89.4	135	21	US-09-791-537-12279	Sequence 12279, A
17	529	89.4	135	21	US-09-791-537-123428	Sequence 123428, A
18	528	89.2	112	21	US-09-791-537-21285	Sequence 21285, A
19	527	89.0	114	21	US-09-791-537-137519	Sequence 137519, A
20	527	89.0	117	21	US-09-791-537-107503	Sequence 107503, A
21	526	88.9	113	21	US-09-791-537-59499	Sequence 59499, A
22	524	88.5	112	11	US-08-700-737-8	Sequence 8, Appl
23	524	88.5	112	16	US-09-254-1808-9	Sequence 9, Appl
24	524	88.5	125	24	US-10-010-9428-6	Sequence 6, Appl
25	524	88.5	132	21	US-09-791-537-78289	Sequence 78289, A
26	523.5	88.4	114	18	US-09-430-048-19	Sequence 19, Appl
27	523.5	88.4	131	18	US-09-430-048-25	Sequence 25, Appl
28	523	88.3	118	21	US-09-791-537-54839	Sequence 54839, A
29	522	88.2	112	7	US-08-331-396-49	Sequence 49, Appl
30	522	88.2	112	7	US-08-331-396A-49	Sequence 49, Appl
31	522	88.2	112	7	US-08-331-396C-49	Sequence 49, Appl
32	522	88.2	112	7	US-08-331-396D-49	Sequence 49, Appl
33	522	88.2	112	7	US-08-331-397-49	Sequence 49, Appl
34	522	88.2	112	7	US-08-331-398-49	Sequence 49, Appl
35	522	88.2	112	11	US-08-759-804-49	Sequence 49, Appl
36	522	88.2	112	21	US-09-791-537-21281	Sequence 21281, A
37	522	88.2	112	21	US-09-791-537-110202	Sequence 110202, A
38	522	88.2	125	21	US-09-791-537-26052	Sequence 26052, A
39	521	88.0	112	21	US-09-791-537-34978	Sequence 34978, A
40	521	88.0	113	21	US-09-791-537-64225	Sequence 64225, A
41	520.5	87.9	113	21	US-09-791-537-137518	Sequence 137518, A
42	520	87.8	112	21	US-09-791-537-110195	Sequence 110195, A
43	518.5	87.6	112	18	US-09-430-048-20	Sequence 20, Appl
44	517.5	87.4	248	19	US-09-517-225E-6	Sequence 6, Appl
45	516	87.2	113	21	US-09-791-537-106796	Sequence 106796, A

ALIGNMENTS

RESULT 1
US-09-538-913-1
; Sequence 1, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hooqenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-1

Query Match	100.0%;	Score 592;	DB 19;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 1e-49;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
..Qy	1	EIVLTQSPSLPVTPGPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLISGSHRA	60	
Db	1	EIVLTQSPSLPVTPGPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLISGSHRA	60	
Qy	61	SGVPDRFSGVSGTDFTLRLISRVAEADVGYVMQGLQSPFTFGPTKVDIKR	113	

Db 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 2

US-09-822-698A-1
; Sequence 1, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of PH1 Fab antibody
US-09-822-698A-1

Query Match 100.0%; Score 592; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA 60

Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA 60

QY 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113

Db 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 3

US-09-822-698A-24
; Sequence 24, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1
US-09-822-698A-24

Query Match 100.0%; Score 592; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA 60

Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA 60

QY 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113

Db 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 4

US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for bivPH1-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match 100.0%; Score 592; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.3e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA 60

Db 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA 186

QY 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113

Db 187 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 239

RESULT 5

US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPH1-IL-2
US-09-822-698A-5

Query Match 100.0%; Score 592; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.3e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA 60

Db 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA 186

QY 61 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113

Db 187 SGVDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 239

RESULT 6

US-09-791-537-56427
; Sequence 56427, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56427
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-56427

Query Match 90.0%; Score 533; DB 21; Length 137;
Best Local Similarity 89.4%; Pred. No. 7.8e-44;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLQKPGSPQLLIYSGSRA 60
Db 21 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLQKPGSPQLLIYSGSRA 80
QY 61 SGVDPFRFSGVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113
Db 81 SGVDPFRFSGVSGTDFTLRISRVEAEDGVYYCMQALQTPFTFGGQTKVEIKR 133

RESULT 11
US-09-490-070-15
; Sequence 15, Application US/09490070
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/025,769
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-070-15

Query Match 89.9%; Score 532; DB 18; Length 113;
Best Local Similarity 88.5%; Pred. No. 7.8e-44;
Matches 100; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLQKPGSPQLLIYSGSRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLQKPGSPQLLIYSGSRA 60
QY 61 SGVDPFRFSGVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVDPFRFSGVSGTDFTLRISRVEAEDGVYYCMQALQTPFTFGGQTKVEIKR 113

RESULT 12
US-09-791-537-86001
; Sequence 86001, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86001
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-86001

Query Match 89.7%; Score 531; DB 21; Length 114;
Best Local Similarity 89.4%; Pred. No. 9.9e-44;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLQKPGSPQLLIYSGSRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLQKPGSPQLLIYSGSRA 60
QY 61 SGVDPFRFSGVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVDPFRFSGVSGTDFTLRISRVEAEDGVYYCMQALQTPFTFGGQTKVEIKR 113

RESULT 13
US-09-791-537-43479
; Sequence 43479, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43479
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-43479

Query Match 89.4%; Score 529; DB 21; Length 116;

Best Local Similarity 89.4%; Pred. No. 1.6e-43;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSHNGVYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 4 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGVYTLDWYLQKPGQSPQLLIYLSNRA 63
QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDGVYYCMQGLQSPFTFGPTGKVDIKR 113
Db 64 SGVPDRFSGSVSGTDFTLKISRVEAEDGVYYCMQALQTPQTFGQGTKEIKR 116

RESULT 14

US-09-791-537-48291
; Sequence 48291, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48291
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-48291

Query Match 89.4%; Score 529; DB 21; Length 117;
Best Local Similarity 89.4%; Pred. No. 1.6e-43;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSHNGVYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGVYTLDWYLQKPGQSPQLLIYLSNRA 64
QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDGVYYCMQGLQSPFTFGPTGKVDIKR 113
Db 65 SGVPDRFSGSVSGTDFTLKISRVEAEDGVYYCMQALQTPQTFGQGTKEIKR 117

RESULT 15

US-09-791-537-129360
; Sequence 129360, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 129360
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-129360

Query Match 89.4%; Score 529; DB 21; Length 118;
Best Local Similarity 89.4%; Pred. No. 1.6e-43;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHSHNGVYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGVYTLDWYLQKPGQSPQLLIYLSNRA 60

QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDGVYYCMQGLQSPFTFGPTGKVDIKR 113
Db 61 SGVPDRFSGSVSGTDFTLKISRVEAEDGVYYCMQALQTPQTFGQGTKEIKR 113
Search completed: March 13, 2003, 15:28:02
Job time : 242.027 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:15:24 ; Search time 41.2885 seconds
(without alignments)
355.800 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 532

Sequence: 1 EIVLTQSLPLVPTGEPAS.....MQGLSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New.*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	592	100.0	131	1	PCT-US02-34249-2
2	592	100.0	131	1	PCT-US02-34249A-2
3	592	100.0	131	6	US-10-279-833-2
4	534	90.2	113	1	PCT-US03-05128-80
5	534	90.2	262	1	PCT-US02-36496-2081
6	534	90.2	262	6	PCT-US02-3418-2081
7	532	89.9	113	5	US-09-490-153-15
8	531	89.7	112	1	PCT-US02-32613-30
9	531	89.7	112	6	US-10-269-805-30
10	526	88.9	112	1	PCT-US02-32613-18
11	526	88.9	112	1	PCT-US02-32613-26
12	526	88.9	112	1	PCT-US02-38550-33
13	526	88.9	112	6	US-10-269-805-18
14	526	88.9	112	6	US-10-269-805-26
15	526	88.9	112	6	US-10-309-762-33
16	524	88.5	112	5	US-09-234-180C-9
17	522	88.2	112	1	PCT-US02-32613-2
18	522	88.2	112	6	US-10-269-805-2
19	521	88.0	112	1	PCT-US02-38550-32
20	521	88.0	112	6	US-10-309-762-32
21	520	87.8	112	1	PCT-US02-32613-28
22	520	87.8	112	6	US-10-269-805-28
23	519	87.7	112	1	PCT-US02-32613-20
24	519	87.7	112	6	US-10-269-805-20
25	517.5	87.4	222	6	US-10-184-508A-6
26	517.5	87.4	222	6	US-10-186-186-6

27	517.5	87.4	222	6	US-10-186-186A-6	Sequence 6, Appli
28	517	87.3	112	1	PCT-US02-32613-44	Sequence 44, Appl
29	517	87.3	112	6	US-10-269-805-44	Sequence 44, Appl
30	515	87.0	219	1	PCT-US02-33556-104	Sequence 104, Appl
31	513	86.7	239	5	US-09-392-095B-8	Sequence 8, Appli
32	513	86.7	239	6	US-10-154-678-8	Sequence 8, Appli
33	512	86.5	112	1	PCT-US02-32613-12	Sequence 12, Appl
34	512	86.5	112	6	US-10-269-805-12	Sequence 12, Appl
35	510	86.1	114	5	US-09-490-153-29	Sequence 29, Appl
36	510	86.1	114	5	US-09-490-153-45	Sequence 45, Appl
37	510	86.1	281	5	US-09-490-153-178	Sequence 178, App
38	508	85.8	110	1	PCT-US02-38550-157	Sequence 157, App
39	508	85.8	110	1	PCT-US02-38550-165	Sequence 165, App
40	508	85.8	110	6	US-10-309-762-157	Sequence 157, App
41	508	85.8	110	6	US-10-309-762-165	Sequence 165, App
42	507	85.6	112	1	PCT-US02-38550-34	Sequence 34, Appl
43	507	85.6	112	5	US-09-936-964A-59	Sequence 59, Appl
44	507	85.6	112	6	US-10-309-762-34	Sequence 34, Appl
45	506	85.5	114	1	PCT-US03-00398-322	Sequence 322, App

ALIGNMENTS

RESULT 1
PCT-US02-34249-2
; Sequence 2, Application PC/TUS0234249
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; FILE REFERENCE: 10280-027W01
; CURRENT APPLICATION NUMBER: PCT/US02/34249
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34249-2

Query Match	100.0%;	Score 592;	DB 1;	Length 131;
Best Local Similarity	100.0%;	Pred. No. 2.9e+44;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA	60	
Db	6	EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA	65	
QY	61	SGVPRFSGSVSGTDTLIRSRVEAEDGVYYCMQGLQSPFTFGPTKVDIKR	113	
Db	66	SGVPRFSGSVSGTDTLIRSRVEAEDGVYYCMQGLQSPFTFGPTKVDIKR	118	

RESULT 2
PCT-US02-34249A-2
; Sequence 2, Application PC/TUS0234249A
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; FILE REFERENCE: 10280-027W01
; CURRENT APPLICATION NUMBER: PCT/US02/34249A
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131

```
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34249A-2

Query Match      100.0%; Score 592; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.9e-44;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 6 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 65

QY 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 66 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 118

RESULT 3
US-10-279-633-2
; Sequence 2, Application US/10279633
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Somers, Veerle
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; TITLE OF INVENTION: VARIATION
; FILE REFERENCE: 10280-027001
; CURRENT APPLICATION NUMBER: US/10/279,633
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-633-2

Query Match      100.0%; Score 592; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.9e-44;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 6 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 65

QY 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 66 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 118

RESULT 4
PCT-US03-05128-80
; Sequence 80, Application PC/TUS0305128
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation, et al
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034W01
; CURRENT APPLICATION NUMBER: PCT/US03/05128
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-05128-80

Query Match      90.2%; Score 534; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 2.8e-39;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
QY 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 5
PCT-US02-36496-2081
; Sequence 2081, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-2081

Query Match      90.2%; Score 534; DB 1; Length 262;
Best Local Similarity 90.3%; Pred. No. 6.1e-39;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 150 EIVLTQSPVSLPVTGPGEPAISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYLSNRA 209

QY 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
Db 210 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 262

RESULT 6
US-10-293-418-2081
; Sequence 2081, Application US/10293418
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
```


Query Match 88.9%; Score 526; DB 1; Length 112;
Best Local Similarity 89.3%; Pred. NO. 1.4e-38;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Query Match 88.9%; Score 526; DB 1; Length 112;
Best Local Similarity 89.3%; Pred. NO. 1.4e-38;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-269-805-18

```

```
Query Match      88.9%; Score 526; DB 6; Length 112;
Best Local Similarity 89.3%; Pred. No. 1.4e-38;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0
```

RESULT 14
US-10-269-805-26
; Sequence 26, Application US/10269805
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

```

RESULT 14
US-10-269-805-26
; Sequence 26, Application US/10269805
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatenIn version 3.1
; SEQ ID NO 26
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-26

```

Search completed: March 13, 2003, 15:29:44
Job time : 42.2885 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:09 ; Search time 19.5577 Seconds
(without alignments)
555.443 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
Sequence: 1 EIVLTQSPVLPVTPGEPAS.....MQGLQSPFTFGPCTKVDIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	90.0	136	2 S40357	Ig kappa chain V-J
2	529	89.4	135	2 S40342	Ig kappa chain - h
3	528	89.2	112	2 S58207	Ig light chain V r
4	527	89.0	117	1 K2HUGM	Ig kappa chain pre
5	524	88.5	132	2 S26882	Ig kappa chain V r
6	522	88.2	112	2 S58206	Ig light chain V r
7	522	88.2	125	2 S40356	Ig kappa chain - h
8	507.5	85.7	126	2 S40339	Ig kappa chain - h
9	505	85.3	121	2 S40371	Ig kappa chain - h
10	500	84.5	113	1 K2HUTW	Ig kappa chain V-I
11	494	83.4	131	2 S40372	Ig kappa chain V-I
12	484	81.8	124	2 S03876	Ig kappa chain V-I
13	478.5	80.8	112	1 K2H0WL	Ig kappa chain V-I
14	478	80.7	123	2 S40319	Ig kappa chain V r
15	473.5	80.0	130	2 S40321	Ig kappa chain - h
16	467.5	79.0	115	1 K2HUCM	Ig kappa chain - h
17	467	78.9	100	2 S24681	Ig kappa chain V-I
18	457	77.2	113	2 PL0203	Ig kappa chain - h
19	457	77.2	114	2 S40375	anti-DNA autoantib
20	455	76.9	113	1 K2H0FR	Ig kappa chain - h
21	452.5	76.4	114	2 S40340	Ig kappa chain V-I
22	449	75.8	131	2 B39276	Ig kappa chain V-J
23	447	75.5	142	2 S22902	Ig light chain pre
24	447	75.5	219	2 S52028	Ig kappa chain V r
25	446	75.3	133	2 S23230	Ig kappa chain - m
26	445.5	75.3	127	2 S40323	Ig kappa chain - h
27	445	75.2	114	2 A32967	Ig kappa chain V-I
28	445	75.2	133	2 S40324	Ig kappa chain V r
29	444	75.0	112	2 A31807	Ig kappa chain V r

30 444 75.0 131 2 B30577 Ig kappa chain pre
31 444 75.0 133 1 K2HURP Ig kappa chain pre
32 444 75.0 219 2 PC4203 Ig kappa chain (mo
33 443 74.8 112 2 I26317 Ig kappa chain V r
34 443 74.8 118 2 PT0359 Ig kappa chain V r
35 443 74.8 197 2 S29593 Ig kappa chain (WM
36 442.5 74.7 126 2 S40341 Ig kappa chain - h
37 442 74.7 112 2 G26317 Ig kappa chain V r
38 442 74.7 112 2 S38719 Ig kappa chain V r
39 442 74.7 115 2 S38715 Ig kappa chain V r
40 442 74.7 122 2 S40338 Ig kappa chain - h
41 441 74.5 112 2 A26317 Ig kappa chain V r
42 441 74.5 112 2 F27887 Ig kappa chain V r
43 441 74.5 112 2 F26317 Ig kappa chain V r
44 441 74.5 113 2 B41940 Ig light chain V r
45 441 74.5 126 2 S40312 Ig kappa chain - h

ALIGNMENTS

RESULT 1

S40357

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40357

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40357

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-136 <KLE>

A:Cross-references: EMBL:X72467

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 533; DB 2; Length 136;
Best Local Similarity 89.4%; Pred. No. 6.7e-42;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYLDWYLOKPGQSPQLIYSSGSHRA 60

Db 21 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYLDWYLOKPGQSPQLIYLGSNRA 80

QY 61 SGVPDRFSGSVSGTDFTLRLSRVEADGVYCYCMOGLQSPFTFGPCTKVDIKR 113

Db 81 SGVPDRFSGSVSGTDFTLRLSRVEADGVYCYCMOGLQSPFTFGPCTKVDIKR 133

RESULT 2

S40342

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40342

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40342

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-135 <KLE>

A:Cross-references: EMBL:X72452; NID:g441372; PID:g441373

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 529; DB 2; Length 135;

```
Best Local Similarity 89.4%; Pred. No. 1.5e-41;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 14 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLSNRA 73
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYVCMQGLQSPFTFGPGTKVDIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQTPRTFGGQTKVEIKR 126
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
S58207
Ig kappa chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C:Accession: S58207
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206
A:Accession: S58207
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 528; DB 2; Length 112;
Best Local Similarity 89.3%; Pred. No. 1.6e-41;
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYVCMQGLQSPFTFGPGTKVDIK 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQTPWTFGGQTKVEIK 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
K2HUGM
Ig kappa chain precursor V-II region (GM607) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A01889; B24452
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.
A:Reference number: A01889; MUID:84191506; PMID:6325927
A:Accession: A01889
A:Molecule type: mRNA
A:Residues: 1-117 <KLO>
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>
F:20-99/Domain: immunoglobulin homology <IMM>
F:27-97/Disulfide bonds: #status predicted

Query Match 89.0%; Score 527; DB 1; Length 117;
Best Local Similarity 89.4%; Pred. No. 2e-41;
```

```
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 5 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLSNRA 64
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYVCMQGLQSPFTFGPGTKVDIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQGLQTPQTFTGGQTKVEIKR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S26882
Ig kappa chain V region (V607) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S26882
R:Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combratio, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A:Title: Megabase inversions in the human genome as physiological events.
A:Reference number: S26882; MUID:90370099; PMID:2118596
A:Accession: S26882
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <WEI>
A:Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 524; DB 2; Length 132;
Best Local Similarity 89.3%; Pred. No. 4.3e-41;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 21 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGQSPQLLIYLSNRA 80
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYVCMQGLQSPFTFGPGTKVDIK 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQTPQTFTGGQTKVEIK 132
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S58206
Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C:Accession: S58206
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitlin
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable regi
A:Reference number: S58206
A:Accession: S58206
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89054; NID:g929640; PIDN:CAA61441.1; PID:g929641
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 522; DB 2; Length 112;
Best Local Similarity 88.4%; Pred. No. 5.5e-41;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db 1 DIVMTQSPVSLPVTGPEPASISCRSSQSLHNSGYNYFDWYLOKPGQSPQLLIYLSNRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYVCMQGLQSPFTFGPGTKVDIK 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 61 SGVPDRFSGSGTDTFLKISRVEADGVVYCMQALQPLTFGGTKVEIK 112
|||||

RESULT 7

S40356

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40356

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40356

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72466; NID:q441400; PIDN:CAA511134.1; PID:q441401

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:25-104/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 88.2%; Score 522; DB 2; Length 125;

Matches 100; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60

Db 10 DIVMTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYLSNRA 69

QY 61 SGVPDRFSGSGTDTFLKISRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113

Db 70 SGVPDRFSGSGTDTFLKISRVEADGVVYCMQGLQPLTFGGTKRVEIKR 122

RESULT 8

S40339

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40339

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40339

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-126 <KLE>

A:Cross-references: EMBL:X72449; NID:q441366; PIDN:CAA51117.1; PID:q441367

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-110/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.7%; Score 507.5; DB 2; Length 126;

Matches 98; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60

Db 16 DIVMTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYLSNRA 75

QY 61 SGVPDRFSGSGTDTFLKISRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 112

Db 76 SGVPDRFSGSGTDTFLKISRVEADGVVYCMQALQ-PWTFGGTKRVEIK 126

RESULT 9

S40371

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40371

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40371

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-121 <KLE>

A:Cross-references: EMBL:X72481; NID:q441430; PIDN:CAA511149.1; PID:q441431

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:13-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.3%; Score 505; DB 2; Length 121;

Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRASGV 63

Db 1 MTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYLSKRASGV 60

QY 64 PDRFSGSVSGTDTFLKISRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113

Db 61 PDRFSGSVSGTDTFLKISRVEADGVVYCMQGLQPLTFGGTKLEIKR 110

RESULT 10

K2HUTW

Ig kappa chain V-II region (Tew) - human (tentative sequence)

C:Species: Homo sapiens (man)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A90370; A92764; A01888

R:Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N.

Biochemistry 12, 3763-3780, 1973

A:Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary au

A:Reference number: A90370; MUID:74148480; PMID:4596149

A:Contents: Bence Jones protein Tew

A:Accession: A90370

A:Molecule type: protein

A:Residues: 1-113 <PUT>

A:Note: This protein was isolated from the urine of a patient with plasma cell dyscra

R:Terry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osserman, E.F.; Glenner, G.G.

J. Clin. Invest. 52, 1276-1281, 1973

A:Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient

A:Reference number: A92764; MUID:73166638; PMID:4700495

A:Contents: amyloid protein Tew

A:Accession: A92764

A:Molecule type: protein

A:Residues: 1-27 <TER>

A:Note: the major amyloid protein appears to be identical with the Bence Jones protei

C:Genetics:

A:Gene: GDB:IGKV2

A:Cross-references: GDB:136265

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: amyloid; heterotetramer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 84.5%; Score 500; DB 1; Length 113;

Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60

Db 1 DIVMTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYALSRA 60

QY 61 SGVPDRFSGSVSGTDTFLKISRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113

|||||

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGYYICMZALQAPITFGQTRLEIKR 113

RESULT 11

S40372

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40372

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40372

A:Status: Preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <LE>

A:Cross-references: EMBL:X72482; NID:g441432; PIDN:CAA51150.1; PID:g441433

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 494; DB 2; Length 131;

Best Local Similarity 83.8%; Pred. No. 2.4e-38;

Matches 93; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60

Db 21 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGHNYLDWYLOKPGQSPQLLIYLGSTRA 80

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGYYICMZALQAPITFGQTRLEIKR 111

Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGYYICMZALQAPITFGQTRLEIKR 131

RESULT 12

S03876

Ig kappa chain V-II region (Inc) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S03876

R:Ferril, G.; Stoppin, M.; Iadarola, P.; Bellotti, V.; Merlini, G.

Biochim. Biophys. Acta 995, 103-108, 1989

A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.

A:Reference number: S03876; MUID:89194238; PMID:2495028

A:Accession: S03876

A:Molecule type: protein

A:Residues: 1-124 <FER>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 484; DB 2; Length 124;

Best Local Similarity 82.3%; Pred. No. 1.9e-37;

Matches 93; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60

Db 1 DIVLTQSPVLPVTPGEPASISCRSSQSLHNSGDNDWYLOKPGSQPIVILGNSRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGYYICMZALQAPITFGQTRLEIKR 113

Db 61 SGVPDRFSGSGGTDFTLLISVGAEDGVYICMZALQAPITFGQTRKVGIR 113

RESULT 13

K2HUMI

Ig kappa chain V-II region (Mil) - human (tentative sequence)

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A01887

R:Dreyer, W.J.; Gray, W.R.; Hood, L.

Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967

A:Title: The genetic, molecular, and cellular basis of antibody formation: some facts

A:Reference number: A01887

A:Accession: A01887

A:Molecule type: protein

A:Residues: 1-112 <DRE>

A:Note: the C region of this chain has the Inv (3) marker

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGKV2

A:Cross-references: GDB:136265

A:Map position: p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 80.8%; Score 478.5; DB 1; Length 112;

Best Local Similarity 78.8%; Pred. No. 5.3e-37;

Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60

Db 1 DIVLTQSPVLPVTPGEPASISCRSSQSLHNSBG-BYLDWYLVZKPGSPZLLIYLSNRA 59

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVYICMZALQAPITFGQTRKVDIKR 113

Db 60 SGVPDRFSGSGGTDFTLKISRVAZBVGYYICMZALQAPITFGGNTNVEIKR 112

RESULT 14

S40319

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40319

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40319

A:Status: Preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: EMBL:X72429; NID:g441326; PIDN:CAA51097.1; PID:g441327

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:26-105/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 478; DB 2; Length 123;

Best Local Similarity 90.0%; Pred. No. 6.5e-37;

Matches 90; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60

Db 11 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYLDWYLOKPGQSPQLLIYLSNRA 70

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVYICMZALQAPITFGQTRLEIKR 100

Db 71 SGVPDRFSGSGGTDFTLKISRVEAEDGVYICMZALQAPITFGQTRLEIKR 110

RESULT 15

S40321

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40321

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40321
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-130 <KLE>
A:Cross-references: EMBL:X72431
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-111/Domain: immunoglobulin homology <IMM>

Query Match	80.0%;	Score 473.5;	DB 2;	Length 130;
Best Local Similarity	80.7%;	Pred. No. 1.8e-36;		
Matches 92;	Conservative 13;	Mismatches 8;	Indels 1;	Gaps 1;

Qy	1	EIVLTFQSPLSLPVTPGEPASISCRSSQSLHS-NGYTYLDWYLOKPGQSPOLLIYSGSHR	59
Db	16	DIVMTQTPLSLFVTPGEPASISCRSSQSLDSDGNTYLDWYLOKPGQSPOLLIYTLISYR	75

Qy	60	ASGVDPDRFSGSVSGTDFTLRISRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKR	113
Db	76	ASGVDPDRFSGSGGTAFTLKISRVEAEDVGLYCMQRIEFPYTFGQGTKLEIKR	129

Search completed: March 13, 2003, 15:17:49
Job time : 19.5577 secs

ID	KV2C_HUMAN	STANDARD;	PRT;	112 AA.
AC	P01616;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-II region MIL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NC	NCBI_Taxid=9606;			
RP	[1]			
RN	SEQUENCE.			
RA	Dreyer W.J., Gray W.R., Hood L.E.;			
RT	"The genetic, molecular, and cellular basis of antibody formation:			
RT	some facts and a unifying hypothesis."			
RT	Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).			
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER			
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
CC	P.I.R; A01887; K2HUML.			
DR	HSSP; P80362; IWL.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig: 1.			
DR	SMART; SM00406; Igv. 1.			
KW	Immunoglobulin V region; Bence-Jones protein.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 33			
FT	DOMAIN 39 53			
FT	DOMAIN 54 60			
FT	DOMAIN 61 92			
FT	DOMAIN 93 101			
FT	DOMAIN 102 111			
FT	DISULFID 23 92			
FT	NON_TER 112 112			
SQ	SEQUENCE 112 AA; 12055 MW; F5B2E2FA7ABE481 CRC64;			
	Query Match 80.8%; Score 478.5; DB 1; Length 112;			
	Best Local Similarity 78.8%; Pred. No. 1.9e-41;			
	Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps			
QY	1 EIVLTQSPLSLTPTVGTGEASISCRSSQSLHSNGYTYLDWYLQKQSPQLLYISGSHRA 60			
Db	:			
Db	1 DIVLTQSPLSLTPTVGTGEASISCRSSQNLLZS8G-BYLDWYLZKPGZSPZLLIYLGSNRA 59			
QY	61 SGVDFRFGSGGDTFLIRISRVEADVGVYVCNQGLQSPFTFGPGTKVDIKR 113			
Db	:			
Db	60 SGVFNRFSGSGGTFTLKISRVAZAVGVYVCNQALQTLPLTFGGTNVEIKR 112			
RESULT 4				
KV2A_HUMAN	STANDARD;	PRT;	115 AA.	
AC	P01614;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-II region Cum.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NC	NCBI_Taxid=9606;			
RN	[1]			
RX	SEQUENCE.			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hiltschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-			
RT	type)."			
RT	hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).			
RN	[2]			
RP	REVIEWS TO 50; 52; 96 AND 97.			
RX	MEDLINE=70063440; PubMed=4188189;			
RA	Hiltschmann N.;			
RT	"Molecular basis of antibody formation."			


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RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR PIR: A01885; K2HUCM.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 79.0%; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.8%; Pred. No. 2.5e-40;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPLVPTGEPASISCRSSQSLHS-NGYTYLDWYLOKPGQSPQLLIYSGSHR 59
DB 2 DIVMTQSPISLPLVPTGEPASISCRSSQSLDSGDNTYLNWYLOKAGQSPQLLIYLSYR 61

QY 60 ASGVPDRFSGSVSGTDFTLIRISRVEADVGVYVCMQGLQSPFTFGPTKVDIKR 113
DB 62 ASGVPDRFSGSGTDFTLKISRVAEDVGVIYCMQRLIEIPYTFGQGTKEIRR 115

RESULT 5
KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR: A01886; K2HURF.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46D996BE CRC64;

Query Match 76.9%; Score 455; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 4.4e-39;
Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPLVPTGEPASISCRSSQSLHSNGYTYLDWYLOKPGQSPQLLIYSGSHR 60
DB 1 DIVMTQSPISLPLVPTLGGPASIQRSSQSLVYRGGTYLEWYLOKPGQSPQLLIYLSYRD 60
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QY 61 SGVPDRFSGSVSGTDFTLIRISRVEADVGVYVCMQGLQSPFTFGPTKVDIKR 113
DB 61 SGVPDRFSGSGTDFTLKISRVAEDVGVIYCMQATSPYTFGQGTKEIRR 113

RESULT 6
KV2F_HUMAN STANDARD; PRT; 133 AA.
ID KV2F_HUMAN
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041952; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; K2HURP.
DR HSSP; P80362; IWTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 75.0%; Score 444; DB 1; Length 133;
Best Local Similarity 75.2%; Pred. No. 6.7e-38;
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPLVPTGEPASISCRSSQSLHSNGYTYLDWYLOKPGQSPQLLIYSGSHR 60
DB 21 DIVMTQSPISLPLVPTLGGPASIQRSSQSLVYSGDNTYLNWYLOKPGQSPQLLIYKVSND 80

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEADVGVYVCMQGLQSPFTFGPTKVDIKR 113
DB 81 SGVPDRFSGSGTDFTLKISRVAEDVGVIYCMQGTHTSWTFGQGTKEIRR 133

RESULT 7
KV2E_MOUSE STANDARD; PRT; 113 AA.
ID KV2E_MOUSE
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
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DT 23-OCT-1986 (Rel. 02, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP [1]
RC TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVM517.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 73.0%; Score 432; DB 1; Length 113;
Best Local Similarity 75.2%; Pred. No. 9e-37;
Matches 85; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPVPVTPGEPASISCRSSQLHNSGYTYLDWYLOKPGQSPQLLYSGSHRA 60
Db 1 DIVMTQVFPVLTGTSASISCRSSKSLHNSGITYLYWYLOKPGQSPQLLYQMSNLA 60

Qy 61 SGVPDRFSGSVSGDTFTLRISRVEADGVVYCMQGLQSPFTFGPKVDIKR 113
Db 61 SGVPDRFSGSVSGDTFTLRISRVEADGVVYCAHNLELPYTFGGTKLEIKR 113

RESULT 8
KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP [1]
RC TISSUE=Hybridoma;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
CC PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KVM526.
DR HSSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
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DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE9A9A4C3A CRC64;

Query Match 72.5%; Score 429; DB 1; Length 113;
Best Local Similarity 72.6%; Pred. No. 1.8e-36;
Matches 82; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPVPVTPGEPASISCRSSQLHNSGYTYLDWYLOKPGQSPQLLYSGSHRA 60
Db 1 DVVMTQTLPLSPVSLGDAQSISCRSSQLVHSNGTYLNWYLOKAGQSPKLLIYKVSNR 60

Qy 61 SGVPDRFSGSVSGDTFTLRISRVEADGVVYCMQGLQSPFTFGPKVDIKR 113
Db 61 SGVPDRFSGSVSGDTFTLRISRVEADGLIYFCSTTHVPTFGGKLEIKR 113

RESULT 9
KV2F_MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP [1]
RC TISSUE=Hybridoma;
RX MEDLINE=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR HSSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 71.5%; Score 423; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 7.2e-36;
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
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OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=79026193; PubMed=100411;
RA Wasserman R.L., Capra J.D.;
RT "The amino acid sequence of the light chain variable region of a
RT canine myeloma immunoglobulin: evidence that the VK subgroups
RT predated mammalian speciation.";
RL Immunohistochemistry 15:303-305(1978).
CC -1- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
CC CHAINS.
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF
CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR PIR; A01907; K2DGGM.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 66.6%; Score 394.5; DB 1; Length 108;
Best Local Similarity 69.0%; Pred. No. 5e-33;
Matches 78; Conservative 13; Mismatches 17; Indels 5; Gaps

QY 1 EIVLTQSPLESLPTVPPGPASISCRSSQSLHNSGYTYLQWYLOKPGSQPLIYSGSHRA 60
Db 1 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DIVMTQPLSLVSPGPASISCRSSQSNL-----DYLNWYLKAGSQSPRLPEQDSQRA 55

QY 61 SGVPDRFSGSVGTDTFLRLSRVEAEDGVYVCMQGLQSPFTFGPTKVDIKR 113
Db 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 SGVPDRFSGSVGTDTFLRLGRVEAEDAGIYCMQRSFPTFTFGQTRLEVR 108

RESULT 12
KV2C_MOUSE
ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 13-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR; A01910; KVM51.
DR HSP; P80362; LWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23 FRAMEWORK-1.

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FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFBD0C4DA2BD3450 CRC64;

Query Match
Best Local Similarity 66.6%; Score 394; DB 1; Length 113;
Matches 78; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLPKPGQSPQLLIYSGSHRA 60
Db 1 DIVITQDELSKPVTSGESVSISSRSKSLYDKGTYLWNFLQGGPQQSPRLIYLMSTRA 60

QY 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVDRFSGSGSGTDFTLISRVKAEDGVVYCCQLVEYPLTFGAGTKLELKR 113

RESULT 13
KV2A_MOUSE STANDARD; PRT; 112 AA.
ID KV2A_MOUSE
AC P01626;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79000273; PubMed=99160;
RA Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
myeloma protein."
RL Blochmistry 17:2703-2707(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
CC CHAIN HAS ALSO BEEN DETERMINED.
DR PIR: A01908; KVM516.
DR HSSP: P80362; 1WTI.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Query Match
Best Local Similarity 65.4%; Score 387; DB 1; Length 112;
Matches 77; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLPKPGQSPQLLIYSGSHRA 60
Db 1 DIVITQDELSKPVTSGESVSISSRSKSLYDKGTYLWNFLQGGPQQSPRLIYLMSTRA 60

QY 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 112
Db 61 SGVDRFSGSGSGTDFTLISRVKAEDGVVYCCQLVEYPLTFGAGTKLELKR 113
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Db 61 SGVDRFSGSGSGTDFTLISRVKAEDGVVYCCQLVEYPLTFGAGTKLELKR 112

RESULT 14
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P18135;
DR 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy."
RT J. Exp. Med. 167:840-852(1988).
EL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLO022; K3HUHA.
DR HSSP: P80362; 1WTI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match
Best Local Similarity 62.5%; Score 370; DB 1; Length 129;
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLPKPGQSPQLLIYSGSHRA 60
Db 21 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLPKPGQSPQLLIYSGSHRA 76

QY 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 77 TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSPRTFGGQTKVEIKR 129

RESULT 15
KV3M_HUMAN STANDARD; PRT; 129 AA.
ID KV3M_HUMAN
AC P18136;
DR 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=88171307; PubMed=3127527;
RA Kips T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLO021; K3HUHI.
DR HSP: P80362; 1WTL.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_LV.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; Iq; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 62.3%; Score 369; DB 1; Length 129;
Best Local Similarity 65.5%; Pred. No. 2.2e-30;
Matches 74; Conservative 14; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPVLSLPTGEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSS---YLAWYQQRPGQAPRLIYGASSRA 76

QY 61 SGVPDRFGSGSGTDFTLRISRAEADGVVYCMQGLSQSPFTFGTKVDIKR 113
Db 77 TGIPTDFSGSGSGTDFTLTISRLEPDPFAVYCCQYGGSSPWTFGGTVKVEIKR 129

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Search completed: March 13, 2003, 15:15:13
Job time : 12.3 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:11:14 ; Search time 40.8538 seconds
(without alignments)
569.918 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
Sequence: I EIVLTQSPFLSLPVTGPGEAS.....MQGLQSPFTFGGCTKVDIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_todent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	457	77.2	238	11	Q99M37	Q99M37 mus musculus
2	444	75.0	239	11	Q8VC55	Q8VC55 mus musculus
3	438	74.0	238	11	Q8VC16	Q8VC16 mus musculus
4	436	73.6	239	4	Q8TCD0	Q8TCD0 homo sapien
5	428.5	72.4	114	4	Q8UL80	Q8UL80 homo sapien
6	406	68.6	104	11	Q9JL82	Q9JL82 mus musculus
7	373	63.0	109	4	Q9UL78	Q9UL78 homo sapien
8	369	62.3	109	4	Q9UL86	Q9UL86 homo sapien
9	351.5	59.4	108	4	Q9UL83	Q9UL83 homo sapien
10	340.5	57.5	111	11	Q920E9	Q920E9 mus musculus
11	325.5	55.0	107	11	Q9ERZ9	Q9ERZ9 mus musculus
12	322	54.4	107	4	Q9UL81	Q9UL81 homo sapien
13	322	54.4	109	4	Q9UL85	Q9UL85 homo sapien
14	316.5	53.5	108	4	Q9UL77	Q9UL77 homo sapien
15	313	52.9	106	5	Q9UL40	Q9UL40 schistosoma
16	309.5	52.3	108	4	Q9UL79	Q9UL79 homo sapien

17	309.5	52.3	234	11	Q8VCP0	Q8VCP0 mus musculus
18	308	52.0	107	4	Q96SA9	Q96SA9 homo sapien
19	306.5	51.8	108	4	Q9UL70	Q9UL70 homo sapien
20	301.5	50.9	214	11	Q9RLA5	Q9RLA5 mus musculus
21	296.5	50.1	298	11	Q9QYF0	Q9QYF0 mus musculus
22	296	50.0	134	11	Q8VDD0	Q8VDD0 mus musculus
23	295.5	49.9	108	11	Q8VIJ0	Q8VIJ0 mus musculus
24	293.5	49.6	109	11	Q920E6	Q920E6 mus musculus
25	288.5	48.7	116	4	Q96PF6	Q96PF6 homo sapien
26	286	48.3	235	11	Q9LW12	Q9LW12 mus musculus
27	284.5	48.1	103	11	Q9JL80	Q9JL80 mus musculus
28	283.5	47.9	99	11	Q9JL74	Q9JL74 mus musculus
29	282.5	47.7	234	11	Q9LWF8	Q9LWF8 mus musculus
30	276.5	46.7	101	11	Q9JL78	Q9JL78 mus musculus
31	276.5	46.7	234	11	Q8R062	Q8R062 mus musculus
32	270.5	45.7	233	11	Q9LWS9	Q9LWS9 mus musculus
33	265.5	44.8	97	11	Q9JL76	Q9JL76 mus musculus
34	255.5	43.2	127	11	Q925S9	Q925S9 mus musculus
35	251.5	42.5	234	11	Q8R028	Q8R028 mus musculus
36	249.5	42.1	109	6	Q9N0W5	Q9N0W5 oryctolagus
37	240.5	40.6	107	11	Q9JL84	Q9JL84 mus musculus
38	235	39.7	233	4	Q8TBC9	Q8TBC9 homo sapien
39	234	39.5	237	4	Q8WTU6	Q8WTU6 homo sapien
40	232	39.2	237	4	Q8WUK4	Q8WUK4 homo sapien
41	223.5	37.8	236	4	Q96E61	Q96E61 homo sapien
42	223	37.7	108	4	Q96SB0	Q96SB0 homo sapien
43	222	37.5	241	11	Q92LA6	Q92LA6 mus musculus
44	214	36.1	110	4	Q8TE63	Q8TE63 homo sapien
45	213.5	36.1	107	4	Q9UL82	Q9UL82 homo sapien

ALIGNMENTS

RESULT 1

Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020235; AAH02035.1; -
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGLike; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 77.2%; Score 457; DB 11; Length 238;

Best Local Similarity 75.2%; Pred. No. 1.7e-43;

Matches 85; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

QY 1 EIVLTQSPFLSLPVTGPGEASISCRSSQSLHNSNGVTYLDWYLRKPGSPQLIYSGSHRA 60

20 DVVMTQTPLSLPVLGDOASISCRSSQSLVHSNGVTYLDWYLRKPGSPQLIYKVSNR 79

QY 61 SGVPDRFSGSGTDFTLRLISRVEADGVGYCMOGLQSPFTFGPGTKVDIKR 113
Db 80 SGVPDRFSGSGTDFTLRLISRVEADGVGYCFQSGSHVPTFGSGTKLEIKR 132

RESULT 2

Q8VC55 PRELIMINARY; PRT; 239 AA.

AC Q8VC55; (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; Igc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.

Query Match 75.0%; Score 444; DB 11; Length 239;

Best Local Similarity 74.3%; Pred. No. 4.9e-42;

Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
QY 1 EIVLTQSPPLSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DVLVTQTPSLPVLNIGDQASISCKSLNSDGFYLDWYLOKPGQSPQLLIYLSNRF 80
QY 61 SGVPDRFSGSGTDFTLRLISRVEADGVGYCMOGLQSPFTFGPGTKVDIKR 113
Db 81 SGVPDRFSGSGTDFTLRLISRVEADGVGYCFQSGSHVPTFGSGTKLEIKR 133

RESULT 3

Q8VC16 PRELIMINARY; PRT; 238 AA.

AC Q8VC16; (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.

DR SMART; SM00407; Igc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 74.0%; Score 438; DB 11; Length 238;

Best Local Similarity 74.3%; Pred. No. 2.3e-41;

Matches 84; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
QY 1 EIVLTQSPPLSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 20 DVLVTQTPSLPVLNIGDQASISCKSLNSDGFYLDWYLOKPGQSPQLLIYKVSNR 79
QY 61 SGVPDRFSGSGTDFTLRLISRVEADGVGYCMOGLQSPFTFGPGTKVDIKR 113
Db 80 SGVPDRFSGSGTDFTLRLISRVEADGVGYCFQSGSHVPTFGSGTKLEIKR 132

RESULT 4

Q8TCDO PRELIMINARY; PRT; 239 AA.

AC Q8TCDO; (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -
KW Hypothetical protein.

Query Match 73.6%; Score 436; DB 4; Length 239;

Best Local Similarity 72.6%; Pred. No. 3.9e-41;

Matches 82; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
QY 1 EIVLTQSPPLSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DVLVTQSPPLSLPVLNIGDQASISCKSLNSDGFYLDWYLOKPGQSPQLLIYKVSNR 80
QY 61 SGVPDRFSGSGTDFTLRLISRVEADGVGYCMOGLQSPFTFGPGTKVDIKR 113
Db 81 SGVPDRFSGSGTDFTLRLISRVEADGVGYCFQSGSHVPTFGSGTKLEIKR 133

RESULT 5

Q9UL80 PRELIMINARY; PRT; 114 AA.

AC Q9UL80; (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";


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RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035034; AAD56270.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 72.4%; Score 428.5; DB 4; Length 114;
Best Local Similarity 73.7%; Pred. No. 1.1e-40;
Matches 84; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLSPLVPTGCEPASISCRSSQSLHNSGYTYLDWYLPKQPGSPQLLIYSGSHRA 60
Db 1 DVMTQSPVLSPLVLTQRPASISCRSSQSPVYSDGNTYLNWFQQRPGSPRLTIYKVSNRD 60

QY 61 SGVPDRFSGSVGTDFTLIRISRVEADGVVYCMQGLQ-SPTFTGCTKVDIKR 113
Db 61 SGVPDRFSGSGTDFTLKISRVEADGVVYCMQGTHTWPTFGGQTKVEIKR 114

RESULT 6
QYJL82 PRELIMINARY; PRT; 104 AA.
AC QYJL82;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALE/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF205024; AAF69322.1; -.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match 68.6%; Score 406; DB 11; Length 104;
Best Local Similarity 75.0%; Pred. No. 3.3e-38;
Matches 78; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 9 LSLPVTGPEASISCRSSQSLHNSGYTYLDWYLPKQPGSPQLLIYSGSHRASGVDPDRFS 68
Db 1 LSLPVSIGQASISCRSSQSLVHTNGNTYLHWYLPKQPGSPKLLIYKVSNRFSGVDPDRFS 60

QY 69 GSVSGTDFTLIRISRVEADGVVYCMQGLQSPFTFGCTKVDIK 112
Db 61 GSGSGTDFTLKISRVEADLVYFCSTHTVPTFGGQTKLEIK 104

RESULT 7
QYJL78 PRELIMINARY; PRT; 109 AA.
AC QYJL78;

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
DE Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 63.0%; Score 373; DB 4; Length 109;
Best Local Similarity 66.4%; Pred. No. 1.9e-34;
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPVLSPLVPTGCEPASISCRSSQSLHNSGYTYLDWYLPKQPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLSPLVPTGCEPASISCRSSQSVSSS---YLAWYQQKPGQAPRLLIYGASSRA 56

QY 61 SGVPDRFSGSVGTDFTLIRISRVEADGVVYCMQGLQSPFTFGCTKVDIKR 113
Db 57 TGIPDRFSGSGTDFTLIRISLEPEDCAVYVCQYQSSPLTGGGQTKVEIKR 109

RESULT 8
QYJL86 PRELIMINARY; PRT; 109 AA.
AC QYJL86;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
DE Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56264.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 62.3%; Score 369; DB 4; Length 109;
Best Local Similarity 67.3%; Pred. No. 5.3e-34;

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RESULT 12
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035033; AAD56269.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 54.4%; Score 322; DB 4; Length 107;
Best Local Similarity 59.3%; Pred. No. 1.1e-28;
Matches 67; Conservative 15; Mismatches 25; Indels 6; Gaps 3;

QY 1 EIVLTQSPPLSLPVTPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPOLLIIYSGSHRA 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQI--SN---YLNWYQKQKGRAPNLLIYASLSQ 55

QY 61 SGVPRFSGSVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113
Db 56 SGVPSRFSGSGGTDTLTISGLQAEAFATYICQSS-YSALTGPGTKVDIR 107

RESULT 13
Q9UL85
ID Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035029; AAD56265.1; -.
DR HSSP: P80362; IWL7.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 54.4%; Score 322; DB 4; Length 109;
Best Local Similarity 58.8%; Pred. No. 1.1e-28;
Matches 67; Conservative 18; Mismatches 23; Indels 6; Gaps 3;

QY 1 EIVLTQSPPLSLPVTPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPOLLIIYSGSHRA 60
Db 1 EIVMTQSPATLSVSPGERATISCVASQS-SSN----LAWYQKQKQAPRLLIYGASTRA 55

QY 61 SGVPRFSGSVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113
Db 56 TGIPARFSGSGGTDTLTISGLQAEAFATYICQYNSWPLTFGGTKVKEIKR 109

RESULT 14
Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; RAD56273.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 53.5%; Score 316.5; DB 4; Length 108;
Best Local Similarity 54.9%; Pred. No. 4.5e-28;
Matches 62; Conservative 18; Mismatches 28; Indels 5; Gaps 1;

QY 1 EIVLTQSPPLSLPVTPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPOLLIIYSGSHRA 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQI-----SSYLNWYQKQKGRAPNLLIYASLSQ 55

QY 61 SGVPRFSGSVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113
Db 56 SGVPSRFSGSGGTDTLTISGLQAEAFATYICQSSYSTSWTFGGTKVKEIKR 108

RESULT 15
Q9UL10
ID Q9UL10 PRELIMINARY; PRT; 106 AA.
AC Q9UL10;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 52.9%; Score 313; DB 5; Length 106;
Best Local Similarity 54.5%; Pred. No. 1.le-27;
Matches 61; Conservative 18; Mismatches 27; Indels 6; Gaps 1;

Qy 1 EIVLTQSPFLSLPVTPGEPASISCSQSLLHSNGYTYLDWYLOKPGSPOLLIIYSGSHRA 60
Db 1 ENLLTQSPAINSA SPGEKVTMTCSASSV-----SYVWYLOKPGSSPRLIIYDTSNLA 54

Qy 61 SGVPDRFSGSVSGTDFTLRISRVAEADVGVVYCMQGLQSPFTFGPGTKVDIK 112
Db 55 SGVPVRFSGSGGTSYSILTISRMEAEADAITYCQOWTSYPFTFGSGTKLELK 106
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Search completed: March 13, 2003, 15:16:56
Job time : 41.8538 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:05:54 ; Search time, 55.3808 Seconds
(without alignments)
291.136 Million cell updates/sec

Title: US-09-822-698A-3
Perfect score: 644
Sequence: 1 QVQIVSGGGLVPGGSLRL.....GGWDPIDYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	644	100.0	121	AAE12706	Human PH1 Fab anti
2	644	100.0	381	AAE12707	Human blyPHJ-IL-2
3	644	100.0	451	AAE12715	Human recombinant
4	548	85.1	121	AAE07029	Human heavy chain
5	543.5	84.4	120	AAW27553	Human Ab heavy chain
6	543.5	84.4	281	AAW27560	Consensus single c
7	541.5	84.1	116	AAE07017	Human heavy chain
8	540.5	83.9	246	ABP45964	Human BlyS binding
9	539	83.7	240	AAU79563	Monoclonal scfv an
10	537.5	83.5	131	AAW13520	Anti-melanoma anti

11	537.5	83.5	239	23	ABP45911	Human BlyS binding
12	537	83.4	117	22	AAE12061	Human anti-tissue
13	537	83.4	313	22	AAU14320	Human novel protei
14	536.5	83.3	240	20	AAU02472	A single chain ant
15	535	83.1	117	18	AAW13532	Anti-melanoma anti
16	533	82.8	119	22	AAU02512	Anti-adiocyte mon
17	532	82.8	246	21	AAV58235	Internalising anti
18	532	82.6	227	22	AAE75051	TRO005 Humab Happa
19	531.5	82.5	118	23	AAU83803	MS-GPC-6 heavy cha
20	531.5	82.5	118	23	ABE57561	HLA-DR-specific pr
21	531.5	82.5	120	22	AAE07022	Human heavy chain
22	530.5	82.4	116	23	AAO21548	Antibody screening
23	529.5	82.2	246	23	ABP45969	Human BlyS binding
24	529	82.1	240	21	AAV15124	Anti-human CTLA-4
25	529	82.1	240	21	AAV15125	Anti-murine CTLA-4
26	528.5	82.1	268	23	AAU97197	Human anti-EGFR si
27	527.5	81.9	122	20	AAW78432	Antibody heavy cha
28	527.5	81.9	122	23	ABE79755	Heavy chain variab
29	527.5	81.9	252	23	ABP45626	Human BlyS binding
30	527	81.8	117	23	ABE05053	Fibronectin isofor
31	527	81.8	121	23	ABE57571	HLA-DR-specific pr
32	527	81.8	245	22	AAE67620	Human leukocyte an
33	526.5	81.8	248	23	ABP44910	Human BlyS binding
34	526.5	81.8	248	23	ABP45445	Human BlyS binding
35	526.5	81.8	250	23	ABP45409	Human BlyS binding
36	525.5	81.6	251	23	ABP45729	Human BlyS binding
37	525	81.5	120	15	AAE54803	SPA-reactive VH re
38	524.5	81.4	116	18	AAW13529	Anti-melanoma anti
39	524.5	81.4	247	23	ABP45912	Human BlyS binding
40	524	81.4	120	15	AAE54802	SPA-reactive VH re
41	524	81.4	120	15	AAE54804	SPA-reactive VH re
42	524	81.4	120	15	AAE54805	SPA-reactive VH re
43	524	81.4	120	15	AAE54806	SPA-reactive VH re
44	524	81.4	123	22	AAE07019	Human heavy chain
45	523.5	81.3	293	22	AAE65715	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAE12706
ID AAE12706 standard; Protein; 121 AA.
XX
AC AAE12706;
XX
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody variable heavy chain region (VH).
XX
XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody.
XX
XX Homo sapiens.
XX
XX
FH Key
FH Region
FH Location/Qualifiers
FT 31..35
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 97..99
FT /label= FR3
FT /note= "Framework region 3"
FT 97..112
FT /note= "VH domain"
FT 99..110
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT 111..112
FT /label= FR4

PT /note= "Framework region 4"

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI: 2001-626437/72.

XX N-PSDB; AAD20731.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member for diagnosing and treating cancer, comprises mucin-1 binding domain or its portion for binding to an epitope of the protein core of mucin-1 -

XX Claim 2; Page 94-95; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1 (MUC-1)-specific binding member comprising an antigen binding domain region having an antibody variable light (VL) or heavy (VH) region, or a complementarity determining region (CDR) of VL or VH. MUC1-specific binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX The binding of MUC1-specific binding member to MUC1 is detected by a detection method selected from enzyme-linked immunosorbent assay, magnetic resonance imaging, scintillation counting, and X-ray film.

XX MUC1-specific binding member is useful for treating cancer, preferably adenocarcinoma, in an individual, where the cancer is present in tissue of the breast, ovary, lung, or bladder of the individual. MUC1-specific binding member is useful for diagnosing and imaging MUC1-expressing cancer cells and tissues, for purifying or isolating non-glycosylated, underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-containing molecules, and for therapeutically or prophylactically treating cancer. The present sequence is anti-MUC1 human PH1 Fab antibody VH region.

XX Sequence 121 AA;

Query Match 100.0%; Score 644; DB 22; Length 121;

Best Local Similarity 100.0%; Pred. No. 3.2e-50;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60

DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120

DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120

QY 121 S 121

DB 121 S 121

RESULT 2

AAE12707

ID AAE12707 standard; Protein; 381 AA.

XX AAE12707;

XX 04-JAN-2002 (first entry)

XX Human b1vPH1-IL-2 immunocytokine protein.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer; breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.

OS Homo sapiens.

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI: 2001-626437/72.

XX N-PSDB; AAD20732.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member for diagnosing and treating cancer, comprises mucin-1 binding domain or its portion for binding to an epitope of the protein core of mucin-1 -

XX Claim 9; Page 95-97; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1 (MUC-1)-specific binding member comprising an antigen binding domain region having an antibody variable light (VL) or heavy (VH) region, or a complementarity determining region (CDR) of VL or VH. MUC1-specific binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX The binding of MUC1-specific binding member to MUC1 is detected by a detection method selected from enzyme-linked immunosorbent assay, magnetic resonance imaging, scintillation counting, and X-ray film.

XX MUC1-specific binding member is useful for treating cancer, preferably adenocarcinoma, in an individual, where the cancer is present in tissue of the breast, ovary, lung, or bladder of the individual. MUC1-specific binding member is useful for diagnosing and imaging MUC1-expressing cancer cells and tissues, for purifying or isolating non-glycosylated, underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-containing molecules, and for therapeutically or prophylactically treating cancer. The present sequence is human b1vPH1-IL-2 immunocytokine protein. b1vPH1 is mucin specific binding portion.

XX Sequence 381 AA;

Query Match 100.0%; Score 644; DB 22; Length 381;

Best Local Similarity 100.0%; Pred. No. 1.1e-49;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60

DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120

DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120

QY 121 S 121

DB 121 S 121

RESULT 3

AAE12715

ID AAE12715 standard; Protein; 451 AA.

XX AAE12715;

XX 04-JAN-2002 (first entry)

XX Human recombinant immunoglobulin (Ig) heavy chain region.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; heavy chain region; cancer; breast; ovary; lung; bladder; cytostatic; therapy; immunoglobulin; Ig.

Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGSTYY	60
Qy	61	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVNDPIDYWGQGLTVTVS	120
Db	61	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVNDPIDYWGQGLTVTVS	120
Qy	121	S	121
Db	121	S	121
RESULT 5			
AAW27553			
ID	AAW27553 standard; Protein; 120 AA.		
XX	AC	AAW27553;	
XX	DT	23-JAN-1998 (first entry)	
XX	DE	Human Ab heavy chain variable region VH3 consensus.	
XX	KW	Human; antibody; preparation; library; VH3; variable region;	
XX	KW	heavy chain; consensus.	
XX	OS	Homo sapiens.	
XX	PN	WO9708320-A1.	
XX	PD	06-MAR-1997.	
XX	PF	19-AUG-1996; 96WO-EP03647.	
XX	PR	18-AUG-1995; 95EP-0113021.	
XX	PA	(MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.	
XX	PI	Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;	
XX	DR	WPI; 1997-179277/16.	
XX	DR	N-PSDB; AAT87951.	
XX	CC	Preparation of human derived antibody gene library - using synthetic	
XX	CC	consensus sequences, and signal consensus antibody gene as universal	
XX	CC	framework for highly diverse antibody libraries	
XX	CC	Example 1; Fig 5D; 436pp; English.	
XX	CC	The present sequence is the human antibody heavy chain	
XX	CC	variable region synthetic sequence VH3, used in the preparation of	
XX	CC	a human derived antibody gene library.	
XX	SQ	Sequence 120 AA;	
Query Match 84.4%; Score 543.5; DB 18; Length 120;			
Best Local Similarity 87.6%; Pred. No. 3e-41;			
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;			
Qy	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGSTYY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGSTYY	60
Qy	61	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVNDPIDYWGQGLTVTVS	120
Db	61	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVNDPIDYWGQGLTVTVS	120
Qy	121	S	121
Db	120	S	120
RESULT 6			
AAW27560			
ID	AAW27560 standard; Protein; 281 AA.		
XX	AC	AAW27560;	
XX	DT	23-JAN-1998 (first entry)	
XX	DE	Consensus single chain fragment VH3-V-kappa-2.	
XX	KW	Human; antibody; preparation; library; VH3; variable region;	
XX	KW	light chain; heavy chain; V-kappa-2; single chain; consensus.	
XX	OS	Homo sapiens.	
XX	OS	Synthetic.	
XX	PH	Key	
XX	FT	Peptide	
XX	FT	/label= sig_peptide	
XX	FT	22..281	
XX	FT	/label= mat_peptide	
XX	PN	WO9708320-A1.	
XX	PD	06-MAR-1997.	
XX	PF	19-AUG-1996; 96WO-EP03647.	
XX	PR	18-AUG-1995; 95EP-0113021.	
XX	PA	(MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.	
XX	PI	Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;	
XX	DR	WPI; 1997-179277/16.	
XX	DR	N-PSDB; AAT87958.	
XX	CC	Preparation of human derived antibody gene library - using synthetic	
XX	CC	consensus sequences, and signal consensus antibody gene as universal	
XX	CC	framework for highly diverse antibody libraries	
XX	CC	Example 2; Fig 8; 436pp; English.	
XX	CC	The present sequence is the consensus single chain fragment	
XX	CC	VH3-V-kappa-2, which comprises the human antibody	
XX	CC	heavy and light chain variable region consensus sequences VH3 and	
XX	CC	V-kappa-2, was used in the preparation of a human derived antibody	
XX	CC	gene library.	
XX	SQ	Sequence 281 AA;	
Query Match 84.4%; Score 543.5; DB 18; Length 281;			
Best Local Similarity 87.6%; Pred. No. 7.5e-41;			
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;			
Qy	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGSTYY	60
Db	26	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGSTYY	85
Qy	61	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVNDPIDYWGQGLTVTVS	120
Db	86	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS	144
Qy	121	S	121
Db	145	S	145
RESULT 7			
AAE07017			
ID	AAE07017 standard; Protein; 116 AA.		
XX	AC	AAE07017;	
XX	DT	16-OCT-2001 (first entry)	

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 246 AA;
 Query Match 83.9%; Score 540.5; DB 23; Length 246;
 Best Local Similarity 89.3%; Pred. No. 1.2e-40;
 Matches 108; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
 QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVWVROAPGKGLVWVSGISGSGSTYY 60
 DB 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVWVROAPGKGLVWVSAISGSGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIYWGQGLTLTVTS 120
 DB 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIYWGQGLTLTVTS 119
 QY 121 S 121
 DB 120 S 120
 RESULT 9
 AAU79563
 ID AAU79563 standard; Protein; 240 AA.
 AC AAU79563;
 DT 03-SEP-2002 (first entry)
 XX Monoclonal scFv antibody, ME-4C, binding Fibronectin ED-B domain.
 DE
 XX Antibody; single chain antibody variable region fragment; scFv; ME-4C;
 KW human; Fibronectin; ED-B; antiangiogenic; CDR3;
 KW complementarity determining region 3; heavy chain; VH; DP-47;
 KW light chain; VL; DPL-16; 7B89; angiogenesis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 220..229
 FT /note= "CDR3 if the scFv light chain"
 XX
 XX WO200246455-A2.
 XX 13-JUN-2002.
 XX
 XX 06-DEC-2001; 2001WO-EPL4330.
 XX
 XX 06-DEC-2000; 2000IT-FI00247.
 XX (PHIL-) PHILGEN SRL.
 XX Giovannoni L;
 XX
 XX WPI; 2002-452759/48.
 DR N-PSDB; ABK86789.
 XX
 XX Novel process for selecting anti-angiogenesis antibody fragments -
 PT
 XX Claim 5; Page 16-17; 18pp; English.
 PS
 XX The invention discloses a process for selecting anti-angiogenesis
 CC antibody fragments, in which, starting from a highly complex system
 CC containing billions of different binding specificities, several cycles of
 CC filter selection of colonies and of amplification of positive clones are
 CC carried out. The method is an improvement on existing antibody selection
 CC methods by allowing the selection from a large repertoire of antibody
 CC fragments expressed in bacteria. It can also avoid the use of phage
 CC display, identifying directly, the clones expressing the antibody
 CC fragments in soluble form. The invention discloses, in particular, a
 CC monoclonal antibody fragment scFv, ME-4C, produced according to the

CC process, with the CDR3 sequences of the heavy chain VH (DP-47) and the
 CC light chain VL (DPL-16) characterised. The monoclonal antibody was
 CC isolated by the recognition of epitopes from a decapeptide library of the
 CC recombinant protein, 7B89, containing the domains 7, 8 and 9, and more
 CC particularly, ED-B (not defined), of human Fibronectin. The identified
 CC monoclonal antibody fragment scFv ME-4C can act as a reagent in the
 CC determination of angiogenesis in tissue samples in vivo and/or in vitro.
 CC The protein sequence presented is the monoclonal scFv antibody, ME-4C,
 CC binding to the human Fibronectin ED-B domain. The antibody was isolated
 CC from the ETH-2000 library.
 XX
 SQ Sequence 240 AA;
 Query Match 83.7%; Score 539; DB 23; Length 240;
 Best Local Similarity 87.5%; Pred. No. 1.6e-40;
 Matches 105; Conservative 2; Mismatches 9; Indels 4; Gaps 1;
 QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVWVROAPGKGLVWVSGISGSGSTYY 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFRSNAMGVWVROAPGKGLVWVSAISGSGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIYWGQGLTLTVTS 120
 DB 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCAKHTGGVWDPIYWGQGLTLTVTS 116
 RESULT 10
 AAU13520
 ID AAU13520 standard; protein; 131 AA.
 XX
 AC AAU13520;
 XX
 DT 28-OCT-1997 (first entry)
 XX
 XX Anti-melanoma antibody heavy chain clone V13.
 DE
 XX Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
 KW cancer; tumourigenesis; anticancer vaccine.
 KW
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= CDR1
 FT Region 50..66
 FT /label= CDR2
 FT Region 99..105
 FT /label= CDR3
 XX
 XX WO9702479-A2.
 XX
 XX 23-JAN-1997.
 XX
 XX 28-JUN-1996; 96WO-IB01032.
 XX
 XX 30-JUN-1995; 95US-0497647.
 PR
 XX (UYXA) UNIV YALE.
 XX
 XX Cai X, Garen A;
 PI
 XX WPI; 1997-109061/10.
 DR
 XX
 XX Prodn. of human monoclonal anti-tumour antibodies - by screening a
 PT fusion phage library produced using peripheral blood lymphocytes
 PT from a cancer patient
 XX
 XX Claim 19; Page 58; 82pp; English.
 PS
 XX A process for isolating and synthesising human monoclonal anti-tumour
 CC antibodies has been produced. The process involves: (a) constructing at
 CC least one fusion phage library from the peripheral blood lymphocytes
 CC (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:44 ; Search time 18.6154 seconds
(without alignments)
191.249 Million cell updates/sec

Title: US-09-822-698A-3

Perfect score: 644
Sequence: 1 QVQLVQSGGGLVPGGSLRL.....GGVMDPIDWGGGTLVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543.5	84.4	120	4	US-09-025-769B-38
2	543.5	84.4	120	4	US-09-025-769B-63
3	543.5	84.4	281	4	US-09-025-769B-178
4	537.5	83.5	131	4	US-08-983-607-28
5	535	83.1	117	4	US-08-983-607-46
6	527	81.8	120	2	US-08-428-197-20
7	527	81.8	120	5	PCT-US93-10555-20
8	527	81.8	125	5	US-08-428-197-1
9	527	81.8	125	5	PCT-US93-10555-1
10	525	81.5	120	2	US-08-428-197-22
11	525	81.5	120	5	PCT-US93-10555-22
12	524.5	81.4	116	4	US-08-983-607-36
13	524.5	81.4	122	2	US-07-934-373C-21
14	524.5	81.4	122	3	US-08-437-642B-21
15	524.5	81.4	122	4	US-08-146-206C-21
16	524.5	81.4	122	5	PCT-US93-07832-21
17	524	81.4	120	2	US-08-428-197-24
18	524	81.4	120	2	US-08-428-197-26
19	524	81.4	120	2	US-08-428-197-28
20	524	81.4	120	5	PCT-US93-10555-24
21	524	81.4	120	5	PCT-US93-10555-26
22	524	81.4	120	5	PCT-US93-10555-28
23	523	81.2	113	3	US-08-974-899-6
24	520.5	80.8	140	4	US-08-983-607-32
25	520	80.7	117	4	US-09-025-769B-24
26	517	80.3	125	1	US-08-478-039-99
27	517	80.3	125	1	US-08-476-349A-99

28	514	79.8	120	2	US-08-428-197-40	Sequence 40, Appl
29	514	79.8	120	5	PCT-US93-10555-40	Sequence 40, Appl
30	512.5	79.6	263	4	US-09-069-821-3	Sequence 3, Appl
31	512.5	79.6	283	4	US-09-420-592A-6	Sequence 6, Appl
32	511	79.3	119	1	US-07-988-925-11	Sequence 11, Appl
33	511	79.3	119	2	US-08-362-780-11	Sequence 11, Appl
34	511	79.3	120	2	US-08-428-197-30	Sequence 30, Appl
35	511	79.3	120	2	US-08-428-197-32	Sequence 32, Appl
36	511	79.3	120	5	PCT-US93-10555-30	Sequence 30, Appl
37	511	79.3	120	5	PCT-US93-10555-32	Sequence 32, Appl
38	510.5	79.3	123	2	US-08-428-197-38	Sequence 38, Appl
39	510.5	79.3	123	5	PCT-US93-10555-38	Sequence 38, Appl
40	508	78.9	120	2	US-08-428-197-34	Sequence 34, Appl
41	508	78.9	120	5	PCT-US93-10555-34	Sequence 34, Appl
42	508	78.9	123	2	US-08-665-202-30	Sequence 30, Appl
43	505.5	78.5	116	2	US-08-428-197-2	Sequence 2, Appl
44	505.5	78.5	116	5	PCT-US93-10555-2	Sequence 2, Appl
45	505.5	78.5	118	2	US-08-958-201-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-38
; Sequence 38, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. C/O Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/025.769B
; APPLICATION NUMBER: US/09/025.769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-38

Query Match 84.4%; Score 543.5; DB 4; Length 120;
Best Local Similarity 87.6%; Pred. No. 2.5e-46;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 OVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS 119
QY 121 S 121
Db 120 S 120

RESULT 2
US-09-025-769B-63
; Sequence 63, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achlm
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-63

Query Match 84.4%; Score 543.5; DB 4; Length 120;
Best Local Similarity 87.6%; Pred. No. 2.5e-46;
Matches 106; Conservative 9; Mismatches 9; Indels 1; Gaps 1;
QY 1 OVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS 119
QY 121 S 121

Db 120 S 120
RESULT 3
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achlm
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-178

Query Match 84.4%; Score 543.5; DB 4; Length 281;
Best Local Similarity 87.6%; Pred. No. 6.5e-46;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
QY 1 OVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60
Db 26 EVOLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSAISGSGSTYY 85
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120
Db 86 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS 144
QY 121 S 121
Db 145 S 145

RESULT 4
US-08-983-607-28
; Sequence 28, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen


```
US-08-428-197-20
; Sequence 20, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-10555-20

Query Match 81.8%; Score 527; DB 5; Length 120;
Best Local Similarity 84.2%; Pred. No. 1e-44; Indels 0; Gaps 0;
Matches 101; Conservative 7; Mismatches 12;

QY 1 QVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTYY 60
Db 1 QVKLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGKGLWVSDISASGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWMDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCASNGAGWGLPSLDYWGQGLTVTVS 120

RESULT 8
US-08-428-197-1
; Sequence 1, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-428-197-20

Query Match 81.8%; Score 527; DB 2; Length 120;
Best Local Similarity 84.2%; Pred. No. 1e-44; Indels 0; Gaps 0;
Matches 101; Conservative 7; Mismatches 12;

QY 1 QVOLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTYY 60
Db 1 QVKLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGKGLWVSDISASGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWMDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCASNGAGWGLPSLDYWGQGLTVTVS 120

RESULT 7
PCT-US93-10555-20
; Sequence 20, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
```

TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
PCT-US93-10555-1

Query Match 81.8%; Score 527; DB 2; Length 125;
Best Local Similarity 83.2%; Pred. No. 1.le-44;
Matches 104; Conservative 5; Mismatches 12; Indels 4; Gaps 1;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNAMGWVRQAPKGLVWVSGISGGSTYY 60
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLVWVSAISGGSTYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAK----HTGGGVWDPIDYWGQGTLL 116
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCTKGQVLYYSGSYHWFDPWGQGTLL 120
QY 117 VTVSS 121
Db 121 VTVSS 125

RESULT 9

PCT-US93-10555-1
Sequence 1, Application PC/TUS9310555

GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
PCT-US93-10555-1

Query Match 81.8%; Score 527; DB 5; Length 125;
Best Local Similarity 83.2%; Pred. No. 1.le-44;
Matches 104; Conservative 5; Mismatches 12; Indels 4; Gaps 1;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNAMGWVRQAPKGLVWVSGISGGSTYY 60
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLVWVSAISGGSTYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAK----HTGGGVWDPIDYWGQGTLL 116
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCTKGQVLYYSGSYHWFDPWGQGTLL 120
QY 117 VTVSS 121
Db 121 VTVSS 125

RESULT 10

US-08-428-197-22
Sequence 22, Application US/08428197

Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-197-22

Query Match 81.5%; Score 525; DB 2; Length 120;
Best Local Similarity 84.2%; Pred. No. 1.6e-44;
Matches 101; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

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1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLGWVSGISGGSTYY 60
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1 QVKLLESGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPKGLGWVSDISASGGSTYY 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTGGGVWDPIDYWGQGTLTVTS 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTALYLCASSGAGWGLPSLDYWGQGTLTVTS 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
PCT-US93-10555-22
; Sequence 22, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: ED-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-10555-22

Query Match 81.5%; Score 525; DB 5; Length 120;
Best Local Similarity 84.2%; Pred. No. 1.6e-44;
Matches 101; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLGWVSGISGGSTYY 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVKLLESGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPKGLGWVSDISASGGSTYY 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTGGGVWDPIDYWGQGTLTVTS 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTALYLCASSGAGWGLPSLDYWGQGTLTVTS 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-08-983-607-36
; Sequence 36, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 51

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100

Query Match 81.4%; Score 524.5; DB 3; Length 122;
Best Local Similarity 85.3%; pred. No. 1.8e-44;
Matches 104; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

[illegible]

```

RECORD 15
US-08-146-206C-21
; Sequence 21, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146, 206C
; FILING DATE: 17-No. 6407213-1993

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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-21

Query Match      81.4%; Score 524.5; DB 4; Length 122;
Best Local Similarity 85.2%; Pred. No. 1.8e-44;
Matches 104; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
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Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSVISGGSTYY 60
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK-HTGGGVWDPIDYWGQGTLLTV 119
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGRVGYSLGLDYIWGGTLLTV 120
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 120 SS 121
   ||
Db 121 SS 122
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Search completed: March 13, 2003, 15:18:40
Job time : 19.6154 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:09 ; Search time 17.2192 Seconds
(without alignments)
323.890 Million cell updates/sec

Title: US-09-822-698A-3

Perfect score: 644

Sequence: 1 QVOLVQSGGLVPGGSLRL.....GGWDPIDYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	644	100.0	121	10	US-09-822-698A-3
2	644	100.0	381	10	US-09-822-698A-5
3	644	100.0	451	10	US-09-822-698A-26
4	548	85.1	121	10	US-09-840-459-92
5	543.5	84.4	120	12	US-10-025-687-4
6	541.5	84.1	116	10	US-09-840-459-80
7	536.5	83.3	240	9	US-09-968-561A-2
8	536.5	83.3	240	10	US-09-192-854-2
9	531.5	82.5	118	9	US-10-001-934-39
10	531.5	82.5	120	10	US-09-840-459-85
11	528.5	82.1	268	10	US-09-976-118-1
12	524	81.4	123	10	US-09-840-459-82
13	523.5	81.3	288	10	US-09-818-247-22
14	523	81.2	113	10	US-09-056-160B-11
15	523	81.2	119	10	US-09-811-123-3
16	522	81.1	249	12	US-10-039-785-53
17	521	80.9	125	10	US-09-840-459-76
18	521	80.6	125	10	US-09-840-459-84
19	519	80.6	127	10	US-09-840-459-87

20	518.5	80.5	128	10	US-09-840-459-77	Sequence 77, Appl
21	518.5	80.5	128	10	US-09-840-459-79	Sequence 79, Appl
22	515.5	80.0	116	9	US-09-300-425B-19	Sequence 19, Appl
23	515.5	80.0	124	10	US-09-840-459-89	Sequence 89, Appl
24	514.5	79.9	124	10	US-09-840-459-81	Sequence 81, Appl
25	512.5	79.6	263	9	US-09-956-086-3	Sequence 3, Appl
26	512.5	79.6	263	9	US-09-956-087-3	Sequence 3, Appl
27	512.5	79.6	283	9	US-09-985-442-6	Sequence 6, Appl
28	512.5	79.6	283	10	US-09-983-580-6	Sequence 6, Appl
29	511	79.3	449	10	US-09-736-371B-21	Sequence 21, Appl
30	509	79.0	117	10	US-09-840-459-83	Sequence 83, Appl
31	499.5	77.6	443	10	US-09-917-410-4	Sequence 4, Appl
32	498.5	77.4	128	10	US-09-840-459-78	Sequence 78, Appl
33	492.5	76.5	120	10	US-09-229-200A-26	Sequence 26, Appl
34	490	76.1	117	8	US-08-790-540A-2	Sequence 2, Appl
35	490	76.1	117	8	US-08-791-391A-2	Sequence 2, Appl
36	490	76.1	117	9	US-09-900-590-2	Sequence 21, Appl
37	489.5	76.0	120	10	US-09-229-200A-21	Sequence 27, Appl
38	487.5	75.7	120	10	US-09-229-200A-27	Sequence 27, Appl
39	484.5	75.2	120	10	US-09-229-200A-22	Sequence 22, Appl
40	484	75.2	127	10	US-09-811-737-1	Sequence 1, Appl
41	484	75.2	255	10	US-09-811-737-15	Sequence 15, Appl
42	482.5	74.9	118	9	US-09-423-800-56	Sequence 56, Appl
43	482.5	74.9	137	9	US-09-423-800-77	Sequence 77, Appl
44	479.5	74.5	120	10	US-09-229-200A-24	Sequence 24, Appl
45	478.5	74.3	120	10	US-09-229-200A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match 100.0%; Score 644; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.8e-46;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVOLVQSGGLVPGGSLRLSCAASGFTFRSNAMGVRAQPGKGLWVSGISGGSTYY 60
|||||
Db 1 QVOLVQSGGLVPGGSLRLSCAASGFTFRSNAMGVRAQPGKGLWVSGISGGSTYY 60
|||||

QY 61 ADSVKGRFTISRDNSKNTLYLQMSLRADETAVYYCAKHTGGVWDPIIDYWGQGLTVTVS 120
|||||
Db 61 ADSVKGRFTISRDNSKNTLYLQMSLRADETAVYYCAKHTGGVWDPIIDYWGQGLTVTVS 120
|||||

QY 121 S 121

Db 121 S 121

RESULT 2

RESULT 4
US-09-840-459-92
; Sequence 92, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459

PRIOR APPLICATION NUMBER: PCT/US01/03537
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 09/497,625
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: 09/359,193
 PRIOR FILING DATE: 1999-07-22
 PRIOR APPLICATION NUMBER: 09/121,781
 PRIOR FILING DATE: 1998-07-23
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 92
 LENGTH: 121
 TYPE: PRT
 ORGANISM: Homo sapiens
 5'-09-840-459-92

PRIOR APPLICATION NUMBER: 09/359,193
 PRIOR FILING DATE: 1999-07-22
 PRIOR APPLICATION NUMBER: 09/121,781
 PRIOR FILING DATE: 1998-07-23
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 92
 LENGTH: 121

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-92

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Query Match      85.1%; Score 548; DB 10; Length 121;
Best Local Similarity 87.6%; Pred. No. 2.6e-38;
Matches 106; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
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RESULT 5
US-10-025-697-4
; Sequence 4, Application US/10025697
; Patent No. US2002014225A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONST
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,697
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 120

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region

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US-10-025-687-4

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Query Match      84.4%; Score 543.5; DB 12; Length 120;
Best Local Similarity 87.6%; Pred. No. 6.1e-38;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVOLVSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGISGGSTYY 60
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Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSAISGGSTYY 60
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTS 119
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QY 121 S 121
   |
Db 120 S 120
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```

RESULT 6

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US-09-840-459-80
; Sequence 80, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher /
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa

```

```

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840.459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-840-459-80
Query Match      83.3%; Score 536.5; DB 9; Length 240;
Best Local Similarity 86.8%; Pred. No. 4.5e-37;
Matches 105; Conservative 3; Mismatches 8; Indels 5; Gaps 1;

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```

QY 1 QVOLVSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGISGGSTYY 60
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSAISGGSTYY 60
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKSYGA-----FDYWGGQGLTVTS 115
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QY 121 S 121
   |
Db 116 S 116
   |

```

RESULT 8

```

US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian

```

```

; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2

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Query Match      83.3%; Score 536.5; DB 10; Length 240;
Best Local Similarity 86.8%; Pred. No. 4.5e-37;
Matches 105; Conservative 3; Mismatches 8; Indels 5; Gaps 1;

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QY 1 QVOLVSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGISGGSTYY 60
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSAISGGSTYY 60
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKSYGA-----FDYWGGQGLTVTS 115
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 7

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US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:

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Qy	121 S 121
Db	116 S 116

RESULT 9

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US-10-001-934-39
; Sequence 39, Application US/10001934
; Publication No. US20030032782A1
; GENERAL INFORMATION:
; APPLICANT: NAGY, ZOLTAN
; TITLE OF INVENTION: HUMAN PEPTIDES/
; FILE OF INVENTION: KILLING OF CEL
; FILE REFERENCE: GPCG-P01-003
; CURRENT APPLICATION NUMBER: US/10/0
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-934-39

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Query Match 82.5%; Score 531.5; DB 9; Length 118;
Best Local Similarity 87.6%; Pred. NO. 5.7e-37;
Matches 106; Conservative 4; Mismatches 8; Indels 3; Gaps 2;

Qy	1	QVQLVQSGGGLVPGGSLRLS	CAASGFTPRSNAMGVWV	RQAPKGLIEWVSGISCSGSGTYY	60
Db	1	EVQLVESGGGLVPGGSLRLS	CAASGFTSSYAMSVWV	RQAPKGLIEWVSAISGSGSTYY	60
Qy	61	ADSVKGRTTISRNSKNTLY	LQNMURAEDTAVYYCAK	HGTGGGVWDPIDYWGQGLTLVTVS	120
Db	61	ADSVKGRTTISRNSKNTLY	LQNMURAEDTAVYYCAR	--GYGRYSP--DLWGQGLTLVTVS	117
Qy	121	S	121		
Db	118	S	118		

RESULT 10

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US-09-840-459-85
; Sequence 85, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarrant
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-85

```

Query Match	82.5%	Score 531.5;	DB 10;	Length 120;
Best Local Similarity	87.6%;	Pred. NO. 5.8e-37;		
Matches 106;	Conservative	3;	Mismatches 11;	Indels 1;
				Gaps 1;

Qy	60
Db	60
Qy	120
Db	119
Qy	121
Db	120

RESULT 17

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US-09-976-118-1
: Sequence 1, Application US/09976118
: Patent No. US20020058033A1
: GENERAL INFORMATION:
: APPLICANT: Ralsch, Kevin Paul
: APPLICANT: Curiel, David T.
: APPLICANT: Bonner, James Allen
: TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
: TITLE OF INVENTION: Single-Chain Antibodies
: FILE REFERENCE: D6355
: CURRENT APPLICATION NUMBER: US/09/976,118
: CURRENT FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: US 60/240,353
: PRIOR FILING DATE: 2000-10-13
: NUMBER OF SEQ ID NOS: 2
: SEQ ID NO 1
: LENGTH: 268
: TYPE: PRT
: ORGANISM: artificial sequence
: FEATURE:
: OTHER INFORMATION: amino acid sequence of anti-EGFR scFv
: OTHER INFORMATION: clone pSEX81-6
US-09-976-118-1

```

Query Match	82.1%;	Score 528.5;	DB 10;	Length 268;
Best Local Similarity	83.1%;	Pred. NO. 2.3e-36;		
Matches 103;	Conservative	6;	Mismatches 12;	Indels 3;
Gaps	1;			

[illegible]

RESULT 12

```

US-09-840-459-82
: Sequence 82, Application US/09840459
: Patent No. US20020150576A1.
: GENERAL INFORMATION:
: APPLICANT: LaRosa, Gregory J.
: APPLICANT: Horvath, Christopher
: APPLICANT: Newman, Walter
: APPLICANT: Jones, S. Farran
: APPLICANT: O'Brien, Stobhan H.
: APPLICANT: O'Keefe, Theresa
: TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
: TITLE OF INVENTION: METHODS OF USE THEREFOR

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; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-82

Query Match      81.4%; Score 524; DB 10; Length 123;
Best Local Similarity 83.2%; Pred. No. 2.4e-36;
Matches 104; Conservative 6; Mismatches 9; Indels 6; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG---GGVMDPIDYWGQGL 116
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG---GGVMDPIDYWGQGL 116

QY 117 VTVSS 121
Db 119 VTVSS 123

RESULT 13
US-09-818-247-22
; Sequence 22, Application US/09818247
; Patent No. US20020102657A1
; GENERAL INFORMATION:
; APPLICANT: Mostov, Keith E.
; APPLICANT: Chapin, Steven J.
; APPLICANT: Richman-Eisenstat, Janice
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Stalk Region of pIgR and Methods of Use Therein
; FILE REFERENCE: 18062B-000910US
; CURRENT APPLICATION NUMBER: US/09/818,247
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: WO PCT/US01/09699
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,197
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,198
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 22
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Pelb/4AF/myc/6HIS
US-09-818-247-22

Query Match      81.3%; Score 523.5; DB 10; Length 288;
Best Local Similarity 85.4%; Pred. No. 6.2e-36;
Matches 105; Conservative 3; Mismatches 10; Indels 5; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG---GGVMDPIDYWGQGL 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG---GGVMDPIDYWGQGL 120

QY 121 S 121
Db 113 S 113

US-09-056-160B-11
; Sequence 11, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-11

Query Match      81.2%; Score 523; DB 10; Length 113;
Best Local Similarity 85.1%; Pred. No. 2.7e-36;
Matches 103; Conservative 3; Mismatches 7; Indels 8; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG---GGVMDPIDYWGQGL 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG---GGVMDPIDYWGQGL 120

QY 121 S 121
Db 113 S 113
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RESULT 15
US-09-811-123-3
; Sequence 3, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-3

Query Match 81.2%; Score 523; DB 10; Length 119;
Best Local Similarity 85.1%; Pred. No. 2.8e-36;
Matches 103; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

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:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAVISGDDGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVDPIDYWGOGTLVTVS 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARGV--YSLDYWGOGTLVTVS 118

Qy 121 S 121
|
Db 119 S 119

Search completed: March 13, 2003, 15:30:31
Job time : 18.2192 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 15:14:49 ; Search time 257.823 Seconds
(without alignments)
302.582 Million cell updates/sec

Title: US-09-822-698A-3

Perfect score: 644

Sequence: 1 QVOLVQSGGLVPGGSLRL.....GGVWDPIYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main: *

- 1: /cgn2_6/ptodata/2/paa/pctus_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/us06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/us07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/us08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/us081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/us082_COMB.pep.*
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- 9: /cgn2_6/ptodata/2/paa/us085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/us086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/us087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/us088_COMB.pep.*
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- 14: /cgn2_6/ptodata/2/paa/us090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/us091_COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/us092_COMB.pep.*
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- 20: /cgn2_6/ptodata/2/paa/us096_COMB.pep.*
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- 22: /cgn2_6/ptodata/2/paa/us098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/us099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/us100_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/us101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/us102_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/us60_COMB.pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	121	19	US-09-538-913-3
2	644	100.0	121	22	US-09-822-698A-3
3	644	100.0	381	19	US-09-538-913-5
4	644	100.0	381	22	US-09-822-698A-5
5	644	100.0	451	22	US-09-822-698A-26
6	548	85.1	121	1	PCT-US01-03537-92

7	548	85.1	121	18	US-09-497-625-92	Sequence 92, Appl
8	548	85.1	121	18	US-09-497-625A-92	Sequence 92, Appl
9	548	85.1	121	22	US-09-840-459-92	Sequence 92, Appl
10	548	85.1	129	21	US-09-791-537-116631	Sequence 116631,
11	545.5	84.7	229	21	US-09-791-537-128087	Sequence 128087,
12	544.5	84.5	222	1	PCT-US02-12801-152	Sequence 152, App
13	543.5	84.4	120	1	PCT-US02-12202-4	Sequence 4, Appli
14	543.5	84.4	120	18	US-09-490-070-38	Sequence 38, Appl
15	543.5	84.4	120	18	US-09-490-070-63	Sequence 63, Appl
16	543.5	84.4	120	24	US-10-025-687-4	Sequence 4, Appli
17	543.5	84.4	120	25	US-10-125-687-4	Sequence 4, Appli
18	543.5	84.4	281	18	US-09-490-070-178	Sequence 178, App
19	543	84.3	119	21	US-09-791-537-31899	Sequence 31899, A
20	542.5	84.2	124	24	US-10-040-244-16	Sequence 16, Appl
21	542	84.2	119	21	US-09-791-537-79748	Sequence 79748, A
22	542	84.2	145	21	US-09-791-537-19722	Sequence 80, Appl
23	541.5	84.1	116	1	PCT-US01-03537-80	Sequence 80, Appl
24	541.5	84.1	116	18	US-09-497-625A-80	Sequence 110614,
25	541.5	84.1	116	21	US-09-791-537-110614	Sequence 80, Appl
26	541.5	84.1	116	22	US-09-840-459-80	Sequence 80, Appl
27	541.5	84.1	123	21	US-09-791-537-106410	Sequence 106410,
28	541	84.0	221	1	PCT-US02-12801-171	Sequence 171, App
29	541	84.0	224	23	US-09-972-656-68	Sequence 68, Appl
30	541	84.0	224	23	US-09-972-656-68	Sequence 55187, A
31	540.5	83.9	128	21	US-09-791-537-55187	Sequence 1975, Ap
32	540.5	83.9	246	1	PCT-US01-19110-1975	Sequence 1975, Ap
33	540.5	83.9	246	22	US-09-880-748-1975	Sequence 102538,
34	538.5	83.6	120	21	US-09-791-537-102538	Sequence 78365, A
35	538.5	83.6	238	21	US-09-791-537-78365	Sequence 28, Appl
36	537.5	83.5	131	8	US-08-497-647E-28	Sequence 1922, Ap
37	537.5	83.5	239	1	PCT-US01-19110-1922	Sequence 1922, Ap
38	537.5	83.5	239	22	US-09-880-748-1922	Sequence 124246,
39	536.5	83.3	122	21	US-09-791-537-124246	Sequence 116038,
40	536.5	83.3	130	21	US-09-791-537-116038	Sequence 2, Appli
41	536.5	83.3	240	15	US-09-192-854-2	Sequence 2, Appli
42	536.5	83.3	240	19	US-09-511-939-2	Sequence 2, Appli
43	536.5	83.3	240	23	US-09-968-561A-2	Sequence 87873, A
44	535.5	83.2	120	21	US-09-791-537-87873	Sequence 102572,
45	535.5	83.2	122	21	US-09-791-537-102572	

ALIGNMENTS

RESULT 1

US-09-538-913-3

; Sequence 3, Application US/09538913

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Paula

; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: seqlist DYX-15

; CURRENT APPLICATION NUMBER: US/09/538,913

; CURRENT FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 3

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-538-913-3

Query Match 100.0%; Score 644; DB 19; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.le-60;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVOLVQSGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGSGSTYY 60

Db 1 QVOLVQSGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGSGSTYY 60

Qy 61 ADVSKGRTTISRDNKNTLYLQMNLRADETAVYVCAKHTGGVWDPIDYWGQGLTVTVSS 120

|||||

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Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
Qy 121 S 121
|
Db 121 S 121

RESULT 2
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PHI Fab antibody
US-09-822-698A-3

Query Match 100.0%; Score 644; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.1e-60;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
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Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
|
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120

Qy 121 S 121
|
Db 121 S 121

RESULT 3
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPHI-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match 100.0%; Score 644; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
|
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
|
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120

Qy 121 S 121
|
Db 121 S 121

RESULT 4
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPHI-IL-2
US-09-822-698A-5

Query Match 100.0%; Score 644; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
|
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
|
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120

Qy 121 S 121
|
Db 121 S 121

RESULT 5
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1
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Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKDISWGDLGLDYWGQGLTVTS 120
Qy 121 S 121
Db 121 S 121

RESULT 9
US-09-840-459-92
; Sequence 92, Application US/09840459
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 92
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-92

Query Match 85.1%; Score 548; DB 22; Length 121;
Best Local Similarity 87.6%; Pred. No. 3.9e-50;
Matches 106; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSTYY 60

Qy 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120
Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKDISWGDLGLDYWGQGLTVTS 120

Qy 121 S 121
Db 121 S 121

RESULT 10
US-09-791-537-116631
; Sequence 116631, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBR
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116631
; LENGTH: 129
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-791-537-116631

Query Match 85.1%; Score 548; DB 21; Length 129;
Best Local Similarity 87.6%; Pred. No. 4.2e-50;
Matches 106; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSTYY 60

Qy 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120
Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKDISWGDLGLDYWGQGLTVTS 120

Qy 121 S 121
Db 121 S 121

RESULT 11
US-09-791-537-128087
; Sequence 128087, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 128087
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-128087

Query Match 84.7%; Score 545.5; DB 21; Length 229;
Best Local Similarity 88.4%; Pred. No. 1.6e-49;
Matches 107; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

Qy 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 QVOLVESGGGLVQPGGSLRLSCAASGFTFRSYAMSWVRQAPGKGLWVSAISGGSTYY 60

Qy 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120
Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAR-VGVDRWYPADYWGQGLTVTS 119

Qy 121 S 121
Db 120 S 120

RESULT 12
PCT-US02-12801-152
; Sequence 152, Application PC/TUS0212801
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; APPLICANT: Morphosys AG
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00074
; CURRENT APPLICATION NUMBER: PCT/US02/12801
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 222
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```
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-12801-152
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Query Match 84.5%; Score 544.5; DB 1; Length 222;
Best Local similarity 87.6%; Pred. No. 2e-49;
Matches 106; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

Qy	1	QVLVQSGGGVLVQPGGSLRLSCAASGFTTFRSNAMGWVQAQPKGLEWVSGISGGSTYY	60
Db	1	QVLVSEGGGLVQPGGSLRLSCAASGFTTSSYAMSWVQAQPKGLEWVSAISGGSTYY	60
Qy	61	ADSVKGRFTI SRDNSKNTLYQNSLRAREDYAVYCAKHTGGGVWDPIDYWGOGTLVTWS	120
Db	61	ADSVKGRFTI SRDNSKNTLYQNSLRAREDYAVYCAR---GAYFGLDYWGOGTLVTWS	117

Qy	121 S 121
Db	118 S 118

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RESULT 13
PCT-US02-12202-4
; Sequence 4, Application FC/TUS0212202
; GENERAL INFORMATION:
; APPLICANT: Abmaxis, Inc.
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-706
; CURRENT APPLICATION NUMBER: PCT/US02/12202
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
PCT-US02-12202-4

```

Query Match 84.4%; Score 543.5; DB 1; Length 120;
Best Local Similarity 87.6%; Pred. No. 1.2e-49;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps

QY	1	QVQLVQSGGGLVQPGGSLRLISCAASGFTTFRSNAMGWVRAQPKGLEWVSGITSGGGSTYY	60
Db	1	EVQLVESGGGLVQPGGSLRLISCAASGFTTSSYAMSVKVRQAPKGLEWYSAITSGGGSTYY	60
QY	61	ADSVAGRTTISRDNSKNTLYLQMNISRAEDTAVYYCAKHTGGVWDPIDYWGQGTLLVTVS	120
Db	61	ADSVAGRTTISRDNSKNTLYLQMNISRAEDTAVYYCARGGDGPY-AMDYWGQGTLLVTVS	119

QY	121	S	121
		-	
Db	120	S	120

```

RESULT 14
US-09-490-070-38
; Sequence 38, Application US/09490070
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (ZPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/025,769
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 38:
 09-490-070-38

Query Match 84.4%; Score 543.5; DB 18; Length 120;
Best Local Similarity 87.6%; Pred. No. 1.2e-49;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Qy 1 QVQLVQSGGIVQPQGLRLSCAASGFTFRSNAMGWVRQAPKGLEWVSIGSGGGTTY 60
:
db 1 EVLVESGGELVQPQGLRLSCAASGFTSSYAMSWVRQAPKGLEWVSATSGSGGGTTY 60

Qy 61 ADSVKGRFTISRDNKNTLYIQMNSRAEDTAVYYCAKHTGGGVWDPIDYWGQGTLVTVS 120
|||||
|||||
Dp 61 ADSVKGRFTISRDNKNTLYIQMNSRAEDTAVYYCARWGGDGYF-AMDYWGQGTLVTVS 119

QY	121	S	121
Db	120	S	120

RESULT 15
US-09-490-070-63
; Sequence 63, Application US/09490070
; GENERAL INFORMATION:
; APPLICANT: Knapplik, Achim

TITLE OF INVENTION: Protein/(Poly)peptide Libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

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; GPF. 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
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Search completed: March 13, 2003, 15:28:03
Job time : 259.073 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:15:24 ; Search time 44.2115 seconds
(without alignments)
355.800 Million cell updates/sec

Title: US-09-822-698A-3

Perfect score: 644

Sequence: 1 QVLVQSGGLVQGGSLRL.....GGWDPIDYWGQGLTVTVSS 121

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
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7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	543.5	84.4	120	5	US-09-490-153-38
2	543.5	84.4	120	5	US-09-490-153-63
3	543.5	84.4	281	5	US-09-490-153-178
4	541	84.0	224	1	PCT-US02-33556-68
5	540.5	83.9	246	1	PCT-US02-36496-1975
6	540.5	83.9	246	6	US-10-293-418-1975
7	537.5	83.5	239	1	PCT-US02-36496-1922
8	537.5	83.5	239	6	US-10-293-418-1922
9	536.5	83.3	240	5	US-09-968-744A-2
10	535	83.1	244	1	PCT-US02-40597-45
11	535	83.1	244	6	US-10-322-673-45
12	534.5	83.0	223	1	PCT-US02-33556-86
13	532	82.6	243	1	PCT-US02-40597-55
14	532	82.6	243	6	US-10-322-673-55
15	531.5	82.5	122	6	US-10-180-648-13
16	531.5	82.5	467	6	US-10-180-648-2
17	530	82.3	123	1	PCT-US02-32613-59
18	530	82.3	123	6	US-10-269-805-59
19	529.5	82.2	246	1	PCT-US02-36496-1980
20	529.5	82.2	246	6	US-10-293-418-1980
21	528.5	82.1	246	1	PCT-US02-26246A-80
22	527.5	81.9	248	1	PCT-US02-26246A-78
23	527.5	81.9	252	1	PCT-US02-36496-1637
24	527.5	81.9	252	6	US-10-293-418-1637
25	526.5	81.8	248	1	PCT-US02-36496-921
26	526.5	81.8	248	1	PCT-US02-36496-1456

27	526.5	81.8	248	6	US-10-293-418-921	Sequence 921, Appl
28	526.5	81.8	248	6	US-10-293-418-1456	Sequence 1456, Ap
29	526.5	81.8	250	1	PCT-US02-36496-1420	Sequence 1420, Ap
30	526.5	81.8	250	6	US-10-293-418-1420	Sequence 1420, Ap
31	526	81.7	119	1	PCT-US02-38540-18	Sequence 18, Appl
32	526	81.7	119	6	US-10-309-764-18	Sequence 18, Appl
33	526	81.7	138	1	PCT-US02-38540-87	Sequence 87, Appl
34	526	81.7	138	6	US-10-309-764-87	Sequence 87, Appl
35	525.5	81.6	251	1	PCT-US02-36496-1740	Sequence 1740, Ap
36	525.5	81.6	251	6	US-10-293-418-1740	Sequence 1740, Ap
37	525	81.5	123	1	PCT-US02-32613-23	Sequence 23, Appl
38	525	81.5	123	6	US-10-269-805-23	Sequence 23, Appl
39	524.5	81.4	247	1	PCT-US02-36496-1923	Sequence 1923, Ap
40	524.5	81.4	247	6	US-10-293-418-1923	Sequence 1923, Ap
41	524.5	81.4	253	1	PCT-US02-26246A-76	Sequence 76, Appl
42	523	81.2	113	4	US-08-975-329B-6	Sequence 6, Appli
43	523	81.2	113	6	US-10-234-671-11	Sequence 11, Appl
44	523	81.2	119	6	US-10-268-501-6	Sequence 6, Appli
45	521.5	81.0	124	6	US-10-031-722-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-490-153-38

; Sequence 38, Application US/09490153

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,153

; FILING DATE: 24-Jan-2000

; PRIORITY INFORMATION:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,784

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 120 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-490-153-38

```

Qy 61 ADSVKGRTTISRDNKNTLYLQNNLSRAEDTAVVYCAKHTGGVWDPIDYWGQGLTIVTS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTTISRDNKNTLYLQNNLSRAEDTAVVYCARWGGDGFY-AMDYWGQGLTIVTS 119
Qy 121 $ 121
Db 120 $ 120
|
RESULT 3
US-09-490-153-178
; Sequence 178, Application US/09490153
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-09-490-153-178
Query Match 84.4%; Score 543.5; DB 5; Length 281;
Best Local Similarity 87.6%; Pred. No. 2.3e-38;
Matches 106; Conservative 5; Mismatches 9; Indels 1; Gaps
Qy 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGGTTY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 26 EVOLVESGGGLVQPGGSLRLSCAASGFTFSSAMSWVRQAPGKLEWWSAISGSGGTTY 85
Qy 61 ADSVKGRTTISRDNKNTLYLQNNLSRAEDTAVVYCAKHTGGVWDPIDYWGQGLTIVTS 120
Db 86 ADSVKGRTTISRDNKNTLYLQNNLSRAEDTAVVYCARWGGDGFY-AMDYWGQGLTIVTS 144
Qy 121 $ 121
Db 145 $ 145
|

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RESULT 4
PCT-US02-33556-68
; Sequence 68, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Angen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 68
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-33556-68

Query Match 84.0%; Score 541; DB 1; Length 224;
Best Local Similarity 87.6%; Pred. No. 3e-38;
Matches 106; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSVWRQAPGKGLWVSAISGGSTYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIYWGQGLTVTS 120
Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKDRVGYSSLDYWGQGLTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 5
PCT-US02-36496-1975
; Sequence 1975, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1975
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-1975

Query Match 83.9%; Score 540.5; DB 1; Length 246;
Best Local Similarity 89.3%; Pred. No. 3.6e-38;
Matches 108; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFSSYAMSVWRQAPGKGLWVSAISGGSTYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIYWGQGLTVTS 120
Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKEFFGYV-LTDYWGRTLVTS 119
QY 121 S 121
Db 120 S 120

RESULT 6
US-10-293-418-1975
; Sequence 1975, Application US/10293418
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1975
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1975

Query Match 83.9%; Score 540.5; DB 6; Length 246;
Best Local Similarity 89.3%; Pred. No. 3.6e-38;
Matches 108; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFSSYAMSVWRQAPGKGLWVSAISGGSTYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIYWGQGLTVTS 120
Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKEFFGYV-LTDYWGRTLVTS 119
QY 121 S 121
Db 120 S 120

RESULT 7
PCT-US02-36496-1922
; Sequence 1922, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1922
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-1922

Query Match 83.5%; Score 537.5; DB 1; Length 239;
Best Local Similarity 86.0%; Pred. No. 6.2e-38;
Matches 104; Conservative 5; Mismatches 7; Indels 5; Gaps 1;


```
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKVRPGRSGYFDYWGGRGLTVTVS 120
QY 121 S 121
Db 121 S 121

RESULT 11
US-10-322-673-45
; Sequence 45, Application US/10322673
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 45
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM029B01 scFv
US-10-322-673-45

Query Match 83.1%; Score 535; DB 6; Length 244;
Best Local Similarity 87.6%; Pred. No. 1e-37;
Matches 106; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60
Db 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAISGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKVHRCRSGYFDYWGGRGLTVTVS 120
QY 121 S 121
Db 121 S 121

RESULT 12
PCT-US02-33556-86
; Sequence 86, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
PCT-US02-33556-86

Query Match 83.0%; Score 534.5; DB 1; Length 223;
Best Local Similarity 87.5%; Pred. No. 1e-37;
Matches 105; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 2 VOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYYA 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAISGSGSTYYA 61
QY 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVSS 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-TSNAGGPIDYWGQGLTVTVSS 120

RESULT 13
PCT-US02-40597-55
; Sequence 55, Application PC/TUS0240597
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PCT
; CURRENT APPLICATION NUMBER: PCT/US02/40597
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 55
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM075A01 scFv
PCT-US02-40597-55

Query Match 82.6%; Score 532; DB 1; Length 243;
Best Local Similarity 85.1%; Pred. No. 1.8e-37;
Matches 103; Conservative 6; Mismatches 6; Indels 6; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAISGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCVK----GAW--LDYWGRTWTVTVS 114
QY 121 S 121
Db 115 S 115

RESULT 14
US-10-322-673-55
; Sequence 55, Application US/10322673
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
```

; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 55
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM075A01 scFv
US-10-322-673-55

Query Match 82.5%; Score 532; DB 6; Length 243;
Best Local Similarity 85.1%; Pred. No. 1.8e-37;
Matches 103; Conservative 6; Mismatches 6; Indels 6; Gaps 2;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:|||:||||||||||||||||||| ||||||||||||||| |||||||||
Db 1 EVQLLESGGGLVOPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLWVSAISGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKHTGGGVNDPDIYWGQGTLLVTVS 120
:||||:||||||||||||||||||||||| ||| ||| :||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCVK----GAW--LDYWGRTMTVTVS 114

Qy 121 S 121
|
Db 115 S 115

RESULT 15
US-10-180-648-13
; Sequence 13, Application US/10180648
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPG
; FILE REFERENCE: 06843, 0049-00000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-13

Query Match 82.5%; Score 531.5; DB 6; Length 122;
Best Local Similarity 85.5%; Pred. No. 1e-37;
Matches 106; Conservative 4; Mismatches 9; Indels 5; Gaps 2;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
:||||:||||||||||||||||||| ||||||||||||||| |||||||||
Db 1 EVQLLESGGGLVOPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLWVSGITGGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKHTGGGV---WDPIDYWGQGTLLV 117
:||||:||||||||||||||||||||||| ||| ||| :||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKDPGTTVINSW--FDPWGQGTLLV 118

Qy 118 TVSS 121
*.

Db 119 TVSS 122

Search completed: March 13, 2003, 15:29:45
Job time : 45.2115 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:09 ; Search time 20.9423 Seconds
(without alignments)
555.443 Million cell updates/sec

Title: US-09-822-698a-3

Perfect score: 644

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....GGVWDPIDYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR.73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	84.3	119	2 S31107	Ig heavy chain - h
2	542	84.2	119	2 C36005	Ig heavy chain v r
3	535.5	83.2	120	2 S48798	Ig heavy chain v r
4	534	82.9	140	2 S31686	Ig heavy chain v r
5	531	82.5	119	2 S31108	Ig heavy chain - h
6	528	82.0	119	2 D36005	Ig heavy chain v r
7	528	82.0	121	2 I55673	Ig heavy chain - h
8	527	81.8	127	2 S38489	Ig heavy chain - h
9	527	81.8	140	2 S31588	Ig heavy chain v r
10	526	81.7	134	2 S31699	Ig heavy chain v r
11	522	81.1	123	2 S31114	Ig heavy chain - h
12	522	81.1	138	2 S31666	Ig heavy chain v r
13	519	80.6	160	2 S03271	Ig heavy chain pre
14	518.5	80.5	124	2 S20782	Ig heavy chain v r
15	518	80.4	120	2 S36278	Ig heavy chain v r
16	509.5	79.1	112	2 PH1647	Ig heavy chain v r
17	508.5	79.0	116	2 S31110	Ig heavy chain - h
18	503	78.1	109	2 PH1649	Ig heavy chain v r
19	501	77.8	121	2 S19666	Ig heavy chain v r
20	501	77.8	140	2 C30532	Ig heavy chain pre
21	498	77.3	121	2 G36005	Ig heavy chain v r
22	495.5	76.9	108	2 PH1648	Ig heavy chain v r
23	494	76.7	134	2 S31679	Ig heavy chain v r
24	492.5	76.5	122	2 S20772	Ig heavy chain v r
25	492	76.4	121	2 S31113	Ig heavy chain - h
26	492	76.4	143	2 S23624	Ig heavy chain v r
27	490	76.1	135	2 S31598	Ig heavy chain v r
28	489.5	76.0	120	2 S44111	Ig heavy chain v-D
29	489.5	76.0	151	2 A60943	Ig heavy chain pre

```

30      489      75.9      125      2 S30531      Ig heavy chain v r
31      488.5      75.9      114      2 S46390      Ig heavy chain v r
32      488.5      75.9      140      2 S70442      Ig heavy chain pre
33      486.5      75.5      118      2 S31105      Ig heavy chain (su
34      485.5      75.4      114      2 S31120      Ig heavy chain - h
35      482      74.8      119      2 F36005      Ig heavy chain v r
36      481.5      74.8      128      2 S26790      Ig heavy chain v r
37      481.5      74.8      128      2 S31595      Ig heavy chain v r
38      481      74.7      118      2 S31121      Ig heavy chain - h
39      481      74.7      120      2 S36273      Ig heavy chain v r
40      480.5      74.6      114      2 S46391      Ig heavy chain v r
41      480.5      74.6      120      2 S31112      Ig heavy chain - h
42      480.5      74.6      147      2 I37780      Ig variable region
43      480      74.5      117      2 S78486      Ig heavy chain v r
44      480      74.5      132      2 S31603      Ig heavy chain v r
45      479.5      74.5      122      2 E36005      Ig heavy chain v r

```

ALIGNMENTS

RESULT 1

S31107

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C:Accession: S31107

R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur

Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third com

A:Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31107

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-119 <RAA>

A:Cross-references: EMBL:X62955

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <INM>

Query Match 84.3%; Score 543; DB 2; Length 119;

Best Local Similarity 87.6%; Pred. No. 2e-40;

Matches 106; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSNAMGVNRQAPGKLEWVSGISGSGSTVY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVNRQAPGKLEWVSAISGSGSTVY 60

QY 61 ADSVKGRFTISDRNSKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120

Db 61 ADSVKGRFTISDRNSKNTLYLQMNLSRAEDTAVYYCAKDPGASY--FDYWGQGLTVTVS 118

QY 121 S 121

Db 119 S 119

RESULT 2

C36005

Ig heavy chain v region (30pl) - human

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996

C:Accession: C36005

R:Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable g

A:Reference number: A36005; MUID:90349571; PMID:2117273

A:Accession: C36005

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <SCH>

A:Cross-references: GB:M18513

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 542; DB 2; Length 119;
Best Local Similarity 87.6%; Pred. No. 2.4e-40;
Matches 106; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKCLEWVSGISGGSTYY 60
DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSAISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 118

QY 121 S 121
DB 119 S 119

RESULT 3
S48798
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S48798
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48798
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MAH>
A:Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 535.5; DB 2; Length 120;
Best Local Similarity 86.9%; Pred. No. 9e-40;
Matches 106; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSAISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTV 119
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDR--GFWSGYKDYWGQGLTVTV 118

QY 120 SS 121
DB 119 SS 120

RESULT 4
S31686
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31686
R:Guinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31686
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CU1>
A:Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 534; DB 2; Length 140;
Best Local Similarity 86.0%; Pred. No. 1.4e-39;
Matches 104; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSAISGGSTYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
DB 80 SDSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 139
QY 121 S 121
DB 140 S 140

RESULT 5
S31108
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31108
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31108
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62956
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 531; DB 2; Length 119;
Best Local Similarity 85.5%; Pred. No. 2.2e-39;
Matches 106; Conservative 3; Mismatches 7; Indels 8; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSAISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKH---TGGGVWDPIDYWGQGLTV 117
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDRRLTG----TFDYWGQGLTV 115

QY 118 TVSS 121
DB 116 TVSS 119

RESULT 6
D36005
Ig heavy chain V region (M43) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: D36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: D36005
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34024
C:Genetics:

```
A:Gene: GDB:IGH@; IGHDIY1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      82.0%; Score 528; DB 2; Length 119;
Best Local Similarity 86.0%; Pred. No. 4e-39;
Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGSGSTYY 60
Db 1 EVQLLESGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSAISGSGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVNDPDIYWGQGLTVTS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVNDPDIYWGQGLTVTS 118

Qy 121 S 121
Db 119 S 119

RESULT 7
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1995 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I55673
J.Knight, G.B.; Agnello, V.; Bonagura, V.; Barnes, J.L.; Panka, D.J.; Zhang, Q.X.
J. Exp. Med. 178, 1903-1911, 1993
A:Title: Human rheumatoid factor cross-idiotypes. IV. Studies on WA Xid-positive Igm with
tinct from the 17.109 and G6 Xids.
A:Reference number: I55673; MUID:94065558; PMID:8245772
A:Accession: I55673
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-121 <RES>
A:Cross-references: GB:M87268; NID:g186197; PIDN:AAC37536.1; PID:g186198
C:Genetics:

A:Gene: GDB:IGHM
A:Cross-references: GDB:120086; OMIM:147020
A:Map position: 14q32.33-14q32.33
A:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      82.0%; Score 528; DB 2; Length 121;
Best Local Similarity 83.1%; Pred. No. 4.1e-39;
Matches 103; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGSGSTYY 60
Db 1 EVQLLESGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSAISGSGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVNDPDIYWGQGLTV 117
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAAPRHAGS---PPDYWGQGLTV 117

Qy 118 TVSS 121
Db 118 TVSS 121

RESULT 8
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R.Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a p

A:Reference number: S38488
A:Accession: S38489
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:723028; NID:g414025; PIDN:CAA80563.1; PID:g414026
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.8%; Score 527; DB 2; Length 127;
Best Local Similarity 82.0%; Pred. No. 5.2e-39;
Matches 105; Conservative 3; Mismatches 10; Indels 10; Gaps 2;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGSGSTYY 60
Db 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSAISGSGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVNDPDIYWGQGLTV 111
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVNDPDIYWGQGLTV 119

Qy 112 GQGLTVTV 119
Db 120 GQGLTVTV 127

RESULT 9
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31588
R.Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from
A:Reference number: S31585
A:Accession: S31588
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      81.8%; Score 527; DB 2; Length 140;
Best Local Similarity 85.1%; Pred. No. 5.8e-39;
Matches 103; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGSGSTYY 60
Db 20 EVQLLESGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSAISGSGSTYY 79

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVNDPDIYWGQGLTVTS 120
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKDHYSNYYFDYWGQGLTVTS 139

Qy 121 S 121
Db 140 S 140

RESULT 10
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31699
R.Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31585
```

RESULT 12
S31666
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31666
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31595

RESULT 14
S20782
Ig heavy chain v region - human

```
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: S20782
R:Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Description: Analysis of the IgA and IgG rearranged VH repertoire of human cord blood
A:Reference number: S20765
A:Accession: S20782
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <MOR>
A:Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      80.5%; Score 518.5; DB 2; Length 124;
Best Local Similarity 83.9%; Pred. No. 2.e-38;
Matches 104; Conservative 4; Mismatches 13; Indels 3; Gaps 1;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGGSTYY 60
Db 1 EVQLLEGGGGLVQPGGSLRLSCAASGFTFSYAMNVRQAPCKGLEWVSTIISGGSTYY 60

Qy 61 ADSVKGRFTISRNSKNTLYLQMSLRAEDTAVYYCAKH--TGGGVWDPTIDYWGQGLTV 117
Db 61 ADSVKGRFTISRNSKNTLYLQMSLRAEDTAVYYCAKERTAIKGVIPHFYDWGQGLTV 120

Qy 118 TVSS 121
Db 121 TVSS 124

RESULT 15
S36278
Ig heavy chain V region (clone alpha-THY-23) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36278
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; M0ID:93178448; PMID:7679990
A:Accession: S36278
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-120 <GRI>
A:Cross-references: EMBL:Z18830; NID:g33114; PIDN:CAA79282.1; PID:g939894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 518; DB 2; Length 120;
Best Local Similarity 85.8%; Pred. No. 3.e-38;
Matches 103; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGGSTYY 60
Db 1 QVQLQSGGVVQVQGRSMRLSCAASGFNFRSYCMHWVRQAPCKGLEWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRNSKNTLYLQMSLRAEDTAVYYCAKH--TGGGVWDPTIDYWGQGLTVTS 120
Db 61 ADSVKGRFTISRNSKNTLYLQMSLRAEDTAVYYCAKSMIVVARYFDYWGQGLTVTS 120

Search completed: March 13, 2003, 15:17:50
Job time : 21.9423 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:06:24 ; Search time 12.1 Seconds
(without alignments)
414.763 Million cell updates/sec

Title: US-09-822-698a-3
Perfect score: 644
Sequence: 1 QVQLVQSGGGLVPGGSLRL.....GGWDPIDVWGGLTVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	471	73.1	117	1 HV3C_HUMAN	P01764 homo sapien
2	466.5	72.4	114	1 HV3B_HUMAN	P01763 homo sapien
3	456.5	70.9	122	1 HV3A_HUMAN	P01768 homo sapien
4	450.5	70.0	122	1 HV3A_HUMAN	P01768 homo sapien
5	449.5	69.8	116	1 HV3T_HUMAN	P01781 homo sapien
6	447	69.4	121	1 HV3J_HUMAN	P01771 homo sapien
7	438.5	68.1	116	1 HV05_CARAU	P19181 carassius a
8	437.5	67.9	122	1 HV3H_HUMAN	P01769 homo sapien
9	437.5	67.9	126	1 HV3K_HUMAN	P01772 homo sapien
10	435.5	67.6	136	1 HV16_MOUSE	P01783 mus musculu
11	435	67.5	115	1 HV3D_HUMAN	P01765 homo sapien
12	432	67.1	117	1 HV02_CANFA	P01785 canis fami
13	428	66.5	119	1 HV3I_HUMAN	P01770 homo sapien
14	427	66.3	115	1 HV3F_HUMAN	P01767 homo sapien
15	422.5	65.6	120	1 HV3U_HUMAN	P01782 homo sapien
16	419.5	65.1	119	1 HV3M_HUMAN	P01774 homo sapien
17	419	65.1	120	1 HV3E_HUMAN	P01766 homo sapien
18	417.5	64.8	119	1 HV3N_HUMAN	P01775 homo sapien
19	414	64.3	119	1 HV3L_HUMAN	P01773 homo sapien
20	400.5	62.2	114	1 HV01_CANFA	P01784 canis fami
21	398	61.8	117	1 HV54_MOUSE	P18525 mus musculu
22	397.5	61.7	117	1 HV3O_HUMAN	P01776 homo sapien
23	396.5	61.6	97	1 HV56_MOUSE	P18527 mus musculu
24	396	61.5	117	1 HV55_MOUSE	P18526 mus musculu
25	395.5	61.4	119	1 HV3P_HUMAN	P01777 homo sapien
26	395.5	61.4	122	1 HV20_MOUSE	P01789 mus musculu
27	395	61.3	115	1 HV32_MOUSE	P01801 mus musculu
28	394.5	61.3	122	1 HV21_MOUSE	P01790 mus musculu
29	394	61.2	116	1 HV3Q_HUMAN	P01778 homo sapien
30	393.5	61.1	111	1 HV35_MOUSE	P01804 mus musculu
31	393	61.0	113	1 HV30_MOUSE	P01799 mus musculu
32	390	60.6	142	1 HV01_RAT	P01805 rattus norv
33	389	60.4	116	1 HV3R_HUMAN	P01779 homo sapien

RESULT 1
HV3C_HUMAN 388 60.2 113 1 HV27_MOUSE P01796 mus musculu
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
CC EMBL; J00236; AAA53516.1; -;
CC PIR; A02047; H3HU26.
CC EMBL; M35415; AAA58735.1; -;
CC HSP; P01772; 2FB4.
CC Genew; HGNC:5545; IGHV@.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
CC NON_TER 117 117
CC SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;
Query Match 73.1%; Score 471; DB 1; Length 117;
Best Local Similarity 91.8%; Pred. No. 7.9e-40;
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTPRSNAMGWVRQAPGKGLWVSGISGGSGSTYY 60
Db 20 EVQLLEGGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSGSTYY 79
Qy 61 ADSVKGRFTISRNKNTLYLQMNLSRAEDTAVYYCAK 98
Db 80 GDSVKGRFTISRNKNTLYLQMNLSRAEDTAVYYCAK 117

DR HSP: P01772; 2FB4.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT NON_TER 122 122
 FT SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

 Query Match 70.0%; Score 456.5; DB 1; Length 122;
 Best Local Similarity 73.0%; Pred. No. 2.2e-38;
 Matches 89; Conservative 13; Mismatches 19; Indels 1; Gaps

 QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLGWVSGISGGSGSTYY 119
 DB 1 OVELVSGGGVGPVPGSLRSLSCAASGFTTSYAMHWVRQPPGKGLGWAVISYVBGBKYY 60
 QY 61 ADSVKGRFTISDNSKNTLYLQMNLSRAEDTAVYYCAKHTG-CGVNDPDIYWGQGLTVT 119
 DB 61 ABSVKGRFTISDRSKBTLYLQMNLSRAEDTAVYYCARDRLPYGBYRAFNWYWGQGLTVT 120
 QY 120 SS 121
 DB 121 SS 122

 RESULT 4
 HV3A_HUMAN STANDARD; PRT; 122 AA.
 ID AC P01762;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region TRO.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=76033781; PubMed=809331;
 RA Kratzin H., Altevoigt P., Ruban E., Kortt A., Staroscik K.,
 RA Hilschmann N.;
 RT II. The primary structure of a monoclonal IgA-immunoglobulin (IgA TRO.)
 RT structure of the complete IgA-molecule.
 RL Hoppe-Seidler's Z. Physiol. Chem. 356:1337-1342(1975).
 CC -1- MTSCELANEONS; THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
 DR PIR: A02045; A1HUTR.
 DR HSP: P01772; 2FB4.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT NON_TER 122 122
 FT SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

 Query Match 70.0%; Score 450.5; DB 1; Length 122;
 Best Local Similarity 68.3%; Pred. No. 8.7e-38;
 Matches 84; Conservative 16; Mismatches 20; Indels 3; Gaps

 QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLGWVSGISGGSGSTYY 60
 DB 1 QVQLVQSGGGLVPGGSLRLSCVAGSFRDFYMSWIRZTPEKGLZMWVSYIGSGSGSTLY 60
 QY 61 ADSVKGRFTISDNSKNTLYLQMNLSRAEDTAVYYCAKHTGGGVND--PIDYWGQGLTVT 119
 DB 61 ADSVKGRFTISDNNAOKSYLYLZMSLRZTZYVYCAA-TBBFWSTSLBYWGWZGBLVT 119
 QY 119 VSS 121

Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;

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Best Local Similarity 87.8%; Pred. No. 1.3e-36;
Matches 86; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNMYMSWRQPPGKLEWVSIY- SGGSTYY 78

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYYCAK 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYYCAR 116

RESULT 8
HV3K_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR: A02052; M3HUGA.
DR HSP: P01772; 2PB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT MOD_RES 122 122 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 67.9%; Score 437.5; DB 1; Length 122;
Best Local Similarity 68.9%; Pred. No. 1.7e-36;
Matches 84; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVZLVZSGGAVZPGRSLRLSCAASGFSFYAMHWRQAPGKGLZWLVSISYGBBZY 60

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYYCAK-TGGGVWDPIDYWGQGLTV 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AASVKGRFTISRDNKNTLYQMNSLRADTAIVYYCARSGALGSVAGTDYWGQGLTV 120

QY 120 SS 121
||
Db 121 SS 122

RESULT 9
HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
DR PIR: A02055; G1HUKL.
DR PDB: 2PB4; 12-JUL-89.
DR PDB: 2IG2; 12-JUL-89.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 15
FT STRAND 14 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 67.9%; Score 437.5; DB 1; Length 126;
Best Local Similarity 69.8%; Pred. No. 1.7e-36;
Matches 88; Conservative 10; Mismatches 23; Indels 5; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVESGGGVQPGKSLRLSCSSSGFISSYAMVWRQAPGKLEWVAIWDGSDQHY 60

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYYCAKHTGGGVWDP1-----DYWGQGT 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAIVYYCAKHTGGGVWDP1-----DYWGQGT 120

QY 116 LVTVSS 121
|||||
Db 121 PVTVSS 126

RESULT 10
HV16_MOUSE STANDARD; PRT; 136 AA.
AC HV16_MOUSE
ID P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

OX	NCBI_TaxID=9606;
RP	[1]
RP	SEQUENCE.
RR	MEDLINE=78005528; PubMed=409716;
RA	Wang A.-C., Wang I.-Y., Fudenberg H.H.;
RT	"Immunoglobulin structure and genetics. Identity between variable
RT	regions of a mu and a gamma2 chain.";
RL	J. Biol. Chem. 252:7192-7199(1977).
CC	-I- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC	OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC	GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC	IDENTICAL.
DR	PIR: A02048; H3HUTL.
DR	HSSP: P01772; 2FB4.
DR	InterPro: IPR003006; Ig_MHC.
DR	Interfam: IPR003596; Ig_v.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SM00406; IGV; 1.
DR	Immunoglobulin V region.
KW	Immunoglobulin V region.
FT	NON_TER 115 115
FT	SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;
QY	Query Match 67.5%; Score 435; DB 1; Length 115;
DB	Best Local Similarity 71.1%; Pred. NO. 2.8e-36;
DB	Matches 86; Conservative 10; Mismatches 19; Indels 6; Gaps
QY	1 OVOLVQSGGGLVQPGCSLRLSCAASGTFPFSNAGWVRQAPCGKLEWVSGISGGSGTYY 60
DB	1 EVOLLESGGGLVQPGCSLRLSCAASGTFFTSYVMSWVRQAPCGKLGZVWGAIZGLSVSZSY 60
QY	61 ADSVKGRTISRDSKNTLYQLMNSLRAEDTAIVYCAKHTGGVWDPIDYWGQGTLLVTVS 120
DB	61 ABSVKGRTISRDSKNT---MNSLRAEDTAIVYCAKGVSAIY--FBYWGZGTLTVTS 114
QY	121 S 121
DB	115 S 115
RESULT 12	
HW02_CANFA	
ID	HW02_CANFA STANDARD; PRT; 117 AA.
AC	P01785;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig heavy chain V region MOO.
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX	NCBI_TaxID=9615;
OX	[1]
RP	SEQUENCE OF 1-112.
RP	MEDLINE=77242268; PubMed=407924;
RP	Wasserman R.L., Capra J.D.;
RA	"Primary structure of the variable regions of two canine
RT	immunoglobulin heavy chains.";
RL	Biochemistry 16:3160-3168(1977).
CC	[2]
RP	SEQUENCE OF 113-117.
RP	MEDLINE=80077682; PubMed=117299;
RP	McCumber L.J., Capra J.D.;
RA	"The complete amino-acid sequence of a canine mu chain.";
RT	Mol. Immunol. 16:565-570(1979).
CC	-I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC	PIR: A02068; MHDGM.
DR	HSSP: P01772; 2FB4.
DR	InterPro: IPR003006; Ig_MHC.
DR	Interfam: IPR003596; Ig_v.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SM00406; IGV; 1.
KW	Immunoglobulin V region.
FT	NON_TER 117 117

```
SQ SEQUENCE 117 AA; 12703 MW; FCB07309E0A84B35 CRC64;
Query Match 67.1%; Score 432; DB 1; Length 117;
Best Local Similarity 71.9%; Pred. No. 5.6e-36;
Matches 87; Conservative 13; Mismatches 17; Indels 4; Gaps 3;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKGLWVSGISGSGSTYY 60
DB 1 EVKLVEGGDLVQPGGSLRLSCAASGFTFRSSNGMSWVQDPGGELQWADIS-SSQTTY 59
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
DB 60 ADLVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 116
QY 121 S 121
DB 117 S 117

RESULT 13
HV31_HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR; A02050; A2HUBU.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 119
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;
Query Match 66.3%; Score 427; DB 1; Length 115;
Best Local Similarity 68.6%; Pred. No. 1.7e-35;
Matches 83; Conservative 16; Mismatches 16; Indels 6; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKGLWVSGISGSGSTYY 60
DB 1 EVQLVETGGGLVQPGGSLRLSCAASGFTVSBHSMVWVQAPGKALZWVAIY-RGGTTY 59
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
DB 60 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARDLAAA-----RLFQKGTTVTVS 114
QY 121 S 121
DB 115 S 115

RESULT 15
HV30_HUMAN STANDARD; PRT; 120 AA.
AC P01782;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region DOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Steiner L.A., Garcia Pardo A., Margolies M.N.;
RT "Amino acid sequence of the heavy-chain variable region of the
crystallizable human myeloma protein Dob.";
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RL Biochemistry 18:4068-4080(1979).
RN [2]
RP CRYSTALLIZATION.
RX MEDLINE=80020920; PubMed=114208;
RA Steiner L.A., Lopes A.D.;
RT "The crystallizable human myeloma protein Dob has a hinge-region
RT deletion.";
RL Biochemistry 18:4054-4067(1979).
CC -I- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
CC HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
CC DISULFIDE BONDS.
DR PIR: A02065; G1H0DB.
DR HSSP: P01772; 2F8A.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 65.6%; Score 422.5; DB 1; Length 120;
Best Local Similarity 69.1%; Pred. No. 5e-35;
Matches 85; Conservative 10; Mismatches 23; Indels 5; Gaps 2;

QY 1 QVQLVQSGGGLVQPQGGSLRLSCAASGFTFSRNAMGWVRQAPKGLGWVSGISGGGSTYY 60
DB :||||:||||| ||||| ||||| | | ||| ||||| ||||| | ||| |
QY 1 EVQLVESGGDLVQPGRSLRLSCAASGFTFHEYNHHLKQPGKGPFWVSTITWNGGSVLY 60
DB :||||| ||||| : ||||| : ||||| ||||| | : | |||||
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYYCAKHTGGGYWDP--IDYWGQGTLVLT 118
DB :||||| ||||| : ||||| : ||||| ||||| | : | |||||
QY 61 ADSVKGRFAISRDNACKTLYLQNLRLPEDTAIFYCAK--GYIWNNGWFDSWGQGTLVLT 117
DB :|||||
QY 119 VSS 121
DB 118 VSS 120

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Search completed: March 13, 2003, 15:15:13
Job time : 12.1 secs


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RESULT 2
Q9UL71 PRELIMINARY; PRT; 121 AA.
ID Q9UL71 AC Q9UL71
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF03043; AAD56279.1; -.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCEFA5D0736 CRC64;

Query Match 78.7%; Score 507; DB 4; Length 121;
Best Local Similarity 81.0%; Pred. No. 2,7e-42;
Matches 98; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVRQAPGKGLVWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGVVPGGSLRLSCAASGFTFRSNAMGVRQAPGKGLVWVSGISGGSTYY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVNDPIDYWGQGTFTVTS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTALYYCAKGVTTIYDRFDINGQGTMTVTS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 121 S 121
|
Db 121 S 121

RESULT 3
Q8WU38 PRELIMINARY; PRT; 573 AA.
ID Q8WU38 AC Q8WU38
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 63.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC021276; AAF21276.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.

Query Match 75.5%; Score 486.5; DB 4; Length 613;
Best Local Similarity 80.2%; Pred. No. 2.3e-39;
Matches 97; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVRQAPGKGLVWVSGISGGSTYY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 QVQLVESGGGVVPGGSLRLSCAASGFTFRSNAMGVRQAPGKGLVWVSGISGGSTYY 79
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVNDPIDYWGQGTFTVTS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKGVNDPIDYWGQGTMTVTS 138
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 121 S 121
|
Db 139 S 139

RESULT 5
Q9UL90

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DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 75.7%; Score 487.5; DB 4; Length 573;
Best Local Similarity 78.2%; Pred. No. 1.7e-39;
Matches 97; Conservative 8; Mismatches 16; Indels 3; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVRQAPGKGLVWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTFDYAMHWVRQAPGKGLVWVSGISWNSGSIY 79
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGG--GYWDPIDYWGQGTFLV 117
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTALYYCAKHTGGSGSYIGYYGNDVWGQGTTV 139
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 118 TVSS 121
||||
Db 140 TVSS 143
||||

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RESULT 4
Q8WU1 PRELIMINARY; PRT; 613 AA.
ID Q8WU1 AC Q8WU1
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC020240; AAF20240.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 75.5%; Score 486.5; DB 4; Length 613;
Best Local Similarity 80.2%; Pred. No. 2.3e-39;
Matches 97; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVRQAPGKGLVWVSGISGGSTYY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 QVQLVESGGGVVPGGSLRLSCAASGFTFRSNAMGVRQAPGKGLVWVSGISGGSTYY 79
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVNDPIDYWGQGTFTVTS 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKGVNDPIDYWGQGTMTVTS 138
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 121 S 121
|
Db 139 S 139

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RESULT 5
Q9UL90


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ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 75.0%; Score 483; DB 4; Length 113;
Best Local Similarity 78.5%; Pred. No. 5.6e-40;
Matches 95; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSGTYY 60
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYCMHWVRQAPGKGLVWVAFIRYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGTLTVVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----DLNYWGQGTLTVVS 112

Qy 121 S 121
Db 113 S 113

RESULT 6
Q9UL93
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 75.0%; Score 483; DB 4; Length 113;
Best Local Similarity 78.5%; Pred. No. 5.6e-40;
Matches 95; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSGTYY 60
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYCMHWVRQAPGKGLVWVAFIRYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGTLTVVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-----DLNYWGQGTLTVVS 112

Qy 121 S 121
Db 113 S 113

RESULT 6
Q9UL93
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
```

```
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Query Match 74.5%; Score 480; DB 4; Length 116;
Best Local Similarity 80.8%; Pred. No. 1.1e-39;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 2;

Qy 2 VOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSGTYYA 61
Db 1 VOLVESGGGVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKGLVWVAVISYDGSNKYYA 60

Qy 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGTLTVVS 121
Db 61 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA--GGGGL--GLGYWGQGTLTVVS 116

RESULT 7
Q9UL72
ID Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 74.5%; Score 479.5; DB 4; Length 118;
Best Local Similarity 81.0%; Pred. No. 1.3e-39;
Matches 98; Conservative 6; Mismatches 14; Indels 3; Gaps 2;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSGTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNMVNRQAPGKGLSVS-VTYSGGSSYY 59

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGTLTVVS 120
Db 60 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRFGEFL--FDYWGQGTLTVVS 117

Qy 121 S 121
Db 118 S 118

RESULT 8
Q9HCC1
ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Single chain Fv (Fragment).
```

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OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme : isolation from a
RL human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig.Like.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match 73.2%; Score 471.5; DB 4; Length 112;
Best Local Similarity 76.9%; Pred. No. 7.4e-39;
Matches 90; Conservative 11; Mismatches 11; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVQLVESGGGVLPVGGSLRLSCAASGFTFDYGMWSVRQAPGKGLWVSGINWGGSTGY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTV 117
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTV 117
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTV 117
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTV 117

RESULT 9
Q9UL91 ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR ENBL; AF035023; RAD56259.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 73.1%; Score 470.5; DB 4; Length 118;
Best Local Similarity 77.5%; Pred. No. 1e-38;
Matches 93; Conservative 10; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60

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Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
1 EVQLVESGGGLVPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSYISITIIYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVMDPIDYWGQGLTV 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAR---GDSSEAFDIMGQGTMTVTS 117
61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAR---GDSSEAFDIMGQGTMTVTS 117

RESULT 10
Q8TC77 ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 72.4%; Score 466.5; DB 4; Length 471;
Best Local Similarity 75.6%; Pred. No. 1.5e-37;
Matches 93; Conservative 9; Mismatches 18; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
20 EVQLVESGGGLVPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSSSSSYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTG--GGVMDPIDYWGQGLTV 118
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
80 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDLRLQTSYWFYDLWGGRGLTV 138
QY 119 VSS 121
Db 139 VSS 141

RESULT 11
Q9Y509 ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Vh3 protein (Fragment).
GN Vh3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR ENBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

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FT NON_TER 1 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 71.2%; Score 458.5; DB 4; Length 147;
Best Local Similarity 72.7%; Pred. No. 2e-37;
Matches 93; Conservative 7; Mismatches 19; Indels 9; Gaps 2;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGSGSTYY 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVHLVESGGGVVQPGKSLRLSCAASGFTFTYGMSSWVRQAPGKGLDWVALISYDGGTOYY 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRNSKNTLYLQWNSLRADTAVYYCAKHTGGVWDP-----IDYWGQ 113
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AGSVKGRFTISRNSKNTLYLQMTSLRVEDTAVYYCAK--DGNVFDSDVGYIYAGIDYWGQ 118
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 114 GTLVTVSS 121
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 GTLVTVSS 126
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RS SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366345B8 CRC64;

Query Match 70.3%; Score 452.5; DB 4; Length 122;
Best Local Similarity 74.8%; Pred. No. 6.1e-37;
Matches 91; Conservative 8; Mismatches 22; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGSGSTYY 60
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGVVQPGKSLRLSCAASRFTFSNYGMHVRQAPGKGLWVAISNDGSKNFY 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRNSKNTLYLQWNSLRADTAVYYCAKHTGGG-VWDFIDYWGQGLTVV 119
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTIFRDNKSNMMDLQWNSLRADTAVYYCAKDERGLVGTTFDYWGQGLTVV 120
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 SS 121
   ||
Db 121 SS 122
   ||

RESULT 13
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RS SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 70.1%; Score 451.5; DB 11; Length 487;
Best Local Similarity 69.4%; Pred. No. 4.6e-36;
Matches 86; Conservative 14; Mismatches 21; Indels 3; Gaps 1;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGSGSTYY 60
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQTPTEKRLWVAITSDGGSYTY 79
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRNSKNTLYLQWNSLRADTAVYYCAKHTGG--GVWDPIDYWGQGLTV 117
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 PDNVKGRFTISRNANKNNLYLQWNSLRADTAVYYCAKDMGSPYGGYSRFDYWGQGTI 139
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 TVSS 121
   |||
Db 140 TVSS 143
   |||

RESULT 14
Q96K68 PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA FLJ14473 fis, clone MAMMAJ001080, highly similar to Homo
DE sapiens SNC73 protein (SNC73) mRNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RS SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagehara K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027379; BAB55072.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AE4C0E CRC64;
  Query Match          69.8%; Score 449.5; DB 4; Length 494;
  Best Local Similarity 72.1%; Pred. No. 7.3e-36;
  Matches 88; Conservative 11; Mismatches 22; Indels 1; Gaps 1;

QY 1 QVOLVSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
   :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:
Db 20 EVQLVESGGDLVKPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 79
   :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT--GGGVWDPIDYWGQGLTVTV 119
   :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:
Db 80 RDSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT--GGGVWDPIDYWGQGLTVTV 139
   :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:

QY 120 SS 121
   ||
Db 140 SS 141

RESULT 15
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iace A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
   in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

  Query Match          68.9%; Score 444; DB 11; Length 119;
  Best Local Similarity 71.3%; Pred. No. 4e-36;
  Matches 87; Conservative 13; Mismatches 18; Indels 4; Gaps 2;

QY 1 QVOLVSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
   :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:
Db 1 EVQLVESGGDLVKPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60
   :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGYMD-PIDYWGQGLTVTV 119
   :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:
Db 61 PDSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT--GDYDVGFAYWGQGLTVTV 117
   :||||:||||:||||:||||:|:|:|:||||:||||:|:|:|:||||:||||:|:|:|:

QY 120 SS 121
   ||
Db 118 SA 119

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Search completed: March 13, 2003, 15:16:58
 Job time : 45.7462 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:33:09 ; Search time 11.3077 Seconds
(without alignments)
57.066 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_110

Perfect score: 14

Sequence: 1 AKHTGGGVWDPIDY 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications.AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/RCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	121	10	US-09-822-698A-3
2	14	100.0	381	10	US-09-822-698A-5
3	14	100.0	451	10	US-09-822-698A-26
4	13	92.9	14	10	US-09-822-698A-75
5	13	92.9	14	10	US-09-822-698A-97
6	13	92.9	14	10	US-09-822-698A-105
7	12	85.7	14	10	US-09-822-698A-30
8	12	85.7	14	10	US-09-822-698A-31
9	12	85.7	14	10	US-09-822-698A-76
10	12	85.7	14	10	US-09-822-698A-79
11	12	85.7	14	10	US-09-822-698A-83
12	12	85.7	14	10	US-09-822-698A-86
13	12	85.7	14	10	US-09-822-698A-89
14	12	85.7	14	10	US-09-822-698A-90
15	12	85.7	14	10	US-09-822-698A-94
16	12	85.7	14	10	US-09-822-698A-96
17	12	85.7	14	10	US-09-822-698A-100
18	12	85.7	14	10	US-09-822-698A-102
19	12	85.7	14	10	US-09-822-698A-109

20	11	78.6	14	10	US-09-822-698A-78	Sequence 78, Appl
21	11	78.6	14	10	US-09-822-698A-81	Sequence 81, Appl
22	11	78.6	14	10	US-09-822-698A-82	Sequence 82, Appl
23	11	78.6	14	10	US-09-822-698A-88	Sequence 88, Appl
24	11	78.6	14	10	US-09-822-698A-91	Sequence 91, Appl
25	11	78.6	14	10	US-09-822-698A-92	Sequence 92, Appl
26	11	78.6	14	10	US-09-822-698A-93	Sequence 93, Appl
27	11	78.6	14	10	US-09-822-698A-98	Sequence 98, Appl
28	11	78.6	14	10	US-09-822-698A-99	Sequence 99, Appl
29	11	78.6	14	10	US-09-822-698A-101	Sequence 101, Appl
30	11	78.6	14	10	US-09-822-698A-103	Sequence 103, Appl
31	11	78.6	16	10	US-09-822-698A-65	Sequence 65, Appl
32	10	71.4	14	10	US-09-822-698A-32	Sequence 32, Appl
33	10	71.4	14	10	US-09-822-698A-77	Sequence 77, Appl
34	10	71.4	14	10	US-09-822-698A-84	Sequence 84, Appl
35	10	71.4	14	10	US-09-822-698A-107	Sequence 107, Appl
36	10	71.4	16	10	US-09-822-698A-67	Sequence 67, Appl
37	9	64.3	14	10	US-09-822-698A-80	Sequence 80, Appl
38	9	64.3	14	10	US-09-822-698A-104	Sequence 104, Appl
39	8	57.1	14	10	US-09-822-698A-106	Sequence 106, Appl
40	8	57.1	14	10	US-09-822-698A-108	Sequence 108, Appl
41	7	50.0	16	10	US-09-822-698A-41	Sequence 41, Appl
42	7	50.0	16	10	US-09-822-698A-43	Sequence 43, Appl
43	7	50.0	16	10	US-09-822-698A-45	Sequence 45, Appl
44	7	50.0	16	10	US-09-822-698A-47	Sequence 47, Appl
45	7	50.0	16	10	US-09-822-698A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PHI Fab antibody
US-09-822-698A-3

Query Match 100.0% Score 14; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
|||||
Db 97 AKHTGGGVWDPIDY 110

RESULT 2
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US

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; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPHI-IL-2
US-09-822-698A-5

Query Match      100.08; Score 14; DB 10; Length 381;
Best Local Similarity 100.08; Pred. No. 4.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVDPIDY 14
|||||
DB 97 AKHTGGGVDPIDY 110

RESULT 3
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PHI-IgG1
US-09-822-698A-26

Query Match      100.08; Score 14; DB 10; Length 451;
Best Local Similarity 100.08; Pred. No. 4.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVDPIDY 14
|||||
DB 97 AKHTGGGVDPIDY 110

RESULT 4
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

Query Match      92.9%; Score 13; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVDPID 13
|||||
DB 1 AKHTGGGVDPID 13

RESULT 5
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match      92.9%; Score 13; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVDPID 13
|||||
DB 1 AKHTGGGVDPID 13

RESULT 6
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match      92.9%; Score 13; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2 KHTGGGVWDPIY 14
|||||
Db 2 KHTGGGVWDPIY 14

RESULT 7

US-09-822-698A-30
; Sequence 30, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 30
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-30

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
|||||
Db 1 AKHTGGGVWDPI 12

RESULT 8

US-09-822-698A-31
; Sequence 31, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
|||||
Db 1 AKHTGGGVWDPI 12

RESULT 9

US-09-822-698A-76
; Sequence 76, Application US/09822698A
; Patent No. US20020146750A1

; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
|||||
Db 1 AKHTGGGVWDPI 12

RESULT 10

US-09-822-698A-79
; Sequence 79, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 79
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-79

Query Match 85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
|||||
Db 1 AKHTGGGVWDPI 12

RESULT 11

US-09-822-698A-83
; Sequence 83, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30

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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83
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Query Match      85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AKHTGGGVWDPI 12
      |||||
Db 1 AKHTGGGVWDPI 12
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RESULT 12
US-09-822-698A-86
; Sequence 86, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-86
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```
Query Match      85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AKHTGGGVWDPI 12
      |||||
Db 1 AKHTGGGVWDPI 12
```

```
RESULT 13
US-09-822-698A-89
; Sequence 89, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 89
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-89
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```
Query Match      85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AKHTGGGVWDPI 12
      |||||
Db 1 AKHTGGGVWDPI 12
```

```
RESULT 14
US-09-822-698A-90
; Sequence 90, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 90
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-90
```

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Query Match      85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AKHTGGGVWDPI 12
      |||||
Db 1 AKHTGGGVWDPI 12
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RESULT 15
US-09-822-698A-94
; Sequence 94, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 94
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-94
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Query Match      85.7%; Score 12; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AKHTGGGVWDPI 12
      |||||
Db 1 AKHTGGGVWDPI 12
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OM protein - protein search, using sw model
Run on: March 13, 2003, 15:31:49 ; Search time 151.846 Seconds
(without alignments)
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Title: US-09-822-698A-3_COPY_97_110
Perfect score: 14
Sequence: 1 AKHTGGVWDPIDY 14

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Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

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- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pap.*
- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pap.*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pap.*
- 26: /cgn2_6/ptodata/2/paa/US102_COMB.pap.*
- 27: /cgn2_6/ptodata/2/paa/US60_COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	121	19	US-09-538-913-3
2	14	100.0	121	22	US-09-822-698A-3
3	14	100.0	381	19	US-09-538-913-5
4	14	100.0	381	22	US-09-822-698A-5
5	14	100.0	451	22	US-09-822-698A-26
6	13	92.9	14	22	US-09-822-698A-75

7	13	92.9	14	22	US-09-822-698A-97	Sequence 97, Appl
8	13	92.9	14	22	US-09-822-698A-105	Sequence 105, App
9	12	85.7	14	22	US-09-822-698A-30	Sequence 30, Appl
10	12	85.7	14	22	US-09-822-698A-31	Sequence 31, Appl
11	12	85.7	14	22	US-09-822-698A-76	Sequence 76, Appl
12	12	85.7	14	22	US-09-822-698A-79	Sequence 79, Appl
13	12	85.7	14	22	US-09-822-698A-83	Sequence 83, Appl
14	12	85.7	14	22	US-09-822-698A-86	Sequence 86, Appl
15	12	85.7	14	22	US-09-822-698A-89	Sequence 89, Appl
16	12	85.7	14	22	US-09-822-698A-90	Sequence 90, Appl
17	12	85.7	14	22	US-09-822-698A-94	Sequence 94, Appl
18	12	85.7	14	22	US-09-822-698A-96	Sequence 96, Appl
19	12	85.7	14	22	US-09-822-698A-100	Sequence 100, App
20	12	85.7	14	22	US-09-822-698A-102	Sequence 102, App
21	12	85.7	14	22	US-09-822-698A-109	Sequence 109, App
22	11	78.6	14	22	US-09-822-698A-78	Sequence 78, Appl
23	11	78.6	14	22	US-09-822-698A-81	Sequence 81, Appl
24	11	78.6	14	22	US-09-822-698A-82	Sequence 82, Appl
25	11	78.6	14	22	US-09-822-698A-88	Sequence 88, Appl
26	11	78.6	14	22	US-09-822-698A-91	Sequence 91, Appl
27	11	78.6	14	22	US-09-822-698A-92	Sequence 92, Appl
28	11	78.6	14	22	US-09-822-698A-93	Sequence 93, Appl
29	11	78.6	14	22	US-09-822-698A-98	Sequence 98, Appl
30	11	78.6	14	22	US-09-822-698A-99	Sequence 99, Appl
31	11	78.6	14	22	US-09-822-698A-101	Sequence 101, App
32	11	78.6	14	22	US-09-822-698A-103	Sequence 103, App
33	11	78.6	16	22	US-09-822-698A-65	Sequence 65, Appl
34	10	71.4	14	22	US-09-822-698A-32	Sequence 32, Appl
35	10	71.4	14	22	US-09-822-698A-77	Sequence 77, Appl
36	10	71.4	14	22	US-09-822-698A-84	Sequence 84, Appl
37	10	71.4	14	22	US-09-822-698A-107	Sequence 107, App
38	10	71.4	16	22	US-09-822-698A-67	Sequence 67, Appl
39	9	64.3	14	22	US-09-822-698A-80	Sequence 80, Appl
40	9	64.3	14	22	US-09-822-698A-104	Sequence 104, App
41	8	57.1	14	22	US-09-822-698A-106	Sequence 106, App
42	8	57.1	14	22	US-09-822-698A-108	Sequence 108, App
43	7	50.0	16	22	US-09-822-698A-41	Sequence 41, Appl
44	7	50.0	16	22	US-09-822-698A-43	Sequence 43, Appl
45	7	50.0	16	22	US-09-822-698A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-538-913-3
; Sequence 3, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hooogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-3

Query Match 100.0%; Score 14; DB 19; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14

DB 97 AKHTGGGVWDPIDY 110

RESULT 2

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US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 14; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKHTGGVWDPTDY 14
        |||||
Db       97 AKHTGGVWDPTDY 110

RESULT 3
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPH1-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match      100.0%; Score 14; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKHTGGVWDPTDY 14
        |||||
Db       97 AKHTGGVWDPTDY 110

RESULT 4
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
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; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPH1-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 14; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKHTGGVWDPTDY 14
        |||||
Db       97 AKHTGGVWDPTDY 110

RESULT 5
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26

Query Match      100.0%; Score 14; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKHTGGVWDPTDY 14
        |||||
Db       97 AKHTGGVWDPTDY 110

RESULT 6
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75
```

```
Query Match      92.9%; Score 13; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGWDPI 13
   |||||
DB 1 AKHTGGGWDPI 13

RESULT 7
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match      92.9%; Score 13; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGWDPI 13
   |||||
DB 1 AKHTGGGWDPI 13

RESULT 8
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match      92.9%; Score 13; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGGWDPI 14
   |||||
DB 2 KHTGGGWDPI 14

RESULT 9
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US-09-822-698A-30
; Sequence 30, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 30
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-30

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGWDPI 12
   |||||
DB 1 AKHTGGGWDPI 12

RESULT 10
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGWDPI 12
   |||||
DB 1 AKHTGGGWDPI 12

RESULT 11
US-09-822-698A-76
; Sequence 76, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
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```
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
   |||||
Db 1 AKHTGGGVWDPI 12

RESULT 12
US-09-822-698A-79
; Sequence 79, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; SOFTWARE: Microsoft Word
; SEQ ID NO 79
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-79

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
   |||||
Db 1 AKHTGGGVWDPI 12

RESULT 13
US-09-822-698A-83
; Sequence 83, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
   |||||
Db 1 AKHTGGGVWDPI 12

RESULT 14
US-09-822-698A-86
; Sequence 86, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; SOFTWARE: Microsoft Word
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-86

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
   |||||
Db 1 AKHTGGGVWDPI 12

RESULT 15
US-09-822-698A-89
; Sequence 89, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; SOFTWARE: Microsoft Word
; SEQ ID NO 89
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-89

Query Match      85.7%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
   |||||
Db 1 AKHTGGGVWDPI 12

Search completed: March 13, 2003, 15:39:00
Job time : 151.846 secs
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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:32:14 ; Search time 24.2308 Seconds
(without alignments)
75.113 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 14
Sequence: 1 AKHTGGGVWDFIDY 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 596842 seqs, 130003698 residues

Word size : 0

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_New*

1: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	6	42.9	55	1 PCT-US02-32727-11588
2	6	42.9	55	Sequence 11588, A
3	6	42.9	55	US-09-978-825-28218
4	6	42.9	93	US-10-057-498-11588
5	6	42.9	93	Sequence 11588, A
6	6	42.9	93	PCT-US02-32727-9150
7	6	42.9	93	Sequence 9150, Ap
8	6	42.9	330	US-09-978-825-9150
9	6	42.9	435	Sequence 9150, Ap
10	6	42.9	435	US-10-057-498-9150
11	6	42.9	512	Sequence 23794, A
12	6	42.9	512	Sequence 78529, A
13	6	42.9	512	Sequence 78531, A
14	6	42.9	526	US-09-724-676A-78532
15	6	42.9	701	Sequence 78532, A
16	6	42.9	1583	US-10-282-122A-62129
17	6	42.9	1583	Sequence 62129, A
18	6	42.9	1583	Sequence 15149, A
19	5	35.7	38	US-09-978-825-15149
20	5	35.7	51	Sequence 15149, A
21	5	35.7	51	US-10-156-761-15030
22	5	35.7	51	Sequence 15030, A
23	5	35.7	56	US-09-724-676A-87689
24	5	35.7	56	Sequence 87689, A
25	5	35.7	56	PCT-US02-32727-26391
26	5	35.7	56	Sequence 26391, A
27	5	35.7	56	US-09-978-825-26391
28	5	35.7	56	Sequence 26391, A
29	5	35.7	58	US-10-057-498-26391
30	5	35.7	58	Sequence 26391, App
31	5	35.7	58	US-09-593-793A-553
32	5	35.7	58	Sequence 553, App
33	5	35.7	58	US-10-294-025-553

27	5	35.7	66	1	PCT-US02-32727-28218	Sequence 28218, A
28	5	35.7	66	5	US-09-978-825-28218	Sequence 28218, A
29	5	35.7	66	6	US-10-057-498-28218	Sequence 28218, A
30	5	35.7	67	1	PCT-US02-32727-9117	Sequence 9117, Ap
31	5	35.7	67	5	US-09-978-825-9117	Sequence 9117, Ap
32	5	35.7	67	6	US-10-057-498-9117	Sequence 9117, Ap
33	5	35.7	68	1	PCT-US02-32727-28689	Sequence 28689, A
34	5	35.7	68	5	US-09-978-825-28689	Sequence 28689, A
35	5	35.7	68	6	US-10-057-498-28689	Sequence 28689, A
36	5	35.7	77	5	US-09-724-676A-87695	Sequence 87695, A
37	5	35.7	77	5	US-09-724-676A-87695	Sequence 87695, A
38	5	35.7	78	1	PCT-US02-32727-21401	Sequence 21401, A
39	5	35.7	78	5	US-09-978-825-21401	Sequence 21401, A
40	5	35.7	78	6	US-10-057-498-21401	Sequence 21401, A
41	5	35.7	84	5	US-09-724-676A-87694	Sequence 87694, A
42	5	35.7	84	5	US-09-724-676A-87694	Sequence 87694, A
43	5	35.7	93	1	PCT-US02-32727-16769	Sequence 16769, A
44	5	35.7	93	5	US-09-978-825-16769	Sequence 16769, A
45	5	35.7	93	6	US-10-057-498-16769	Sequence 16769, A

ALIGNMENTS

RESULT 1
PCT-US02-32727-11588
; Sequence 11588, Application PC/TUS0232727

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois

; APPLICANT: Zhang, Yanni

; APPLICANT: Wang, Siqing

; APPLICANT: Jen, Shylan

; APPLICANT: Lodes, Michael

; APPLICANT: Benson, Darin

; APPLICANT: Jones, Robert

; APPLICANT: Carter, Darrick

; APPLICANT: Barth, Brenda

; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: PCT/US02/32727

; CURRENT FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 11588

; LENGTH: 55

; TYPE: PRT

; ORGANISM: Propioni acnes

PCT-US02-32727-11588

Query Match

Best Local Similarity

Matches

QY

Db

3 HTGGGV 8

37 HTGGGV 42

42.9% Score 6; DB 1; Length 55;

100.0% Pred. No. 28;

6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

```

; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-11588

Query Match 42.9%; Score 6; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8
Db 37 HTGGGV 42

RESULT 3
US-10-057-498-11588
; Sequence 11588, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-11588

Query Match 42.9%; Score 6; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8
Db 37 HTGGGV 42

RESULT 4
PCT-US02-32727-9150
; Sequence 9150, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

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; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-9150

Query Match 42.9%; Score 6; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGVWD 10
Db 10 GGGVWD 15

RESULT 5
US-09-978-825-9150
; Sequence 9150, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-9150

Query Match 42.9%; Score 6; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGVWD 10
Db 10 GGGVWD 15

RESULT 6
US-10-057-498-9150
; Sequence 9150, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes

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US-10-057-498-9150

Query Match 42.9%; Score 6; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGVVD 10
| | | | |
Db 10 GGVVD 15

RESULT 7

US-10-366-683-23794
; Sequence 23794, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nolling, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: PATH03-04
; CURRENT APPLICATION NUMBER: US/10/366,683
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23794
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-23794

Query Match 42.9%; Score 6; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VWDPID 13
| | | | |
Db 103 VWDPID 108

RESULT 8

US-09-724-676-78529
; Sequence 78529, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78529
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78529

Query Match 42.9%; Score 6; DB 5; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7
| | | | |
Db 396 KHTGGG 401

RESULT 9

US-09-724-676A-78529
; Sequence 78529, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78529
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78529

Query Match 42.9%; Score 6; DB 5; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7
| | | | |
Db 396 KHTGGG 401

RESULT 10

US-10-369-493-11831
; Sequence 11831, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11831
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-11831

Query Match 42.9%; Score 6; DB 6; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGG 6
| | | | |
Db 32 AKHTGG 37

RESULT 11

US-09-724-676-78531
; Sequence 78531, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78531
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78531

Query Match 42.9%; Score 6; DB 5; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 KHTGGG 7
Db      473 KHTGGG 478

RESULT 12
US-09-724-676A-78531
; Sequence 78531, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78531
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78531

Query Match      42.9%; Score 6; DB 5; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KHTGGG 7
Db      473 KHTGGG 478

RESULT 13
US-09-724-676-78532
; Sequence 78532, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78532
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78532

Query Match      42.9%; Score 6; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KHTGGG 7
Db      487 KHTGGG 492

RESULT 14
US-09-724-676A-78532
; Sequence 78532, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78532
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78532

Query Match      42.9%; Score 6; DB 6; Length 701;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 HTGGGV 8
Db      75 HTGGGV 80

US-09-724-676A-78532
; Sequence 62129, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62129
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-62129

Query Match      42.9%; Score 6; DB 6; Length 701;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 HTGGGV 8
Db      75 HTGGGV 80

Search completed: March 13, 2003, 15:39:54
Job time : 25.2308 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:29:54 ; Search time 14.5385 Seconds
 (without alignments)
 92.574 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
 Perfect score: 14
 Sequence: 1 AKHTGGGWDPIDY 14

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR.73:*
 1: pir1.*
 2: pir2.*
 3: pir3.*
 4: pir4.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	42.9	114	2	T08411
2	6	42.9	193	2	C82683
3	6	42.9	436	2	H84121
4	6	42.9	511	2	A54676
5	6	42.9	1123	2	S20497
6	5	35.7	10	2	H60787
7	5	35.7	10	2	D60788
8	5	35.7	10	2	B60787
9	5	35.7	10	2	A60788
10	5	35.7	10	2	C60589
11	5	35.7	10	2	D60588
12	5	35.7	71	2	T26663
13	5	35.7	72	2	T48971
14	5	35.7	75	2	A59147
15	5	35.7	101	2	S22454
16	5	35.7	107	2	S58218
17	5	35.7	113	2	S25575
18	5	35.7	119	2	T08142
19	5	35.7	119	2	D83723
20	5	35.7	119	2	T48745
21	5	35.7	120	2	C53482
22	5	35.7	130	1	S52339
23	5	35.7	130	1	JC2234
24	5	35.7	130	2	T18510
25	5	35.7	133	2	C97301
26	5	35.7	144	2	F64094
27	5	35.7	145	1	A35932
28	5	35.7	145	2	D70938
29	5	35.7	150	2	AH3482

30	5	35.7	155	2	C86206
31	5	35.7	158	2	C95159
32	5	35.7	158	2	C98025
33	5	35.7	160	2	G69376
34	5	35.7	163	2	A70847
35	5	35.7	168	2	D82310
36	5	35.7	169	2	A40522
37	5	35.7	170	2	H87704
38	5	35.7	175	2	A71680
39	5	35.7	175	2	A97742
40	5	35.7	181	1	I41314
41	5	35.7	185	2	F95008
42	5	35.7	188	2	B95365
43	5	35.7	189	1	S74659
44	5	35.7	189	2	D69128
45	5	35.7	189	2	A87254

ALIGNMENTS

RESULT 1
 T08411
 hypothetical protein fl8B3.180 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
 C:Accession: T08411
 R:Querier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Sala, submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16409
 A:Accession: T08411
 A:Molecule type: DNA
 A:Residues: 1-114 <QUE>
 A:Cross-references: EMBL:AL049862; GSPDB:GN000061; ATSP:F18B3.180
 A:Experimental source: cultivar Columbia; BAC clone F18B3
 C:Genetics:
 A:Gene: ATSP:F18B3.180
 A:Map position: 3
 C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match 42.9%; Score 5; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	GGWVDP	11
Db	99	GGWVDP	104

RESULT 2
 C82683
 disulfide oxidoreductase XF1436 [Imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: C82683
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: C82683
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-193 <SIM>
 A:Cross-references: GB:AE003973; GB:AE003849; NID:g9106438; PIDN:AAF84245.1; GSPDB:GN
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
 Briones, M.R.P.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carri
 as-Neto, E.; Docena, C.; El-Dorfi, H.; Facincaui, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 8

B60787 sperm-activating peptide (Thr-5 speract) - sea urchin (Hemicentrotus pulcherrimus)
C:Species: Hemicentrotus pulcherrimus
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: B60787

R:Yoshino, K.I.; Kajiyama, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
A:Reference number: A60787; MUID:88242184; PMID:3378407
C:Accession: B60787

A:Molecule type: protein
A:Residues: 1-10 <SU2>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 9

A60788 sperm-activating peptide (Thr-5 speract) - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: A60788

R:Suzuki, N.; Kajiyama, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
A:Reference number: A60787; MUID:88242184; PMID:3378407
C:Accession: A60788

A:Molecule type: protein
A:Residues: 1-10 <SU2>
C:Comment: This oligopeptide from egg jelly is one of several from this species. Unlike
of the repeats in the known precursor (see PIR:A34543).
C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 10

C60589 sperm-activating peptide (Thr-5 SAP-I) - Echinometa mathaei
C:Species: Echinometa mathaei
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: C60589
R:Yoshino, K.I.; Kajiyama, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe

otus nudus, Echinometa mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527

A:Accession: C60589
A:Molecule type: protein
A:Residues: 1-10 <VOS>
A:Note: an identical peptide was isolated from Echinometa mathaei type A and type B
C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 11

D60588 sperm-activating peptide (Thr-5 SAP-I) - sea urchin (Strongylocentrotus nudus)
N:Alternate names: speract homolog
C:Species: Strongylocentrotus nudus
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: D60588
R:Yoshino, K.I.; Kajiyama, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yama
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related
otus nudus, Echinometa mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: D60588
A:Molecule type: protein
A:Residues: 1-10 <VOS>
C:Superfamily: unassigned animal peptides

Query Match 35.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 5 TGGGV 9

RESULT 12

T26663 hypothetical protein Y38E10A.m - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26663
R:Wallis, J.

submitted to the EMBL Data Library, September 1999
A:Reference number: Z20252
A:Accession: T26663
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-71 <WIL>
A:Cross-references: EMBL:AL110484; NID:el542205; PIDN:CAR54404.1; CESP:Y38E10A.m
A:Experimental source: clone Y38E10A
C:Genetics:
A:Gene: CESP:Y38E10A.m

Query Match 35.7%; Score 5; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 32 TGGGV 36

RESULT 13

T48971 hypothetical protein F14D17.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unsel, M.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25008
A:Accession: T48971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-72 <J0R>
A:Cross-references: EMBL:AL353992; GSPDB:GN00061; ATSP:F14D17.20
A:Experimental source: cultivar Columbia; BAC clone F14D17
C:Genetics:
A:Gene: ATSP:F14D17.20
A:Map position: 3
A:Introns: 42/3

Query Match 35.7%; Score 5; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGVW 9
|||||
Db 66 GGGVW 70

RESULT 14
A69147
hypothetical protein MTH364 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: A69147
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:96037514; PMID:9371463
A:Accession: A69147
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-75 <MTH>
A:Cross-references: GB:AF000822; GB:AF000666; NID:g2621420; PIDN:AAB84870.1; PID:g262142
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH364
A:Start codon: TTG

Query Match 35.7%; Score 5; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 23 TGGGV 27

RESULT 15
S22454
ribosomal protein L2 REP - wood tobacco mitochondrion (fragment)
C:Species: mitochondrion Nicotiana sylvestris (wood tobacco)
C:date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 21-Jul-2000
C:Accession: S22454
R:Vitart, V.; de Paeppe, R.; Mathieu, C.; Chetrit, P.; Vedel, F.
Mol. Gen. Genet. 233, 193-200, 1992
A:Title: Amplification of substoichiometric recombinant mitochondrial DNA sequences in a
A:Reference number: S22454; MUID:92293115; PMID:1376403
A:Accession: S22454
A:Molecule type: DNA
A:Residues: 1-101 <VIT>
A:Cross-references: EMBL:X66519; NID:g396185; PIDN:CAA47138.1; PID:g396186
C:Genetics:
A:Genome: mitochondrion

C:Superfamily: Escherichia coli ribosomal protein L2
C:Keywords: mitochondrion

Query Match 35.7%; Score 5; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
|||||
Db 73 TGGGV 77

Search completed: March 13, 2003, 15:33:40
Job time : 16.5385 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:18:49 ; Search time 7.53846 Seconds
(without alignments)
77.027 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_l10
Perfect score: 14
Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6	42.9	511	1 DHAX_HUMAN	P49419 homo sapien
2	6	42.9	1123	1 PHYA_SOLTU	P30733 solanum tub
3	6	42.9	1124	1 PHY1_TOBAC	P33530 nicotiana t
4	5	35.7	68	1 YYY4_HUMAN	Q9ui36 homo sapien
5	5	35.7	114	1 PT11_STYPL	P28203 styela plic
6	5	35.7	119	1 THH2_BRANA	Q39362 brassica na
7	5	35.7	129	1 RS1A_HUMAN	P39027 homo sapien
8	5	35.7	129	1 RS1A_ICTPU	Q90yq8 ictalurus p
9	5	35.7	144	1 RL15_HAEIN	P44353 haemophilus
10	5	35.7	145	1 ANGL_MOUSE	P21570 mus musculu
11	5	35.7	169	1 PLMN_RAT	Q01177 rattus norv
12	5	35.7	181	1 FMKA_ECOLI	P04738 escherichia
13	5	35.7	184	1 VP50_BPAPS	Q9TLp8 bacterioph
14	5	35.7	189	1 AROK_SYNY3	P72796 synecocyst
15	5	35.7	197	1 VG23_BPMO2	Q38362 mycobacteri
16	5	35.7	197	1 VG23_BPML5	Q05229 mycobacteri
17	5	35.7	201	1 CLPP_AQUAE	O67357 aquifex aeo
18	5	35.7	207	1 CLPP_YEREN	Q60107 yersinia en
19	5	35.7	208	1 CLPP_XYLFA	Q9pe41 xyella fas
20	5	35.7	223	1 RLA_MYCBO	O06045 mycobacteri
21	5	35.7	223	1 RLA_MYCTU	P95050 mycobacteri
22	5	35.7	229	1 H1S4_PYRAE	Q8zy14 pyrobaculum
23	5	35.7	238	1 MOTB_TREPA	Q07887 treponema p
24	5	35.7	240	1 HLXX_ACTPL	P23619 actinobacil
25	5	35.7	241	1 PYRE_TRETH	P96076 thermus the
26	5	35.7	245	1 PELA_HAEIN	P43751 haemophilus
27	5	35.7	245	1 T2M4_METJA	Q58723 methanococc
28	5	35.7	261	1 YY00_MYCLE	Q49741 mycobacteri
29	5	35.7	262	1 RS2_THEMEA	Q9wzml thermotoga
30	5	35.7	265	1 H1S4_XYLFA	Q9pbc9 xyella fas
31	5	35.7	270	1 L181_CHLEU	Q03965 chlamydomon
32	5	35.7	270	1 URED_SYNY3	P73047 synecocyst
33	5	35.7	285	1 NADC_MYCTU	O06594 mycobacteri

34	5	35.7	294	1 TOXR_VIBCH	P15795 vibrio chol
35	5	35.7	296	1 SAPR_STRPU	P11761 strongyloce
36	5	35.7	297	1 EZV3_CHLRE	Q08356 chlamydomon
37	5	35.7	303	1 Y722_SYNY3	P72667 synecocyst
38	5	35.7	304	1 LST_HAEIN	Q48211 haemophilus
39	5	35.7	319	1 AES_ECOLI	P23872 escherichia
40	5	35.7	325	1 YC83_MYCTU	Q10611 mycobacteri
41	5	35.7	333	1 EBP2_SCHPO	O13802 schizosacch
42	5	35.7	337	1 TAT_HTLV2	P03410 human t-cel
43	5	35.7	343	1 SLAM_MOUSE	Q9gum4 mus musculu
44	5	35.7	344	1 JUNE_MOUSE	P09450 mus musculu
45	5	35.7	344	1 JUNE_RAT	P24898 rattus norv

ALIGNMENTS

RESULT 1
DHAX_HUMAN
ID DHAX_HUMAN STANDARD; PRT; 511 AA.
AC P49419;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiquitin (EC 1.2.1.1).
GN ALDH7A1 OR ATQ1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
.. OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, Liver, and Placenta;
RX MEDLINE=94375061; PubMed=8088832;
RA Lee P., Kuhl W., Gelbart F., Kamimura T., West C., Beutler E.;
RT "Homology between a human protein and a protein of the green garden pea.";
RL Genomics 21:371-378(1994).
CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC STRONGEST. TO PEA 26G.
CC -----
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CC -----
CC EMBL; S74728; AAB31966.1; -.
DR HSSP; P51977; IBSX.
DR Genew; HGNC:877; ALDH7A1.
DR MIM; 107323; -.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR Pfam; PF00171; aldehyd; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; FALSE_NEG.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Oxidoreductase; NAD.
FT NP_BIND 246 251 NAD (ADP PART) (BY SIMILARITY).
FT ACT_SITE 268 268 BY SIMILARITY.
FT ACT_SITE 302 302 BY SIMILARITY.
SQ SEQUENCE 511 AA; 55366 MW; 08F6F7672C948E2C CRC64;

Query Match 42.98; Score 6; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7
|||||
Db 472 KHTGGG 477

RESULT 2

PHYA_SOLTU STANDARD; PRT; 1123 AA.
 AC P30733;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phytochrome A.
 GN PHYA.
 OS Solanum tuberosum (Potato).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Desiree;
 RX MEDLINE=92163018; PubMed=1536928;
 RA Heyer A., Gatz C.;
 RT "Isolation and characterization of a cDNA-clone coding for potato
 type A phytochrome.";
 RL Plant Mol. Biol. 18:535-544(1992).
 CC -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
 CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
 CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
 CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
 CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
 CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
 CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
 CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
 CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
 CC PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS
 CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
 CC -!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
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 CC -----
 CC EMBL; S84872; AAB21533.2; -.
 CC PIR; S20497; S20497.
 CC InterPro; IPR003594; ATPbind_ATPase.
 CC InterPro; IPR003018; GAF.
 CC InterPro; IPR004359; HIS_KIN_sig.
 CC InterPro; IPR003661; HIS_KIN.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000700; PAS-assoc_C.
 CC InterPro; IPR000014; PAS_domain.
 CC InterPro; IPR001294; Phytochrome.
 CC Pfam; PF00360; phytochrome; 1.
 CC Pfam; PF00512; signal; 1.
 CC Pfam; PF00989; PAS; 2.
 CC Pfam; PF01590; GAF; 1.
 CC Pfam; PF02518; HATPase_c; 1.
 CC PRINTS; PR01033; PHYTOCHROME.
 CC SMART; SM00065; GAF; 1.
 CC SMART; SM00387; HATPase_c; 1.
 CC SMART; SM00388; HSKA; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC TIGRFAMs; TIGR00229; sensory_box; 1.
 CC PROSITE; PS50109; HIS_KIN; 1.
 CC PROSITE; PS50113; PAC; 1.
 CC PROSITE; PS50112; PAS; 2.
 CC PROSITE; PS00245; PHYTOCHROME_1; 1.

DR PROSITE; PS50046; PHYTOCHROME_2; 1.
 KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
 KW Repeat; Multigene family.
 FT DOMAIN 617 687 PAS 1.
 FT DOMAIN 690 746 PAC.
 FT DOMAIN 747 821 PAS 2.
 FT DOMAIN 901 1118 HISTIDINE KINASE.
 FT BINDING 323 323 CHROMOPHORE.
 SQ SEQUENCE 1123 AA; 124689 MW; 3A97062A5DFB29EA CRC64;
 Query Match 42.9%; Score 6; DB 1; Length 1123;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HTGGGV 8
 Db 1058 HTGGGV 1063
 |||||
 |||||
 RESULT 3
 ID PHY1_TOBAC STANDARD; PRT; 1124 AA.
 AC P35530;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phytochrome A1.
 GN PHYA1.
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94143494; PubMed=8310074;
 RA Adam E., Deak M., Kay S., Chua N.H., Nagy F.;
 RT "Sequence of a tobacco (Nicotiana tabacum) gene coding for type A
 phytochrome.";
 RL Plant Physiol. 101:1407-1408(1993).
 CC -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
 CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
 CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
 CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
 CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
 CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
 CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
 CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
 CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
 CC PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS
 CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
 CC -!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
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 CC -----
 CC EMBL; X66784; CAA47284.1; -.
 CC InterPro; IPR003594; ATPbind_ATPase.
 CC InterPro; IPR003018; GAF.
 CC InterPro; IPR004359; HIS_KIN_sig.
 CC InterPro; IPR003661; HIS_KIN.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000700; PAS-assoc_C.


```
DR InterPro; IPR000014; PAS_domain.  
DR InterPro; IPR001294; Phytochrome.  
DR Pfam; PF00360; phytochrome; 1.  
DR Pfam; PF00512; signal; 1.  
DR Pfam; PF00989; PAS; 2.  
DR Pfam; PF01590; GAF; 1.  
DR Pfam; PF02518; HATPase_c; 1.  
DR PRINTS; PR01033; PHYTOCHROME.  
DR SMART; SM00065; GAF; 1.  
DR SMART; SM00387; HATPase_c; 1.  
DR SMART; SM00388; HSKA; 1.  
DR SMART; SM00086; PAC; 1.  
DR SMART; SM00091; PAS; 2.  
DR TIGRFS; TIGR00229; sensory_box; 1.  
DR PROSITE; PS50109; HIS_KIN; 1.  
DR PROSITE; PS50113; PAC; 1.  
DR PROSITE; PS50112; PAS; 2.  
DR PROSITE; PS00245; PHYTOCHROME_1; 1.  
DR PROSITE; PS0046; PHYTOCHROME_2; 1.  
KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;  
KW Repeat; Multigene family.  
FT DOMAIN 617 687 PAS 1.  
FT DOMAIN 690 746 PAC.  
FT DOMAIN 747 821 PAS 2.  
FT DOMAIN 901 1118 HISTIDINE KINASE.  
FT BINDING 323 323 CHROMOPHORE (BY SIMILARITY).  
SQ SEQUENCE 1124 AA; 124296 MW; 4C2938CFE9A5F130 CRC64;  
  
Query Match 42.9%; Score 6; DB 1; Length 1124;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 HTGGGV 8  
|||||  
Db 1058 HTGGGV 1063  
  
RESULT 4  
YYV4_HUMAN  
ID YYV4_HUMAN STANDARD; PRT; 68 AA.  
AC Q9U156;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Very very hypothetical protein from MEG3 locus (protein PR00518).  
GN MEG3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal liver;  
RA Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,  
RA Liu M., He F.;  
RT "Functional prediction of the coding sequences of 50 new genes deduced  
RT by analysis of cDNA clones from human fetal liver."  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP PROBABLE FUNCTION AS A RNA.  
RA Miyoshi N., Wagatsuma H., Wakana S., Shiroishi T., Nomura M.,  
RA Aisaka K., Kohda T., Surani M.A., Kaneko-Ishino T., Ishino F.;  
RT "Identification of an imprinted gene, Meg3/Gtl2 and its human  
RT homologue MEG3, first mapped on mouse distal chromosome 12 and human  
RT chromosome 14q."  
RL Genes Cells 5:211-220(2000).  
CC -!- CAUTION: There is no evidence of expression of this protein. The  
CC MEG3 (Maternally Expressed) gene probably encodes for a RNA.  
CC  
-----  
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-----  
DR EMBL; AF090934; AAF24048.1; -.  
DR MIM; 605636; -.  
DR Genew; HGNC:14575; MEG3.  
KW Hypothetical protein.  
SQ SEQUENCE 68 AA; 7791 MW; DDC6B78EC2981B99 CRC64;  
  
Query Match 35.7%; Score 5; DB 1; Length 68;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 KHTGG 6  
|||||  
Db 22 KHTGG 26  
  
RESULT 5  
PTL1_STYPL  
ID PTL1_STYPL STANDARD; PRT; 114 AA.  
AC P28203;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Protein-tyrosine phosphatase 11 (EC 3.1.3.48) (Fragment).  
GN STY 11.  
OS Styela plicata (Sea squirt).  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
OC Stolidobranchia; Styelidae; Styela.  
OX NCBI_TaxID=7726;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91139172; PubMed=1704870;  
RA Matthews R.J., Flores E., Thomas M.L.;  
RT "Protein tyrosine phosphatase domains from the protochordate Styela  
RT plicata."  
RL Immunogenetics 33:33-41(1991).  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
-----  
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-----  
DR EMBL; M37996; AAA29829.1; -.  
DR HSSP; P28827; IRPM.  
DR InterPro; IPR000340; DS-phosphatase.  
DR InterPro; IPR000387; TYR_phosphatase.  
DR InterPro; IPR000242; Tyr_PP.  
DR Pfam; PF00102; Y-phosphatase; 1.  
DR SMART; SM00012; YTPC_DSPC; 1.  
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; PARTIAL.  
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; PARTIAL.  
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.  
KW Hydrolase.  
KW NON_TER  
FT NON_TER 1 1  
FT NON_TER 114 114  
SQ SEQUENCE 114 AA; 13566 MW; 1FBF565A3D1F8945 CRC64;  
  
Query Match 35.7%; Score 5; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AKHTG 5  
|||||  
Db 106 AKHTG 110
```

```
RESULT 6
THH2_BRANA STANDARD; PRT; 119 AA.
AC Q39362;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioresoxin H-type 2 (TRX-H-2).
GN THL-2.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Pistill;
RC MEDLINE=96434547; PubMed=8837514;
RA Bower M.S., Matias D.D., Fernandes-Carvalho E., Mazzurco M., Gu T.,
RA Rothstein S.J., Goring D.R.;
RT "Two members of the thioresoxin-h family interact with the kinase
RT domain of a Brassica S locus receptor kinase.";
RL Plant Cell 8:1641-1650(1996).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of the active center dithiol to a disulfide.
CC The H form is known to activate a number of cytosolic enzymes (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN FLORAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. PLANT H-TYPE.
-----
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-----
DR EMBL; U59380; AB53695.1; -
DR HSSP; P10599; IERV.
DR InterPro; IPR000063; Thiores.
DR Pfam; PF00085; thiores; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFS; TIGR01068; thioresoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Redox-active center; Electron transport; Multigene family.
KW DISULFID 40 43 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 119 AA; 12949 MW; 84A9985C618B1246 CRC64;
Query Match 35.7%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKHTG 5
| | | |
DB 111 AKHTG 115
RESULT 7
RS1A_HUMAN STANDARD; PRT; 129 AA.
AC P39027; P39031; Q9BV24;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S15a.
GN RPS15A.
OS Homo sapiens (Human), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
-----
OX NCBI_TaxID=9606, 10116;
[1]
RN SEQUENCE FROM N.A.
RP SPECIES=Human;
RC Schwabe G.;
RA Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP SPECIES=Human; TISSUE=Carcinoma;
RA Mays G., Burchert-Graeve M.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP SPECIES=Human;
RA Shichiho S., Itoh K.;
RT "Identification of immuno-peptidomics that recognized by tumor-reactive
RT CTL generated from TIL of colon cancer patients.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RP SPECIES=Human; TISSUE=Eye, and Skin;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE OF 43-53 FROM N.A.
RP SPECIES=Human;
RC MEDLINE=98248690; PubMed=9582194;
RA Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N.,
RA Hudson T.J., Tanaka T., Page D.C.;
RT "A map of 75 human ribosomal protein genes.";
RL Genome Res. 8:509-523(1998).
[6]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-37.
RP SPECIES=Rat; STRAIN=Sprague-Dawley; TISSUE=Liver;
RC MEDLINE=94242014; PubMed=8185605;
RA Chan Y.-L., Olivera J., Paz V., Wool I.G.;
RT "The primary structure of rat ribosomal protein S15a.";
RL Biochem. Biophys. Res. Commun. 200:1498-1504(1994).
CC -1- SIMILARITY: BELONGS TO THE S8P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS
CC 23 TO 36 DUE TO PROBABLE FRAMESHIFT ERRORS.
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-----
DR EMBL; X62691; CAA44568.1; ALT_FRAME.
DR EMBL; X84407; CAA59127.1; -
DR EMBL; AB062400; BAB93487.1; -
DR EMBL; BC001697; AAH01697.1; -
DR EMBL; BC030569; AAH30569.1; -
DR EMBL; AB007154; BAA28592.1; -
DR EMBL; X77953; CAA54918.1; -
DR PIR; S22051; S22051.
DR PIR; JC2234; JC2234.
DR Genew; HGNC:10389; RPS15A.
DR MIM; 603674; -
DR InterPro; IPR000630; Ribosomal_S8.
DR Pfam; PF00410; Ribosomal_S8; 1.
DR Prodom; PD001098; Ribosomal_S8; 1.
DR PROSITE; PS00053; RIBOSOMAL_S8; 1.
KW Ribosomal protein.
FT INIT_MET 0
FT CONFLICT 39 39 V -> L (IN REF. 2).
FT CONFLICT 78 78 F -> S (IN REF. 4; AAH01697).
SQ SEQUENCE 129 AA; 14708 MW; 4D95D7EE94E3A1E2 CRC64;
Query Match 35.7%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 58;
```

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KHTGG 6
|||||
Db 118 KHTGG 122

RESULT 8
RS1A_ICTPU
ID RS1A_ICTPU STANDARD; PRT; 129 AA.
AC Q90YQ8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S15a.
GN RPS15A.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12095691;
RA Karsi A., Patterson A., Peng J., Liu Z.-J.;
RT "Translational machinery of channel catfish: I. A transcriptomic
RT approach to the analysis of 32 40S ribosomal protein genes and their
RT expression.";
RL Gene 291:177-186(2002).
CC -!- SIMILARITY: BELONGS TO THE S8P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
CC EMBL: AF402824; AAK95198.1; ALT INIT.
CC TIGR: HI0797;
CC InterPro: IPR000630; Ribosomal_S8.
CC Pfam: PF00410; Ribosomal_S8; 1.
CC PROSITE: PS00053; RIBOSOMAL_S8; 1.
CC Ribosomal protein.
CC INIT_MET 0
CC SEQUENCE 129 AA; 14613 MW; 503D34786583D7A7 CRC64;
BY SIMILARITY.
QY 2 KHTGG 6
|||||
Db 118 KHTGG 122

RESULT 9
RL15_HAEIN
ID RL15_HAEIN STANDARD; PRT; 144 AA.
AC P44353;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L15.
GN RPL0 OR RPL15 OR HI0797.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;

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RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL: U32762; AAC22455.1;
CC TIGR: HI0797;
CC InterPro: IPR001196; Ribosomal_L15.
CC Pfam: PF00256; L15; 1.
CC TIGRFAMs: TIGR01071; rplO_bact; 1.
CC PROSITE: PS00475; RIBOSOMAL_L15; 1.
CC Ribosomal protein; rRNA-binding; Complete proteome.
CC SEQUENCE 144 AA; 15072 MW; F0CFC80684DC64C5 CRC64;
Query Match 35.7%; Score 5; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TGGGV 8
|||||
Db 42 TGGGV 46

RESULT 10
ANGI_MOUSE
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,

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CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC
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 CC
 CC EMBL; U22516; AAA91366.1; -
 CC PIR; A35932; A35932.
 CC HSSP; P03950; 1A4Y.
 CC MGD; MGI:88022; Ang.
 CC PIRam; PF00074; RNaseA; 1.
 CC PRINTS; PR00794; RIBONUCLEASE.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNaseA_Pc; 1.
 CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
 CC Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 CC Protein synthesis inhibitor; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 145 ANGIOGENIN.
 CC MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
 CC
 CC ACT_SITE 37 37 BY SIMILARITY.
 CC ACT_SITE 64 64 BY SIMILARITY.
 CC ACT_SITE 137 137 BY SIMILARITY.
 CC DISULFID 50 104 BY SIMILARITY.
 CC DISULFID 63 115 BY SIMILARITY.
 CC DISULFID 81 130 BY SIMILARITY.
 CC SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;
 SQ
 Query Match 35.7%; Score 5; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KHTGG 6
 Db 105 KHTGG 109
 |||||
 RESULT 11
 ID PLMN_RAT STANDARD; PRT; 169 AA.
 AC Q01177;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN PLG.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=91250378; PubMed=1645711;
 RA Kanalas J.J.; Makker S.P.;
 RT Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RT receptor site for plasminogen.;
 RL J. Biol. Chem. 266:10825-10829(1991).
 CC -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,

CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-I-Xaa > Arg-I-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC
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 CC
 CC EMBL; M62832; AAA41884.1; -
 CC PIR; A40522; A40522.
 CC HSSP; P00747; 1PMK.
 CC MEROPS; S01.233; -
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR001254; Ser-protease_Try.
 CC Pfam; PF00051; kringle; 2.
 CC ProDom; PD000395; Kringle; 2.
 CC SMART; SM00130; KR; 1.
 CC PROSITE; PS00021; KRINGLE_1; 1.
 CC PROSITE; PS50070; KRINGLE_2; 2.
 CC PROSITE; PS50240; TRYPSIN_DOM; PARTIAL.
 CC PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
 CC PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
 CC Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 CC Tissue remodeling; Blood coagulation; Kringle; Repeat.
 CC NON_TER 1 1
 CC DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
 CC DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
 CC DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
 CC DISULFID 34 112 BY SIMILARITY.
 CC DISULFID 55 95 BY SIMILARITY.
 CC DISULFID 83 107 BY SIMILARITY.
 CC NON_TER 169 169
 CC SEQUENCE 169 AA; 18401 MW; 77A54214C49D010C CRC64;
 SQ
 Query Match 35.7%; Score 5; DB 1; Length 169;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TGGGV 8
 Db 115 TGGGV 119
 |||||
 RESULT 12
 ID FMKA_ECOLI STANDARD; PRT; 181 AA.
 AC P04738;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE K88 fimbrial protein A precursor.
 GN FAEC.
 OS Escherichia coli.
 CC Plasmid pF205.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 CC NCBI_TaxID=562;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=84264326; PubMed=6086572;
RA Mooi F.R., van Buuren M., Koopman G., Roosendaal B., de Graaf F.K.;
RT "K88ab gene of Escherichia coli encodes a fimbria-like protein
RL distinct from the K88ab fimbrial adhesin.";
RJ J. Bacteriol. 159:482-487(1984).
RN [2]
RP SEQUENCE OF 160-181 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=86176742; PubMed=2870470;
RA Mooi F.R., Claassen I., Bakker D., Kuipers H., de Graaf F.K.;
RT "Regulation and structure of an Escherichia coli gene coding for an
RL outer membrane protein involved in export of K88ab fimbrial
RJ subunits.";
RN Nucleic Acids Res. 14:2443-2457(1986).
RL -!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -!- SUBUNIT: K88 FIMBRIA, 0.1-1 MICROMETER IN LENGTH AND 7 NANOMETERS
CC IN DIAMETER, IS COMPOSED OF ABOUT 100 IDENTICAL SUBUNITS.
CC -!- SUBCELLULAR LOCATION: PREDOMINANTLY LOCATED AT THE TIP OF THE
CC FIMBRIAE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00940; CAA25454.1; -.
CC DR EMBL; X00940; CAA25454.1; -.
CC KW Fimbria; Signal; Plasmid.
CC FT SIGNAL 1 21
CC FT CHAIN 22 181 K88 FIMBRIAL PROTEIN A.
CC FT DISULFID 37 84 PROBABLE.
CC SQ SEQUENCE 181 AA; 13066 MW; 44EA049DA025D011 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
DB 14 TGGGV 18

RESULT 13
VP50_BPAPS STANDARD; PRT; 184 AA.
ID Q9TIP8;
AC VP50_BPAPS
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative protein P50.
GN 50
OS Bacteriophage APSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC unclassified Podoviridae.
OX NCBI_TaxID=106199;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99420383; PubMed=10489345;
RA van der Wilk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
RL the secondary endosymbiont of acyrthosiphon pisum.";
RJ Virology 262:104-113(1999).
CC -----
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CC -----
CC EMBL; AF157835; AAF03993.1; -.
CC DR Hypothetical protein.
CC KW Hypothetical protein.
CC SQ SEQUENCE 184 AA; 20416 MW; EB705FA272B6768F CRC64;

Query Match 35.7%; Score 5; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGV 8
DB 160 TGGGV 164

RESULT 14
AROK_SYNY3 STANDARD; PRT; 189 AA.
ID AROK_SYNY3
AC P72796;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Shikimate kinase (EC 2.7.1.71) (SK).
GN AROK OR SLL1669.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Suglura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fifth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (probable).
CC -!- SIMILARITY: BELONGS TO THE SHIKIMATE KINASE FAMILY.
CC -----
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CC -----
CC EMBL; D90300; BAA16811.1; -.
CC DR HSP; P10880; ISHK.
CC DR InterPro; IPR000623; SHIK_kinase.
CC DR Pfam; PF01202; SKI; 1.
CC DR PRINTS; PR01100; SHIKIMTKINASE.
CC DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
CC Aromatic amino acid biosynthesis; Transferase; Kinase; ATP-binding;
KW Complete proteome.
FT NP_BIND 19 26 ATP (POTENTIAL).
FT SQ SEQUENCE 189 AA; 20697 MW; 41727D4EC6E585D9 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Fri Mar 14 09:39:59 2003

QY 4 TGGGV 8
 |||||
 Db 88 TGGGV 92

RESULT 15
 VG23_BPMD2
 ID VG23_BPMD2 STANDARD; PRT; 197 AA.
 AC Q38362; O64217;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Major tail protein GP23 (Major coat protein).
 GN 23.
 OS Mycobacteriophage D29.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC unclassified Siphoviridae.
 OX NCBI_TaxID=28369;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shramm Y., Wyse J., Mink S., Suissa M., Kuhn J.;
 RT "Cloning, sequence and expression of the gene coding for the major
 RL coat protein of Mycobacteriophage D29."; Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98300335; PubMed=9636706;
 RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
 RT "Genome structure of mycobacteriophage D29: implications for phage
 evolution."; J. Mol. Biol. 279:143-164(1998).
 CC -----
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 CC -----
 DR EMBL; X70353; CAA49811.1; -;
 KW Coats protein.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT CONFLICT 25 25 H -> P (IN REF. 1).
 FT CONFLICT 176 176 K -> E (IN REF. 1).
 SQ SEQUENCE 197 AA; 21183 MW; 548580298149564D CRC64;
 Query Match 35.7%; Score 5; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. NO. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DPIDY 14
 |||||
 Db 86 DPIDY 90

Search completed: March 13, 2003, 15:32:06
 Job time : 9.53846 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:28:09 ; Search time 26.9231 Seconds
(without alignments)
107.144 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 14
Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	42.9	114	10 Q9SVK9	Q9svk9 arabidopsis
2	6	42.9	131	4 Q8WY0	Q8wyo0 homo sapien
3	6	42.9	164	16 Q98HY2	Q98hy2 rhizobium l
4	6	42.9	181	13 Q91665	Q91665 xenopus lae
5	6	42.9	192	5 Q9N6S3	Q9n6s3 leishmania
6	6	42.9	193	16 Q9PDE3	Q9pde3 xylella fas
7	6	42.9	381	16 Q98CL9	Q98cl9 rhizobium l
8	6	42.9	436	16 Q9K6F3	Q9k6f3 bacillus ha
9	6	42.9	474	16 Q98MD0	Q98md0 rhizobium l
10	6	42.9	502	16 Q8Y012	Q8y012 ralstonia s
11	6	42.9	511	4 Q9BUL4	Q9bul4 homo sapien
12	6	42.9	511	11 Q9BDF1	Q9bdf1 mus musculu
13	6	42.9	614	16 Q98212	Q98212 rhizobium l
14	6	42.9	1068	10 Q9FF3	Q9fff3 arabidopsis
15	6	42.9	1123	10 Q41331	Q41331 lycopersico
16	5	35.7	46	15 Q80812	Q80812 human t-lym

17	5	35.7	52	12 Q98809	Q98809 yam mosaic
18	5	35.7	53	15 Q992L1	Q992l1 human t-cel
19	5	35.7	57	10 Q9SAT4	Q9sat4 nicotiana t
20	5	35.7	71	5 Q9NAJ8	Q9naj8 caenorhabdi
21	5	35.7	72	10 Q9LX10	Q9lxi0 arabidopsis
22	5	35.7	75	17 Q26464	Q26464 methanobact
23	5	35.7	77	15 Q9198	Q9198 human t-lym
24	5	35.7	78	5 Q8WR25	Q8wr25 anopheles g
25	5	35.7	85	11 Q9JHY3	Q9jhy3 mus musculu
26	5	35.7	90	16 Q931P1	Q931p1 staphylococ
27	5	35.7	94	5 Q9VM00	Q9vm00 drosophila
28	5	35.7	101	8 Q08712	Q08712 nicotiana s
29	5	35.7	102	2 Q9LCA9	Q9lca9 rhodocyclus
30	5	35.7	103	16 Q9KJ66	Q9k166 streptomyc
31	5	35.7	107	2 Q51490	Q51490 pseudomonas
32	5	35.7	109	10 Q9FJ20	Q9fj20 arabidopsis
33	5	35.7	110	11 Q9D905	Q9d9u5 mus musculu
34	5	35.7	111	5 Q8WPS3	Q8wps3 trypanosoma
35	5	35.7	117	2 Q9RH52	Q9rh52 streptomyc
36	5	35.7	117	11 Q9D466	Q9d466 mus musculu
37	5	35.7	118	6 Q95JT4	Q95jt4 macaca fasc
38	5	35.7	119	16 Q9KFF7	Q9kff7 bacillus ha
39	5	35.7	122	10 Q9LW24	Q9lw24 arabidopsis
40	5	35.7	124	8 Q35862	Q35862 schistosoma
41	5	35.7	127	13 Q90YQ8	Q90yq8 ictalurus p
42	5	35.7	128	8 Q954T6	Q954t6 dugesia pol
43	5	35.7	130	4 Q9BV24	Q9bv24 homo sapien
44	5	35.7	130	5 Q77395	Q77395 plasmodium
45	5	35.7	130	13 Q91A74	Q91a74 paralichthy

ALIGNMENTS

RESULT 1

ID Q9SVK9 PRELIMINARY; PRT; 114 AA.
AC Q9SVK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Hypothetical 12.9 kDa protein.
GN F18B3.180.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_taxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M., F.,
RA Meves H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetier F.,
RA Salanoubat M.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049862; CAB42919.1; -
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12923 MW; F8156E1465887DBB CRC64;

Query Match 42.9%; Score 6; DB 10; Length 114;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGVWDP 11

|||||

Db 99 GGVWDP 104

RESULT 2

Q8WY0

ID	Q8WY0	PRELIMINARY;	PRT;	131 AA.
AC	Q8WY0;			
DT	01-MAR-2002 (TReMBLrel. 20, Created)			
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)			
DE	Hypothetical 13.9 kDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,			
RA	Wan D.F., Gu J.R.;			
RT	"Novel human cDNA clones with function of inhibiting cancer cell			
RT	growth."			
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF289615; AAL5799.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 131 AA; 13879 MW; BID6A5917F3608ED CRC64;			
Query Match 42.9%; Score 6; DB 4; Length 131;				
Best Local Similarity 100.0%; Pred. No. 21;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	4 TGGGVW 9			
Db	29 TGGGVW 34			
RESULT 3				
Q98HY2	PRELIMINARY;	PRT;	164 AA.	
ID	Q98HY2			
AC	Q98HY2;			
DT	01-OCT-2001 (TReMBLrel. 18, Created)			
DT	01-OCT-2001 (TReMBLrel. 18, Last sequence update)			
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)			
DE	Hypothetical protein ms18626.			
GN	MS18626.			
OS	Rhizobium loti (Mesorhizobium loti).			
OC	Bacteria; Proteobacteria; alpha subdlvision; Rhizobiaceae group;			
OC	Phyllobacteriaceae; Mesorhizobium.			
OX	NCBI_TaxID=381;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MAFF303099;			
RC	MEDLINE=21082930; PubMed=11214968;			
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,			
RA	Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,			
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,			
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,			
RA	Takeuchi C., Yamada M., Tabata S.;			
RT	"Complete genome structure of the nitrogen-fixing symbiotic bacterium			
RT	Mesorhizobium loti."			
RL	DNA Res. 7:331-338 (2000).			
DR	EMBL; AP003000; BAB49734.1; -			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 164 AA; 16680 MW; 8489A02A3C55D76D CRC64;			
Query Match 42.9%; Score 6; DB 16; Length 164;				
Best Local Similarity 100.0%; Pred. No. 26;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 AKHTGG 6			
Db	90 AKHTGG 95			
RESULT 4				
Q91665	PRELIMINARY;	PRT;	181 AA.	
ID	Q91665			
AC	Q91665;			
DT	01-NOV-1996 (TReMBLrel. 01, Created)			
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)			
DE	CTX (Fragment).			
GN	Gl.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FF;			
RC	MEDLINE=96210130; PubMed=8625968;			
RA	Chretien I., Robert J., Marcuz A., Garcia-Sanz J.A., Courtet M.,			
RA	Du Pasquier L.;			
RT	"CTX, a novel molecule specifically expressed on the surface of			
RT	cortical thymocytes in Xenopus."			
RL	Eur. J. Immunol. 26:780-791(1996).			
DR	EMBL; U43393; AAC59860.1; -			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR003600; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; IG; 1.			
DR	SMART; SM00410; IG-like; 1.			
FT	NON_TER 1			
SQ	SEQUENCE 181 AA; 19380 MW; 6A558F6C824EDC16 CRC64;			
Query Match 42.9%; Score 6; DB 13; Length 181;				
Best Local Similarity 100.0%; Pred. No. 28;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	3 HTGGGV 8			
Db	154 HTGGGV 159			
RESULT 5				
Q9N6S3	PRELIMINARY;	PRT;	192 AA.	
ID	Q9N6S3			
AC	Q9N6S3;			
DT	01-OCT-2000 (TReMBLrel. 15, Created)			
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TReMBLrel. 15, Last annotation update)			
DE	L7535.14.			
GN	L822.2 OR L7535.14.			
OS	Leishmania major.			
OC	Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.			
OX	NCBI_TaxID=5664;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FRIEDLIN;			
RA	Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,			
RA	Cawthra J., Marsolini F., Sunkin S., Stuart K.D.;			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FRIEDLIN;			
RA	Myler P.J.;			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AC005893; AAF31031.1; -			
DR	EMBL; AC005767; AAF27953.1; -			
DR	EMBL; AC005766; AAF28379.1; -			
SQ	SEQUENCE 192 AA; 19650 MW; 0CE9460B1FB5A9C4 CRC64;			
Query Match 42.9%; Score 6; DB 5; Length 192;				
Best Local Similarity 100.0%; Pred. No. 30;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	3 HTGGGV 8			
Db	129 HTGGGV 134			


```

RESULT 6
Q9PDE3 ID Q9PDE3 PRELIMINARY; PRT; 193 AA.
AC Q9PDE3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Disulfide oxidoreductase.
GN XF1436.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
[1]
SEQUENCE FROM N.A.
RX STRAIN=9A5C;
MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Canargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Froime M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Slyks M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL: AE003973; AAF84245.1; -.
DR InterPro: IPR001853; DSSA.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF01323; DSSA; 1.
DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 193 AA; 21305 MW; 552DC6D86B4F555D CRC64;

Query Match 42.9%; Score 6; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWDP 11
Db 68 GGWDP 73

[11111]

RESULT 7
Q98C19 ID Q98C19 PRELIMINARY; PRT; 381 AA.
AC Q98C19;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical protein mlr5331.
GN MLR5331.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
[1]
SEQUENCE FROM N.A.
RX STRAIN=9A5C;
MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Canargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Froime M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Slyks M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL: AE003973; AAF84245.1; -.
DR InterPro: IPR001853; DSSA.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF01323; DSSA; 1.
DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 193 AA; 21305 MW; 552DC6D86B4F555D CRC64;

Query Match 42.9%; Score 6; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGWDP 11
Db 68 GGWDP 73

[11111]

RESULT 8
Q9K6F3 ID Q9K6F3 PRELIMINARY; PRT; 436 AA.
AC Q9K6F3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH oxidase (nox).
GN BH3776.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
[1]
SEQUENCE FROM N.A.
RX STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -/- COFACTOR: FAD (BY SIMILARITY).
DR EMBL: AF001519; BAB07495.1; -.
DR HSSP: P37062; INHP.
DR InterPro: IPR001327; FAD_pyr_redox.
DR InterPro: IPR000205; NAD_binding.
DR InterPro: IPR000103; Pyridine_redox_2.
DR InterPro: IPR001100; Pyr_redox.
DR InterPro: IPR004099; Pyr_redox.
DR Pfam: PF00070; pyr_redox; 1.

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DR Pfam: PF02852; pyr_redox_dim; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEII.
DR PRINTS; PR00469; PNDRTASEII.
DR ProDom: PD000139; FAD_pyr_redox; 1.
DR FAD; Flavoprotein; Oxidoreductase; Complete proteome.
KW SEQUENCE 436 AA; 47376 MW; 6B7997FD763FF732 CRC64;

Query Match 42.9%; Score 6; DB 16; Length 436;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GWDPI 12
DB 424 GWDPI 429

RESULT 9
ID Q98MD0 PRELIMINARY; PRT; 474 AA.
AC Q98MD0;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glutamyl-trna synthetase.
GN MRL0628.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AF002995; BAB48183.1; -.
DR InterPro; IPR004527; GltX_bact.
DR InterPro; IPR000924; GltX-trna-synt_1c.
DR Pfam; PF00749; trna-synt_1c; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMs; TIGR00464; gltX_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-trna synthetase; Complete proteome.
SQ SEQUENCE 474 AA; 51491 MW; 7A2F5D16AFF4DAFB CRC64;

Query Match 42.9%; Score 6; DB 16; Length 474;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGG 6
DB 32 AKHTGG 37

RESULT 10
ID Q8Y012 PRELIMINARY; PRT; 502 AA.
AC Q8Y012;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Probable transporter transmembrane protein.
GN RSC1233 OR RS02740.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

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OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646063; CAD14935.1; -.
DR InterPro; IPR001248; Cyt_pur_permease.
DR Pfam; PF02133; Transp_cyt_pur; 1.
DR TIGRFAMs; TIGR00800; ncs1; 1.
KW Complete proteome.
SQ SEQUENCE 502 AA; 53783 MW; 7F72D191E74030C0 CRC64;

Query Match 42.9%; Score 6; DB 16; Length 502;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VWDPID 13
DB 304 VWDPID 309

RESULT 11
ID Q9BUL4 PRELIMINARY; PRT; 511 AA.
AC Q9BUL4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Antiquitin 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL; BC002515; AAH02515.1; -.
DR HSP; P51977; 1BXS.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR Pfam; PF00171; aldehyd; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 511 AA; 55366 MW; 6B39D6B5383F7A93 CRC64;

Query Match 42.9%; Score 6; DB 4; Length 511;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGG 7
DB 472 KHTGG 477

RESULT 12
ID Q9DBF1 PRELIMINARY; PRT; 511 AA.
AC Q9DBF1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE DNA segment, Chr 18, Wayne state university 181, expressed (unknown)

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DE (Protein for MGC:18699).

GN D18WSu181E.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=LIVER;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinaawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,

RA Saito T., Okazaki Y., Gyojbori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Salivary Gland;

RA Strausberg R.;

RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

DR EMBL; AK004991; BAB23726.1; -.

DR EMBL; BC012407; AAH12407.1; -.

DR MGD; MGI:107847; D18WSu181E.

DR InterPro; IPR002086; Aldehyde_dehydr.

DR Pfam; PF00171; aldedh; 1

DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.

DR Oxidoreductase.

SW SEQUENCE 511 AA; 55644 MW; 37952CEC7C5F3A85 CRC64;

Query Match 42.9%; Score 6; DB 11; Length 511;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGG 7

DB 472 KHTGGG 477

RESULT 13

Q98212

ID Q98212 PRELIMINARY; PRT; 614 AA.

AC Q98212;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE DNA methyltransferase.

GN ML19056.

OS Rhizobium loti (Mesorhizobium loti).

OG Plasmid pMla.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).

DR EMBL; AP003015; BAB54474.1; -.

DR InterPro; IPR001091; CN4_MetTransf.

DR InterPro; IPR002295; D21N6_mtfase.

DR InterPro; IPR002941; N6/N4_Mtase.

DR InterPro; IPR002052; N6_Mtase.

DR Pfam; PF01555; N6/N4_Mtase; 1.

DR PRINTS; PR00506; D21N6MTFRASE.

DR PRINTS; PR00508; S21N4MTFRASE.

DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.

KW Transferase; Methyltransferase; Plasmid; Complete proteome.

SQ SEQUENCE 614 AA; 69230 MW; 14507EDDAE0FBCE CRC64;

Query Match 42.9%; Score 6; DB 16; Length 614;

Best Local Similarity 100.0%; Pred. No. 86;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HTGGGV 8

DB 116 HTGGGV 121

RESULT 14

Q9FFF3

ID Q9FFF3 PRELIMINARY; PRT; 1068 AA.

AC Q9FFF3;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Low density lipoprotein B-like protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Magnoliophyta; Streptophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=97471969; PubMed=9330910;

RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,

RA Miyajima N., Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence

RT features of the 1.6 Mb regions covered by twenty physically assigned

RT Pl clones.";

RL DNA Res. 4:215-230(1997).

DR EMBL; AB005242; BAB09597.1; -.

KW Lipoprotein.

SW SEQUENCE 1068 AA; 118802 MW; D696E592DD4B991C CRC64;

Query Match 42.9%; Score 6; DB 10; Length 1068;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGVW 9

DB 484 TGGGVW 489

RESULT 15

Q41331

ID Q41331 PRELIMINARY; PRT; 1123 AA.

AC Q41331;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE PHYA protein (Phytochrome A).

GN PHYA.

OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. UC82B;
 RX MEDLINE=98346008; PubMed=9681030;
 RA Lazarova G.I., Cordonnier-Pratt M.M., Kerckhoffs L.J.,
 RA Brandstadter J., Matsui M., Pratt L.H., Kendrick R.E.;
 RT "Molecular analysis of PHA in wild-type and phytochrome A-deficient
 RT mutants of tomato";
 RL Plant J. 14:653-662(1998).
 RN [2]
 RP SEQUENCE OF 165-277 FROM N.A.
 RC STRAIN=UC-82B;
 RX MEDLINE=96191281; PubMed=8616214;
 RA Hauser B.A., Cordonnier-Pratt M.M., Daniel-Vedele F., Pratt L.H.;
 RT "The phytochrome gene family in tomato includes a novel subfamily";
 RL Plant Mol. Biol. 29:1143-1155(1995).
 DR EMBL; AJ001916; CAA05089.1; -;
 DR EMBL; U32345; AAC49297.1; -;
 DR EMBL; AJ001915; CAA05088.1; -;
 DR EMBL; AJ001913; CAA05086.1; -;
 DR EMBL; AJ001914; CAA05087.1; -;
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR003018; GAF.
 DR InterPro: IPR003661; His_kinA.
 DR InterPro: IPR004359; HIS_KIN_sig.
 DR InterPro: IPR001610; PAC.
 DR InterPro: IPR000700; PAS-assoc_C.
 DR InterPro: IPR000014; PAS_domain.
 DR InterPro: IPR001294; Phytochrome.
 DR InterPro: IPR001680; WD40.
 DR Pfam; PF01590; GAF; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00989; PAS; 2.
 DR Pfam; PF00360; phytochrome; 1.
 DR Pfam; PF00512; signal; 1.
 DR PRINTS; PR01033; PHYTOCHROME.
 DR SMART; SM00065; GAF; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HSKA; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR TIGRfams; TIGR00229; sensory_box; 1.
 DR PROSITE; PS00245; PHYTOCHROME_1; 1.
 DR PROSITE; PS50046; PHYTOCHROME_2; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
 KW Phytochrome.
 SQ SEQUENCE 1123 AA; 124659 MW; 0432ADCCCFDF0FB1 CRC64;

Query Match 42.9%; Score 6; DB 10; Length 1123;
 Best Local Similarity 100.0%; Pred. No. 1.5e-02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 HTGGGV 8
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 Db 1058 HTGGGV 1063

Search completed: March 13, 2003, 15:33:05
 Job time : 29.9231 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:05:54 ; Search time 6.40769 Seconds
(without alignments)
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	85	100.0	121	22	AAE12706 Human PH1 Fab anti
2	85	100.0	381	22	AAE12707 Human b1vPH1-IL-2
3	85	100.0	451	22	AAE12715 Human recombinant
4	84	98.8	14	22	AAE12764 Human PH1 Fab anti
5	82	96.5	14	22	AAE12758 Human PH1 Fab anti
6	81	95.3	14	22	AAE12770 Human PH1 Fab anti
7	80	94.1	14	22	AAE12748 Human PH1 Fab anti
8	80	94.1	14	22	AAE12769 Human PH1 Fab anti
9	79	92.9	14	22	AAE12771 Human PH1 Fab anti
10	78	91.8	14	22	AAE12719 Human PH1 Fab anti

11	78	91.8	14	22	AAE12740 Human PH1 Fab anti
12	78	91.8	14	22	AAE12741 Human PH1 Fab anti
13	78	91.8	14	22	AAE12759 Human PH1 Fab anti
14	78	91.8	14	22	AAE12762 Human PH1 Fab anti
15	77	90.6	14	22	AAE12749 Human PH1 Fab anti
16	77	90.6	14	22	AAE12754 Human PH1 Fab anti
17	77	90.6	14	22	AAE12773 Human PH1 Fab anti
18	76	89.4	14	22	AAE12746 Human PH1 Fab anti
19	76	89.4	14	22	AAE12747 Human PH1 Fab anti
20	76	89.4	14	22	AAE12753 Human PH1 Fab anti
21	76	89.4	14	22	AAE12774 Human PH1 Fab anti
22	75	88.2	14	22	AAE12742 Human PH1 Fab anti
23	75	88.2	14	22	AAE12743 Human PH1 Fab anti
24	75	88.2	14	22	AAE12768 Human PH1 Fab anti
25	74	87.1	14	22	AAE12750 Human PH1 Fab anti
26	74	87.1	14	22	AAE12772 Human PH1 Fab anti
27	73	85.9	14	22	AAE12718 Human PH1 Fab anti
28	73	85.9	14	22	AAE12744 Human PH1 Fab anti
29	73	85.9	14	22	AAE12751 Human PH1 Fab anti
30	73	85.9	14	22	AAE12756 Human PH1 Fab anti
31	73	85.9	14	22	AAE12766 Human PH1 Fab anti
32	73	85.9	16	22	AAE12735 Human PH1 Fab anti
33	72	84.7	14	22	AAE12755 Human PH1 Fab anti
34	72	84.7	14	22	AAE12761 Human PH1 Fab anti
35	72	84.7	14	22	AAE12763 Human PH1 Fab anti
36	72	84.7	14	22	AAE12765 Human PH1 Fab anti
37	72	84.7	14	22	AAE12767 Human PH1 Fab anti
38	72	84.7	16	22	AAE12734 Human PH1 Fab anti
39	71	83.5	16	22	AAE12736 Human PH1 Fab anti
40	70	82.4	14	22	AAE12717 Human PH1 Fab anti
41	70	82.4	14	22	AAE12720 Human PH1 Fab anti
42	70	82.4	14	22	AAE12739 Human PH1 Fab anti
43	69	81.2	14	22	AAE12738 Human PH1 Fab anti
44	69	81.2	14	22	AAE12757 Human PH1 Fab anti
45	68	80.0	14	22	AAE12745 Human PH1 Fab anti

ALIGNMENTS

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RESULT 1
AAE12706
ID AAE12706 standard; Protein; 121 AA.
XX
AC AAE12706;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody variable heavy chain region (VH).
XX
KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody.
XX
OS Homo sapiens.
XX
FH Key
FH Region
FT Location/Qualifiers
FT 31..35
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 97..99
FT /label= FR3
FT /note= "Framework region 3"
FT 97..112
FT /note= "VH domain"
FT 99..110
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT 111..112
FT /label= FR4

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FT XX /note= "Framework region 4"
PN XX
PD XX WO200175110-A2.
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
XX
XX 30-MAR-2000; 2000US-0538913.
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX N-PSDB; AAD20731.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX its portion for binding to an epitope of the protein core of mucin-1
XX
XX Claim 2; Page 94-95; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
XX (MUC-1)-specific binding member comprising an antigen binding domain
XX region having an antibody variable light (VL) or heavy (VH) region,
XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX The binding of MUC1-specific binding member to MUC1 is detected by a
XX detection method selected from enzyme-linked immunosorbent assay,
XX magnetic resonance imaging, scintillation counting, and x-ray film.
XX MUC1-specific binding member is useful for treating cancer, preferably
XX adenocarcinoma, in an individual, where the cancer is present in tissue
XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX binding member is useful for diagnosing and imaging MUC1-expressing
XX cancer cells and tissues, for purifying or isolating non-glycosylated,
XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX containing molecules, and for therapeutically or prophylactically
XX treating cancer. The present sequence is anti-MUC1 human PH1 Fab
XX antibody VH region.
XX
XX Sequence 121 AA;
XX
XX Query Match 100.0%; Score 85; DB 22; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-06;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AKHTGGGVNDPIDY 14
XX | | | | | | | | | |
XX Db 97 AKHTGGGVNDPIDY 110
XX
XX RESULT 2
XX AAEL12707
XX ID AAEL12707 standard; Protein; 381 AA.
XX AC AAEL12707;
XX
XX DT 04-JAN-2002 (first entry)
XX
XX DE Human b1vPH1-IL-2 immunocytokine protein.
XX
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
XX breast; ovary; lung; bladder; cytotstatic; therapy; immunocytokine.
XX
XX OS Homo sapiens.
XX
XX PN WO200175110-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US10589.
XX
XX

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PR 30-MAR-2000; 2000US-0538913.
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX N-PSDB; AAD20732.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX its portion for binding to an epitope of the protein core of mucin-1
XX
XX Claim 9; Page 95-97; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
XX (MUC-1)-specific binding member comprising an antigen binding domain
XX region having an antibody variable light (VL) or heavy (VH) region,
XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX The binding of MUC1-specific binding member to MUC1 is detected by a
XX detection method selected from enzyme-linked immunosorbent assay,
XX magnetic resonance imaging, scintillation counting, and x-ray film.
XX MUC1-specific binding member is useful for treating cancer, preferably
XX adenocarcinoma, in an individual, where the cancer is present in tissue
XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX binding member is useful for diagnosing and imaging MUC1-expressing
XX cancer cells and tissues, for purifying or isolating non-glycosylated,
XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX containing molecules, and for therapeutically or prophylactically
XX treating cancer. The present sequence is human b1vPH1-IL-2
XX immunocytokine protein. b1vPH1 is mucin specific binding portion.
XX
XX Sequence 381 AA;
XX
XX Query Match 100.0%; Score 85; DB 22; Length 381;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AKHTGGGVNDPIDY 14
XX | | | | | | | | | |
XX Db 97 AKHTGGGVNDPIDY 110
XX
XX RESULT 3
XX AAEL12715
XX ID AAEL12715 standard; Protein; 451 AA.
XX AC AAEL12715;
XX
XX DT 04-JAN-2002 (first entry)
XX
XX DE Human recombinant immunoglobulin (Ig) heavy chain region.
XX
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX heavy chain region; cancer; breast; ovary; lung; bladder;
XX cytotstatic; therapy; immunoglobulin; Ig.
XX
XX OS Homo sapiens.
XX
XX PN WO200175110-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US10589.
XX
XX 30-MAR-2000; 2000US-0538913.
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX

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DR N-PSDB; AAD20745.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Claim 12; Page 106-108; 126pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human recombinant immunoglobulin
 CC (19) heavy chain region (variable VH and CH constant heavy chain).
 XX

SQ Sequence 451 AA;

Query Match 100.0%; Score 85; DB 22; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14

|||||

Db 97 AKHTGGGVWDPIDY 110

RESULT 4

AAE12764

ID AAE12764 standard; peptide; 14 AA.

XX AAE12764;

XX 04-JAN-2002 (first entry)

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #31.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..2

XX Region 3..14 /label= Framework_region_3

XX Region 3..14 /label= Complementarity_determining_region_3

XX WO200175110-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Example 2; Page 123; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 98.8%; Score 84; DB 22; Length 14;

Best Local Similarity 92.9%; Pred. No. 5.8e-07;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14

|||||

Db 1 AKHTGGGVWDPIDY 14

RESULT 5

AAE12758

ID AAE12758 standard; peptide; 14 AA.

XX AAE12758;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #25.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..2

XX Region 3..14 /label= Framework_region_3

XX Region 3..14 /label= Complementarity_determining_region_3

XX WO200175110-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 122; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

SQ

Query Match 96.5%; Score 82; DB 22; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.2e-06;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKHTGGVWDPIDY 14

DB 1 AKHTGGVWDPMDY 14

|||||

RESULT 6

AAE12770

ID AAE12770 standard; peptide; 14 AA.

XX AC AAE12770;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #37.

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderixx MPG;

XX DR WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 125; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

SQ

Query Match 95.3%; Score 81; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KHTGGVWDPIDY 14

DB 2 KHTGGVWDPIDY 14

|||||

RESULT 7

AAE12748

ID AAE12748 standard; peptide; 14 AA.

XX AC AAE12748;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #15.

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderixx MPG;

XX DR WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 120; 126pp; English.

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 94.1%; Score 80; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.6e-06;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPIDY 14
 |||||

Db 1 AKHTGGGVNDPIDY 14

RESULT 8

AAE12769
 ID AAE12769 standard; peptide; 14 AA.

XX AAE12769;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #36.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 1..2 /label= Framework_region_3

FT Region 3..14 /label= Complementarity_determining_region_3

FT WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

PS Example 2; Page 124; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC the binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 94.1%; Score 80; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.6e-06;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPIDY 14
 |||||

Db 1 AKHTGGGVNDPIDY 14

RESULT 9

AAE12771
 ID AAE12771 standard; peptide; 14 AA.

XX AAE12771;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #38.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 1..2 /label= Framework_region_3

FT Region 3..14 /label= Complementarity_determining_region_3

FT WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

PS Example 2; Page 125; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 92.9%; Score 79; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 3.7e-06;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
 ||||| |||||
 Db 1 AKHTGAGVWDPIDY 14

RESULT 10
 AAE12719
 ID AAE12719 standard; peptide; 14 AA.
 AC AAE12719;
 XX
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #3.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotstatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

WO200175110-A2.
 11-OCT-2001.
 30-MAR-2001; 2001WO-US10589.
 30-MAR-2000; 2000US-0538913.
 (DYAX-) DYAX CORP.
 Hoogenboom HRJM, Henderikx MPG;
 WPI; 2001-626437/72.

Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or
 its portion for binding to an epitope of the protein core of mucin-1 -
 Claim 2; Page 75; 126pp; English.
 The invention relates to an isolated tumour-associated antigen mucin-1
 (MUC-1)-specific binding member comprising an antigen binding domain
 region having an antibody variable light (VL) or heavy (VH) region,
 or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.

CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 91.8%; Score 78; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
 ||||| |||||
 Db 1 AKHTGGVWDPIDY 14

RESULT 11
 AAE12740
 ID AAE12740 standard; peptide; 14 AA.

AC AAE12740;
 XX
 DT 04-JAN-2002 (first entry)

DE Human PH1 Fab antibody VH region FR3-CDR3 variant #7.

XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotstatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

WO200175110-A2.
 11-OCT-2001.
 30-MAR-2001; 2001WO-US10589.
 30-MAR-2000; 2000US-0538913.
 (DYAX-) DYAX CORP.
 Hoogenboom HRJM, Henderikx MPG;
 WPI; 2001-626437/72.
 Novel isolated tumor-associated antigen mucin-1-specific binding member
 for diagnosing and treating cancer, comprises mucin-1 binding domain or
 its portion for binding to an epitope of the protein core of mucin-1 -
 Example 2; Page 119; 126pp; English.

The invention relates to an isolated tumour-associated antigen mucin-1
 (MUC-1)-specific binding member comprising an antigen binding domain
 region having an antibody variable light (VL) or heavy (VH) region,
 or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating MUC1 epitope-
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX Sequence 14 AA;

Query Match

Best Local Similarity 91.8%; Score 78; DB 22; Length 14;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPID 13

Db 1 AKHTGGGVNDPID 13

RESULT 12

AAE12741
 ID AAE12741 standard; peptide: 14 AA.

XX
 AC AAE12741;

XX
 DT 04-JAN-2002 (first entry)

XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #8.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX
 OS Homo sapiens.

XX
 FH Key

FT Region

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

FT WO200175110-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US10589.

PF 30-MAR-2000; 2000US-0538913.

PR (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

for diagnosing and treating cancer, comprises mucin-1 binding domain or

its portion for binding to an epitope of the protein core of mucin-1

Example 2; Page 119; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

(MUC-1)-specific binding member comprising an antigen binding domain

or a complementarity determining region (CDR) of VL or VH. MUC1-specific

binding member is useful for diagnosing cancer, preferably adenocarcinoma

The binding of MUC1-specific binding member to MUC1 is detected by a

detection method selected from enzyme-linked immunosorbent assay,

magnetic resonance imaging, scintillation counting, and x-ray film.

XX MUC1-specific binding member is useful for treating cancer, preferably

adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 XX Sequence 14 AA;

Query Match

Best Local Similarity 91.8%; Score 78; DB 22; Length 14;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPID 14

Db 1 AKHTGGGVNDPID 14

RESULT 13

AAE12759
 ID AAE12759 standard; peptide: 14 AA.

XX
 AC AAE12759;

XX
 DT 04-JAN-2002 (first entry)

XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #26.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

KW cytostatic; therapy; PH1 antibody; variant.

XX
 OS Homo sapiens.

XX
 FH Key

FT Region

FT 1..2

FT /label= Framework_region_3

FT 3..14

FT /label= Complementarity_determining_region_3

FT WO200175110-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US10589.

PF 30-MAR-2000; 2000US-0538913.

PR (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

for diagnosing and treating cancer, comprises mucin-1 binding domain or

its portion for binding to an epitope of the protein core of mucin-1

Example 2; Page 122; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

(MUC-1)-specific binding member comprising an antigen binding domain

or a complementarity determining region (CDR) of VL or VH. MUC1-specific

binding member is useful for diagnosing cancer, preferably adenocarcinoma

The binding of MUC1-specific binding member to MUC1 is detected by a

detection method selected from enzyme-linked immunosorbent assay,

magnetic resonance imaging, scintillation counting, and x-ray film.

XX MUC1-specific binding member is useful for treating cancer, preferably

adenocarcinoma, in an individual, where the cancer is present in tissue

of the breast, ovary, lung, or bladder of the individual. MUC1-specific

binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;
 SQ Query Match 91.8%; Score 78; DB 22; Length 14;
 Best Local Similarity 92.9%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AKHTGGVWDPIY 14
 |||||
 DB 1 AKHTGGVWDPIY 14

RESULT 14
 AAEL2762
 ID AAE12762 standard; peptide; 14 AA.
 XX AC AAEL2762;
 XX DT 04-JAN-2002 (first entry)
 XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #29.
 XX KW Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 XX KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 XX KW cytostatic; therapy; PH1 antibody; variant.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 123; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 XX region having an antibody variable light (VL) or heavy (VH) region,
 XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
 XX The binding of MUC1-specific binding member to MUC1 is detected by a
 XX detection method selected from enzyme-linked immunosorbent assay,
 XX magnetic resonance imaging, scintillation counting, and X-ray film.
 XX MUC1-specific binding member is useful for treating cancer, preferably
 XX adenocarcinoma, in an individual, where the cancer is present in tissue
 XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 XX binding member is useful for diagnosing and imaging MUC1-expressing
 XX cancer cells and tissues, for purifying or isolating non-glycosylated,
 XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;
 SQ Query Match 91.8%; Score 78; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKHTGGVWDPID 13
 |||||
 DB 1 AKHTGGVWDPID 13

RESULT 15
 AAEL2749
 ID AAE12749 standard; peptide; 14 AA.
 XX AC AAEL2749;
 XX DT 04-JAN-2002 (first entry)
 XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #16.
 XX KW Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 XX KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 XX KW cytostatic; therapy; PH1 antibody; variant.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 120; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 XX (MUC-1)-specific binding member comprising an antigen binding domain
 XX region having an antibody variable light (VL) or heavy (VH) region,
 XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
 XX The binding of MUC1-specific binding member to MUC1 is detected by a
 XX detection method selected from enzyme-linked immunosorbent assay,
 XX magnetic resonance imaging, scintillation counting, and X-ray film.
 XX MUC1-specific binding member is useful for treating cancer, preferably
 XX adenocarcinoma, in an individual, where the cancer is present in tissue
 XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 XX binding member is useful for diagnosing and imaging MUC1-expressing
 XX cancer cells and tissues, for purifying or isolating non-glycosylated,
 XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 XX containing molecules, and for therapeutically or prophylactically
 XX treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX
SQ

Sequence 14 AA;

Query Match

90.6%; Score 77; DB 22; Length 14;

Best Local Similarity 85.7%;

Pred. No. 7.9e-06;

Matches 12; Conservative 2;

Mismatches 0;

Indels 0;

Gaps 0;

QY 1 AKHTGGGVNDPIDY 14

1:|||||

Db 1 ARHTGGGVNDPINY 14

Search completed: March 13, 2003, 15:14:41
Job time : 6.40769 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	47	55	3	573	1	US-08-200-512-2
2	43.5	51	2	774	4	US-09-346-237-8
3		42	49	4	421	3
4	41	48	2	160	4	US-09-370-838-189
5	40	47	1	123	6	5171845-1
6	40	47	1	544	4	US-08-687-530-30
7	38	44	7	28	3	US-08-978-741-14
8	38	44	7	28	4	US-09-333-729A-14
9	38	44	7	109	4	US-09-134-001C-3523
10	38	44	7	328	4	US-09-300-672-2
11	38	44	7	397	3	US-08-978-741-6
12	38	44	7	397	4	US-08-333-729A-7
13	38	44	7	447	3	US-08-508-761B-6
14	38	44	7	738	1	US-07-985-458-3
15	38	44	7	941	4	US-09-074-658-75
16	38	44	7	944	2	US-08-867-941-23
17	38	44	7	944	2	US-08-867-941-24
18	38	44	7	944	4	US-09-074-658-23
19	38	44	7	944	4	US-09-074-658-24
20	37	43	5	409	3	US-09-075-215A-17
21	37	43	5	720	4	US-09-296-284-25
22	37	43	5	754	4	US-09-296-284-4
23	37	43	5	848	4	US-08-976-255-10
24	37	43	5	983	4	US-09-134-001C-3814
25	36	42	4	20	4	US-08-992-877-65
26	36	42	4	79	2	US-08-499-676A-13
27	36	42	4	152	3	US-08-916-043-2

ORIGINAL SOURCE:
ORGANISM: PSEUDOMONAS TESTOSTERONI
FEATURE: (R, repeat if necessary)
NAME/KEY: PROTEIN
LOCATION: 1..573
OTHER INFORMATION: /note = Delta
OTHER INFORMATION: dehydrogenase protein of Pseudomonas
OTHER INFORMATION: testosterone
US-08-200-512-2

Query Match 55.3%; Score 47; DB 1; Length 573;
Best Local Similarity 54.5%; Pred. No. 7.4;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGVWDPIDY 14
DB 47 SGGGIWIPLYN 57

RESULT 2

US-09-346-237-8
Sequence 8, Application US/09346237A

Patent No. 6265197
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629,200-US
CURRENT APPLICATION NUMBER: US/09/346,237A
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: PA 1998 00868
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: 60/094,353
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 8
LENGTH: 774
TYPE: PRT
ORGANISM: Favobacterium odoratum

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(774)
OTHER INFORMATION: Isoamylase
US-09-346-237-8

Query Match 51.2%; Score 43.5; DB 4; Length 774;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 HTG-GGVWDPID 13
DB 329 HTGEGGAWSPD 340

RESULT 3

US-09-032-372-3
Sequence 3, Application US/09032372

Patent No. 6008337
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,372
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0478 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNOT23
CLONE: 1693222
US-09-032-372-3

Query Match 49.4%; Score 42; DB 3; Length 421;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDP 11
DB 274 AKHTGGGMPD 284

RESULT 4

US-09-370-838-189
Sequence 189, Application US/09370838

Patent No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 189
LENGTH: 160
TYPE: PRT
ORGANISM: Homo sapien
US-09-370-838-189

Query Match 48.2%; Score 41; DB 4; Length 160;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9
DB 149 AKHTGGGPW 157

RESULT 5
5171845-1
; Patent No. 5171845
; APPLICANT: SPIK, GENEVIEVE; TARTAR, ANDRE; MONTREUIL, JEAN
; TITLE OF INVENTION: PROTEIN HOMOLOGUE OF HUMAN ANGIOGENIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392.977
; FILING DATE: 18-NOV-1988
; SEQ ID NO: 1:
; LENGTH: 123
5171845-1

Query Match 47.1%; Score 40; DB 6; Length 123;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
|| ||| |
DB 85 GGGVWDPCQY 94

RESULT 6
US-08-687-590-30
; Sequence 30, Application US/08687590
; Patent No. 6255070
; GENERAL INFORMATION:
; APPLICANT: Willison, Keith Robert
; APPLICANT: Kubota, Hiroshi
; APPLICANT: Ashworth, Alan
; TITLE OF INVENTION: Folding Proteins
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,590
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/00192
; FILING DATE: 31-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401791.0
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9418234.2
; FILING DATE: 09-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 084619-00000005
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-687-590-30

Query Match 47.1%; Score 40; DB 4; Length 544;
Best Local Similarity 46.2%; Pred. No. 95;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 AKHTGGVWDPID 13
|:| |:| :|
DB 466 ARHAQGGMWYGV 478

RESULT 7
US-08-978-741-14
; Sequence 14, Application US/08978741
; Patent No. 6100076
; GENERAL INFORMATION:
; APPLICANT: Yang Wang, Michael W. Spellman
; TITLE OF INVENTION: O-Fucosyltransferase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,741
; FILING DATE: 26-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/792498
; FILING DATE: 31
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1041P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-978-741-14

Query Match 44.7%; Score 38; DB 3; Length 28;
Best Local Similarity 50.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 HTGGVWDPIDY 14
| | | | |
DB 8 HMPAGSWDPAGY 19

RESULT 8
US-09-333-729A-14
; Sequence 14, Application US/09333729A
; Patent No. 6270987
; GENERAL INFORMATION:
; APPLICANT: Wang, Yang
; APPLICANT: Spellman, Michael W.
; TITLE OF INVENTION: O-Fucosyltransferase
; FILE REFERENCE: P1041P1-Substitute
; CURRENT APPLICATION NUMBER: US/09/333,729A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: US 08/798,741
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 14
; LENGTH: 28

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid insert encoded protein.
NAME/KEY: unsure
LOCATION: 23, 25
OTHER INFORMATION: unknown amino acid
US-09-333-729A-14

Query Match 44.7%; Score 38; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 HTGGGVWDPIDY 14
| | | | |
DB 8 HMPAGSWDPAGY 19

RESULT 9
US-09-134-001C-3523
Sequence 3523, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3523
LENGTH: 109
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3523

Query Match 44.7%; Score 38; DB 4; Length 109;
Best Local Similarity 45.5%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 HTGGGVWDPID 13
| | | | |
DB 27 HTLEGWHPVE 37

RESULT 10
US-09-300-672-2
Sequence 2, Application US/09300672
Patent No. 6248937
GENERAL INFORMATION:
APPLICANT: Finkelstein, Ruth R.
APPLICANT: Lynch, Tim
APPLICANT: Goodman, Howard M.
APPLICANT: Wang, Ming-Li
TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
FILE REFERENCE: 480.89(RV)
CURRENT APPLICATION NUMBER: US/09/300,672
CURRENT FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 328
TYPE: PRT
ORGANISM: Arabidopsis
US-09-300-672-2

Query Match 44.7%; Score 38; DB 4; Length 328;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 HTGGGVWDPID 13
| | | | |
DB 311 HNWGSIWDFID 321

RESULT 11
US-08-978-741-6
Sequence 6, Application US/08978741
Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-978-741-6

Query Match 44.7%; Score 38; DB 3; Length 397;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 HTGGGVWDPIDY 14
| | | | |
DB 32 HMPAGSWDPAGY 43

RESULT 12
US-09-333-729A-7
Sequence 7, Application US/09333729A
Patent No. 6270987
GENERAL INFORMATION:
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 7
LENGTH: 397

;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Plasmid insert encoded protein.
US-09-333-729A-7

Query Match 44.7%; Score 38; DB 4; Length 397;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 HTGGGVDPIDY 14
| | | | |
Db 32 HMPAGSWDPAGY 43

RESULT 13
US-08-508-761B-6
; Sequence 6, Application US/08508761B
; Patent No. 6027920
; GENERAL INFORMATION:
; APPLICANT: Joliff, Gwennael
; APPLICANT: Guyonvarch, Arnel
; APPLICANT: Duchiron, Francis
; APPLICANT: Renaud, Michel
; TITLE OF INVENTION: System for Protein Expression and
; SECRETION ESPECIALLY IN CORYNEBACTERIA
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,761B
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09652
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09870
; FILING DATE: 02-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58525NA
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-508-761B-6

Query Match 44.7%; Score 38; DB 3; Length 447;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HTGGGVWD 10
| | | | |
Db 304 HTDGSWD 311

RESULT 14

US-07-985-458-3
; Sequence 3, Application US/07985458
; Patent No. 5344777
; GENERAL INFORMATION:
; APPLICANT: Tamaki, Toshiaki
; APPLICANT: Takemura, Hiroshi
; APPLICANT: Tayama, Kenji
; APPLICANT: Fukaya, Masahiro
; APPLICANT: Okumura, Hajime
; APPLICANT: Kawamura, Yoshiya
; TITLE OF INVENTION: Structural Gene of Membrane-Bound
; ALCOHOL DEHYDROGENASE COMPLEX, PLASMID
; CONTAINING THE SAME AND TRANSFORMED ACETIC ACID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frischauf, Holtz, Goodman & Woodward, P.C.
; STREET: 600 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2088
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.72 mb
; COMPUTER: IBM PC compatible (NEC PC-9801 ES)
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII Form
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/985,458
; FILING DATE: 19921203
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,221
; FILING DATE: 20-FEB-1991
; APPLICATION NUMBER: 73440/1990
; FILING DATE: 26-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Herbert
; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 910134/HG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)972-1400
; TELEFAX: (212)370-1622
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: MATURE PEPTIDE
; LOCATION: 36 to 738
; IDENTIFICATION METHOD: N-terminal sequences of the
; IDENTIFICATION METHOD: purified protein having a molecular weight of about
; IDENTIFICATION METHOD: 72,000
; ORIGINAL SOURCE:
; ORGANISM: Acetobacter altoacetigenes
; STRAIN: MH-24
; PUBLICATION INFORMATION:
; AUTHORS: Tamaki, Toshiaki
; AUTHORS: Fukaya, Masahiro
; AUTHORS: Takemura, Hiroshi
; AUTHORS: Tayama, Kenji
; AUTHORS: Okumura, Hajime
; AUTHORS: Kawamura, Yoshiya
; AUTHORS: Nishiyama, Makoto
; AUTHORS: Horinouchi, Sueharu and
; AUTHORS: Beppu, Teruhiko
; TITLE: Cloning and Sequencing of the Gene Cluster
; Encoding Two Subunits of Membrane-Bound
; TITLE: Alcohol Dehydrogenase from Acetobacter
; TITLE: polyoxogenes

JOURNAL: Biochimica et Biophysica Acta.
VOLUME: 1088
PAGES: 292-300
DATE: 1991
US-07-985-458-3

Query Match 44.7%; Score 38; DB 1; Length 738;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
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Db 276 GGTWVDSIVY 285

RESULT 15
US-09-074-658-75
; Sequence 75, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: Quijun Wang
; APPLICANT: Yang, Yan-ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-074-658-75

Query Match 44.7%; Score 38; DB 4; Length 941;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 3 HTGGG-VWDPIDY 14
: |||| : |||:
Db 326 YTGGRILPDPMDY 339

Search completed: March 13, 2003, 15:18:41
Job time : 3.15385 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run On: March 13, 2003, 15:17:09 ; Search time 1.99231 Seconds
(without alignments)
323.890 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110

Perfect score: 85

Sequence: 1 AKHTGGGVNDPIDY 14

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Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications.AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pcp.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	85	100.0	121	10	US-09-822-698A-3
2	85	100.0	381	10	US-09-822-698A-5
3	85	100.0	451	10	US-09-822-698A-26
4	84	98.8	14	10	US-09-822-698A-99
5	82	96.5	14	10	US-09-822-698A-93
6	81	95.3	14	10	US-09-822-698A-105
7	80	94.1	14	10	US-09-822-698A-83
8	80	94.1	14	10	US-09-822-698A-104
9	79	92.9	14	10	US-09-822-698A-106
10	78	91.8	14	10	US-09-822-698A-31
11	78	91.8	14	10	US-09-822-698A-75
12	78	91.8	14	10	US-09-822-698A-76
13	78	91.8	14	10	US-09-822-698A-94
14	78	91.8	14	10	US-09-822-698A-97
15	77	90.6	14	10	US-09-822-698A-84
16	77	90.6	14	10	US-09-822-698A-89
17	77	90.6	14	10	US-09-822-698A-108
18	76	89.4	14	10	US-09-822-698A-81
19	76	89.4	14	10	US-09-822-698A-82

20	76	89.4	14	10	US-09-822-698A-88	Sequence 88, Appl
21	76	89.4	14	10	US-09-822-698A-109	Sequence 109, Appl
22	75	88.2	14	10	US-09-822-698A-77	Sequence 77, Appl
23	75	88.2	14	10	US-09-822-698A-78	Sequence 78, Appl
24	75	88.2	14	10	US-09-822-698A-103	Sequence 103, Appl
25	74	87.1	14	10	US-09-822-698A-85	Sequence 85, Appl
26	74	87.1	14	10	US-09-822-698A-107	Sequence 107, Appl
27	73	85.9	14	10	US-09-822-698A-30	Sequence 30, Appl
28	73	85.9	14	10	US-09-822-698A-79	Sequence 79, Appl
29	73	85.9	14	10	US-09-822-698A-86	Sequence 86, Appl
30	73	85.9	14	10	US-09-822-698A-91	Sequence 91, Appl
31	73	85.9	14	10	US-09-822-698A-101	Sequence 101, Appl
32	73	85.9	16	10	US-09-822-698A-57	Sequence 67, Appl
33	72	84.7	14	10	US-09-822-698A-90	Sequence 90, Appl
34	72	84.7	14	10	US-09-822-698A-96	Sequence 96, Appl
35	72	84.7	14	10	US-09-822-698A-98	Sequence 98, Appl
36	72	84.7	14	10	US-09-822-698A-100	Sequence 100, Appl
37	72	84.7	14	10	US-09-822-698A-102	Sequence 102, Appl
38	72	84.7	16	10	US-09-822-698A-65	Sequence 65, Appl
39	71	83.5	16	10	US-09-822-698A-69	Sequence 69, Appl
40	70	82.4	14	10	US-09-822-698A-29	Sequence 29, Appl
41	70	82.4	14	10	US-09-822-698A-32	Sequence 32, Appl
42	70	82.4	14	10	US-09-822-698A-74	Sequence 74, Appl
43	69	81.2	14	10	US-09-822-698A-73	Sequence 73, Appl
44	69	81.2	14	10	US-09-822-698A-92	Sequence 92, Appl
45	68	80.0	14	10	US-09-822-698A-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match 100.0%; Score 85; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVNDPIDY 14
|||||
Db 97 AKHTGGGVNDPIDY 110

RESULT 2
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US

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; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific Immunocytokine biVPH1-IL-2
US-09-822-698A-5
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Query Match 100.0%; Score 85; DB 10; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AKHTGGGVWDPIDY 14
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Db 97 AKHTGGGVWDPIDY 110
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RESULT 3
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
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; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
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; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26
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Query Match 100.0%; Score 85; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AKHTGGGVWDPIDY 14
|||||
Db 97 AKHTGGGVWDPIDY 110
|||||
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RESULT 4
US-09-822-698A-99
; Sequence 99, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
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; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-99
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Query Match 98.8%; Score 84; DB 10; Length 14;
Best Local Similarity 92.9%; Pred. No. 7.9e-07;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AKHTGGGVWDPIDY 14
|||||
Db 1 AKHTGGGVWDPIDY 14
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RESULT 5
US-09-822-698A-93
; Sequence 93, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 93
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-93
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Query Match 96.5%; Score 82; DB 10; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AKHTGGGVWDPIDY 14
|||||
Db 1 AKHTGGGVWDPIDY 14
|||||
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RESULT 6
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
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; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105
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Query Match 95.3%; Score 81; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

Query Match 91.8%; Score 78; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPID 13
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPID 13

RESULT 12

US-09-822-698A-76
; Sequence 76, Application US/09822698A
; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 76

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-76

Query Match 91.8%; Score 78; DB 10; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.4e-06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPIGY 14

RESULT 13

US-09-822-698A-94

; Sequence 94, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 94

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-94

Query Match 91.8%; Score 78; DB 10; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.4e-06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPIHY 14

RESULT 14

US-09-822-698A-97

; Sequence 97, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 97

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-97

Query Match 91.8%; Score 78; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPID 13
| | | | | | | | | | | | | | | |
Db 1 AKHTGGGVWDPID 13

RESULT 15

US-09-822-698A-84

; Sequence 84, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 84

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-84

Query Match 90.6%; Score 77; DB 10; Length 14;
Best Local Similarity 85.7%; Pred. No. 9.1e-06;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPIDY 14
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Db 1 AKHTGGGVWDPINY 14

Search completed: March 13, 2003, 15:30:31
Job time : 1.99231 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model
Run on: March 13, 2003, 15:14:49 ; Search time 29,8308 seconds
(without alignments)
302.582 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110
Perfect score: 85
Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Pending_Patents_AA_Main:*
- 1: /cgn2_6/ptodata/2/paa/US06_COMB.pcp.*
 - 2: /cgn2_6/ptodata/2/paa/US07_COMB.pcp.*
 - 3: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
 - 4: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*
 - 5: /cgn2_6/ptodata/2/paa/US10_COMB.pcp.*
 - 6: /cgn2_6/ptodata/2/paa/US11_COMB.pcp.*
 - 7: /cgn2_6/ptodata/2/paa/US12_COMB.pcp.*
 - 8: /cgn2_6/ptodata/2/paa/US13_COMB.pcp.*
 - 9: /cgn2_6/ptodata/2/paa/US14_COMB.pcp.*
 - 10: /cgn2_6/ptodata/2/paa/US15_COMB.pcp.*
 - 11: /cgn2_6/ptodata/2/paa/US16_COMB.pcp.*
 - 12: /cgn2_6/ptodata/2/paa/US17_COMB.pcp.*
 - 13: /cgn2_6/ptodata/2/paa/US18_COMB.pcp.*
 - 14: /cgn2_6/ptodata/2/paa/US19_COMB.pcp.*
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 - 16: /cgn2_6/ptodata/2/paa/US21_COMB.pcp.*
 - 17: /cgn2_6/ptodata/2/paa/US22_COMB.pcp.*
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 - 19: /cgn2_6/ptodata/2/paa/US24_COMB.pcp.*
 - 20: /cgn2_6/ptodata/2/paa/US25_COMB.pcp.*
 - 21: /cgn2_6/ptodata/2/paa/US26_COMB.pcp.*
 - 22: /cgn2_6/ptodata/2/paa/US27_COMB.pcp.*
 - 23: /cgn2_6/ptodata/2/paa/US28_COMB.pcp.*
 - 24: /cgn2_6/ptodata/2/paa/US29_COMB.pcp.*
 - 25: /cgn2_6/ptodata/2/paa/US30_COMB.pcp.*
 - 26: /cgn2_6/ptodata/2/paa/US31_COMB.pcp.*
 - 27: /cgn2_6/ptodata/2/paa/US32_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	ID	Description
1	85	100.0	121	19	US-09-538-913-3	Sequence 3, Appli
2	85	100.0	121	22	US-09-822-698A-3	Sequence 3, Appli
3	85	100.0	381	22	US-09-538-913-5	Sequence 5, Appli
4	85	100.0	381	22	US-09-822-698A-5	Sequence 5, Appli
5	85	100.0	451	22	US-09-822-698A-26	Sequence 26, Appli
6	84	98.8	14	22	US-09-822-698A-99	Sequence 99, Appli

7	82	96.5	14	22	US-09-822-698A-93	Sequence 93, Appli
8	81	95.3	14	22	US-09-822-698A-105	Sequence 105, Appli
9	80	94.1	14	22	US-09-822-698A-83	Sequence 83, Appli
10	80	94.1	14	22	US-09-822-698A-104	Sequence 104, Appli
11	79	92.9	14	22	US-09-822-698A-106	Sequence 106, Appli
12	78	91.8	14	22	US-09-822-698A-31	Sequence 31, Appli
13	78	91.8	14	22	US-09-822-698A-75	Sequence 75, Appli
14	78	91.8	14	22	US-09-822-698A-94	Sequence 94, Appli
15	78	91.8	14	22	US-09-822-698A-97	Sequence 97, Appli
16	77	90.6	14	22	US-09-822-698A-84	Sequence 84, Appli
17	77	90.6	14	22	US-09-822-698A-89	Sequence 89, Appli
18	77	90.6	14	22	US-09-822-698A-108	Sequence 108, Appli
19	77	90.6	14	22	US-09-822-698A-81	Sequence 81, Appli
20	76	89.4	14	22	US-09-822-698A-82	Sequence 82, Appli
21	76	89.4	14	22	US-09-822-698A-88	Sequence 88, Appli
22	76	89.4	14	22	US-09-822-698A-109	Sequence 109, Appli
23	75	88.2	14	22	US-09-822-698A-77	Sequence 77, Appli
24	75	88.2	14	22	US-09-822-698A-78	Sequence 78, Appli
25	75	88.2	14	22	US-09-822-698A-103	Sequence 103, Appli
26	74	87.1	14	22	US-09-822-698A-85	Sequence 85, Appli
27	74	87.1	14	22	US-09-822-698A-107	Sequence 107, Appli
28	74	87.1	14	22	US-09-822-698A-30	Sequence 30, Appli
29	73	85.9	14	22	US-09-822-698A-79	Sequence 79, Appli
30	73	85.9	14	22	US-09-822-698A-86	Sequence 86, Appli
31	73	85.9	14	22	US-09-822-698A-91	Sequence 91, Appli
32	73	85.9	14	22	US-09-822-698A-101	Sequence 101, Appli
33	73	85.9	14	22	US-09-822-698A-90	Sequence 90, Appli
34	73	85.9	14	22	US-09-822-698A-96	Sequence 96, Appli
35	72	84.7	14	22	US-09-822-698A-98	Sequence 98, Appli
36	72	84.7	14	22	US-09-822-698A-100	Sequence 100, Appli
37	72	84.7	14	22	US-09-822-698A-65	Sequence 65, Appli
38	72	84.7	14	22	US-09-822-698A-69	Sequence 69, Appli
39	72	84.7	14	22	US-09-822-698A-32	Sequence 32, Appli
40	71	83.5	16	22	US-09-822-698A-74	Sequence 74, Appli
41	71	83.5	16	22	US-09-822-698A-73	Sequence 73, Appli
42	70	82.4	14	22		
43	70	82.4	14	22		
44	70	82.4	14	22		
45	69	81.2	14	22		

ALIGNMENTS

RESULT 1
US-09-538-913-3
; Sequence 3, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEROOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-3

Query Match 100.0%; Score 85; DB 19; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKHTGGVWDPIDY 14
Db 97 AKHTGGVWDPIDY 110

RESULT 2

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US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match 100.0%; Score 85; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | |
Db 97 AKHTGGGVWDPIDY 110

RESULT 3
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for bivPH1-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match 100.0%; Score 85; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | |
Db 97 AKHTGGGVWDPIDY 110

RESULT 4
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
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; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPH1-IL-2
US-09-822-698A-5

Query Match 100.0%; Score 85; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | |
Db 97 AKHTGGGVWDPIDY 110

RESULT 5
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26

Query Match 100.0%; Score 85; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGGVWDPIDY 14
| | | | | | | | | | | | | | |
Db 97 AKHTGGGVWDPIDY 110

RESULT 6
US-09-822-698A-99
; Sequence 99, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-99
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```
Query Match          98.8%; Score 84; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 7e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   |||||:|||||:|
Db 1 AKHTGGVWDPIDY 14

RESULT 7
US-09-822-698A-93
; Sequence 93, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 93
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-93

Query Match          96.5%; Score 82; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.4e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   |||||:|||||:|
Db 1 AKHTGGVWDPIDY 14

RESULT 8
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match          95.3%; Score 81; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KHTGGVWDPIDY 14
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Db 2 KHTGGVWDPIDY 14

RESULT 9
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US-09-822-698A-83
; Sequence 83, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match          94.1%; Score 80; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   |||||:|||||:|
Db 1 AKHTGGVWDPIDY 14

RESULT 10
US-09-822-698A-104
; Sequence 104, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 104
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-104

Query Match          94.1%; Score 80; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
   |||||:|||||:|
Db 1 AKHTGGVWDPIDY 14

RESULT 11
US-09-822-698A-106
; Sequence 106, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
```

```

; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 106
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-106

```

```

Query Match          92.9%; Score 79; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.3e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 AKHTGGVWDPIDY 14
      ||||| |||||
Db 1 AKHTGAGVDPIDY 14

```

```

RESULT 12
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

```

```

Query Match          91.8%; Score 78; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 AKHTGGVWDPIDY 14
      ||||| |||||
Db 1 AKHTGGVWDPIDY 14

```

```

RESULT 13
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

```

```

Query Match          91.8%; Score 78; DB 22; Length 14;

```

```

Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKHTGGVWDPID 13
      ||||| |||||
Db 1 AKHTGGVWDPID 13

RESULT 14
US-09-822-698A-76
; Sequence 76, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

```

```

Query Match          91.8%; Score 78; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 AKHTGGVWDPIDY 14
      ||||| |||||
Db 1 AKHTGGVWDPIDY 14

```

```

RESULT 15
US-09-822-698A-94
; Sequence 94, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 94
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-94

```

```

Query Match          91.8%; Score 78; DB 22; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 AKHTGGVWDPIDY 14
      ||||| |||||
Db 1 AKHTGGVWDPIDY 14

```

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Search completed: March 13, 2003, 15:28:04
Job time : 31.0808 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:15:24 ; Search time 5.11538 Seconds
(without alignments)
355.800 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_l10

Perfect score: 85

Sequence: 1 AKHTGGVMDPIDY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US05_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	45	52.9	218	6 US-10-282-122A-50009	Sequence 50009, A
2	44	51.8	330	6 US-10-366-683-23794	Sequence 23794, A
3	43	50.6	57	1 PCT-US02-32727-17567	Sequence 17567, A
4	43	50.6	57	5 US-09-978-825-17567	Sequence 17567, A
5	43	50.6	57	6 US-10-057-498-17567	Sequence 17567, A
6	43	50.6	799	6 US-10-282-122A-49879	Sequence 49879, A
7	42	49.4	152	6 US-10-156-761-10926	Sequence 10926, A
8	41	48.2	222	5 US-09-724-676-80033	Sequence 80033, A
9	41	48.2	222	5 US-09-724-676A-80033	Sequence 80033, A
10	41	48.2	251	6 US-10-282-122A-46525	Sequence 46525, A
11	41	48.2	264	1 PCT-US02-40225-3079	Sequence 3079, Ap
12	41	48.2	264	6 US-10-320-797-3079	Sequence 3079, Ap
13	41	48.2	275	5 US-09-724-676-80034	Sequence 80034, A
14	41	48.2	275	5 US-09-724-676A-80034	Sequence 80034, A
15	41	48.2	295	5 US-09-724-676-80022	Sequence 80022, A
16	41	48.2	295	5 US-09-724-676-80028	Sequence 80028, A
17	41	48.2	295	5 US-09-724-676-80037	Sequence 80037, A
18	41	48.2	295	5 US-09-724-676A-80022	Sequence 80022, A
19	41	48.2	295	5 US-09-724-676A-80028	Sequence 80028, A
20	41	48.2	295	5 US-09-724-676A-80037	Sequence 80037, A
21	41	48.2	300	6 US-10-282-122A-46309	Sequence 46309, A
22	41	48.2	348	5 US-09-724-676-80023	Sequence 80023, A
23	41	48.2	348	5 US-09-724-676-80029	Sequence 80029, A
24	41	48.2	348	5 US-09-724-676-80038	Sequence 80038, A
25	41	48.2	348	5 US-09-724-676A-80023	Sequence 80023, A
26	41	48.2	348	5 US-09-724-676A-80029	Sequence 80029, A

27	41	48.2	348	5 US-09-724-676A-80038	Sequence 80038, A
28	41	48.2	385	5 US-09-724-676-80041	Sequence 80041, A
29	41	48.2	385	5 US-09-724-676A-80041	Sequence 80041, A
30	41	48.2	420	5 US-09-724-676-80025	Sequence 80025, A
31	41	48.2	420	5 US-09-724-676A-80025	Sequence 80025, A
32	41	48.2	438	5 US-09-724-676-80020	Sequence 80020, A
33	41	48.2	438	5 US-09-724-676A-80020	Sequence 80020, A
34	41	48.2	473	5 US-09-724-676-80026	Sequence 80026, A
35	41	48.2	473	5 US-09-724-676-80035	Sequence 80035, A
36	41	48.2	473	5 US-09-724-676A-80026	Sequence 80026, A
37	41	48.2	473	5 US-09-724-676A-80035	Sequence 80035, A
38	41	48.2	687	6 US-10-369-493-7152	Sequence 7152, Ap
39	41	48.2	692	6 US-10-369-493-4397	Sequence 4397, Ap
40	41	48.2	710	6 US-10-156-761-14284	Sequence 14284, A
41	41	48.2	795	6 US-10-282-122A-47364	Sequence 47364, A
42	40.5	47.6	672	6 US-10-156-761-8104	Sequence 8104, Ap
43	40	47.1	34	6 US-10-203-138A-13646	Sequence 13646, A
44	40	47.1	93	1 PCT-US02-32727-9150	Sequence 9150, Ap
45	40	47.1	93	5 US-09-978-825-9150	Sequence 9150, Ap

ALIGNMENTS

RESULT 1

US-10-282-122A-50009
Sequence 50009, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELTRA 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50009
LENGTH: 218
TYPE: PRT
ORGANISM: Burkholderia mallei
US-10-282-122A-50009

Query Match 52.9%; Score 45; DB 6; Length 218;
Best Local Similarity 58.3%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KHTGGGVWDPID 13
:|:||||| |
Db 79 RHSGGGRWPP 90

RESULT 2
US-10-366-683-23794
; Sequence 23794, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rudenfield, Marc J.
; APPLICANT: Nollinger, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-04
; CURRENT APPLICATION NUMBER: US/10/366,683
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23794
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-23794

Query Match 51.8%; Score 44; DB 6; Length 330;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGVWDPID 13
|:||||| |
Db 101 GSVWDPID 108

RESULT 3
PCT-US02-32727-17567
; Sequence 17567, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-17567

Query Match 50.6%; Score 43; DB 1; Length 57;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KHTGGGVWDP 11
:|:|||| |
Db 17 RHSGGGRWPP 26

RESULT 4
US-09-978-825-17567
; Sequence 17567, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-17567

Query Match 50.6%; Score 43; DB 5; Length 57;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KHTGGGVWDP 11
:|:|||| |
Db 17 RHSGGGRWPP 26

RESULT 5
US-10-057-498-17567
; Sequence 17567, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-17567

Query Match 50.6%; Score 43; DB 6; Length 57;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KHTGGGVWDP 11
:|:|||| |
Db 17 RHSGGGRWPP 26

RESULT 6
US-10-282-122A-49879
; Sequence 49879, Application US/10282122A


```

; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49879
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49879

Query Match 50.6%; Score 43; DB 6; Length 799;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AKHTGGVWDPIDY 14
Db 511 AAETGGQWEPKNY 524

RESULT 7
US-10-156-761-10926
; Sequence 10926, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697

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; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10926
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10926

Query Match 49.4%; Score 42; DB 6; Length 152;
Best Local Similarity 32.1%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 16; Gaps 1;

QY 2 KHTG-----GGVMDPID 13
Db 104 RHTGGEWTTGGDHWVTPDGLWDPID 131

RESULT 8
US-09-724-676-80033
; Sequence 80033, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80033
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-80033

Query Match 48.2%; Score 41; DB 5; Length 222;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9
Db 76 AKHTPGGPW 84

RESULT 9
US-09-724-676A-80033
; Sequence 80033, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80033
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-80033

Query Match 48.2%; Score 41; DB 5; Length 222;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9
Db 76 AKHTPGGPW 84

RESULT 10
US-10-282-122A-46525
; Sequence 46525, Application US/10282122A
; GENERAL INFORMATION:

```

```
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46525
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46525

Query Match 48.2%; Score 41; DB 6; Length 251;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGGGVWDPI 12
      |||| ||
DB 152 TGGGGWGPI 160

RESULT 11
PCT-US02-40225-3079
; Sequence 3079, Application PC/TUS0240225
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; APPLICANT: Eroshkin, Alexey M.
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: 10182-021-228
; CURRENT APPLICATION NUMBER: PCT/US02/40225
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3079
; LENGTH: 264
; TYPE: PRT

US-09-822-698a-3_copy_97_110_1.rapn

; ORGANISM: Cryptococcus neoformans
PCT-US02-40225-3079
Query Match 48.2%; Score 41; DB 1; Length 264;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 HTGGGVWDPI 13
      : |||| |
DB 233 YKGTGVWTPVD 243

RESULT 12
US-10-320-797-3079
; Sequence 3079, Application US/10320797
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS A
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3079
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3079

Query Match 48.2%; Score 41; DB 6; Length 264;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 HTGGGVWDPI 13
      : |||| |
DB 233 YKGTGVWTPVD 243

RESULT 13
US-09-724-676-80034
; Sequence 80034, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80034
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (97)..(98)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (107)..(107)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-724-676-80034

Query Match 48.2%; Score 41; DB 5; Length 275;
Best Local Similarity 77.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGVW 9
      |||| |
```

Db 76 AKHTPGGPW 84

RESULT 14
US-09-724-676A-80034
; Sequence 80034, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80034
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (97)..(98)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (107)..(107)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-724-676A-80034

Query Match 48.2%; Score 41; DB 5; Length 275;
Best Local Similarity 77.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGW 9
|||||||
Db 76 AKHTPGGPW 84

RESULT 15
US-09-724-676-80022
; Sequence 80022, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80022
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-80022

Query Match 48.2%; Score 41; DB 5; Length 295;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKHTGGGW 9
|||||||
Db 149 AKHTPGGPW 157

Search completed: March 13, 2003, 15:29:46
Job time : 6.11538 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:09 ; Search time 2.42308 seconds
(without alignments)
555.443 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110

Perfect score: 85
Sequence: 1 AKHGGGVWDPIDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	55.3	573	2 A41319	3-oxosteroid 1-dehydrogenase
2	45	52.9	381	2 B97182	acyl-protein synthetase, luxE [imported] - Clostridium acetobutylicum
3	44	51.8	125	1 B43825	angiotensin - rabbit
4	43	50.6	71	2 A34768	ORF1 protein - Orf
5	43	50.6	304	2 H82984	hypothetical prote
6	43	50.6	435	2 H87412	conserved hypothet
7	43	50.6	536	2 T08241	gas-vesicle operon
8	43	50.6	536	2 S15183	gas-vesicle operon
9	42.5	50.0	597	2 G75070	hypothetical prote
10	42.5	50.0	598	2 B71095	hypothetical prote
11	42	49.4	255	2 S26020	cytochrome-c oxida
12	41	48.2	42	2 E95061	peptide pheromone
13	41	48.2	182	2 S17005	Anrl protein - yea
14	41	48.2	300	2 F69997	hypothetical prote
15	40	47.1	114	2 T08411	hypothetical prote
16	40	47.1	158	2 E86498	pts IIA Protein [i
17	40	47.1	158	2 E72124	pts iia protein -
18	40	47.1	193	2 C82683	disulfide oxidore
19	40	47.1	241	2 AC0596	histidine utilizat
20	40	47.1	291	2 E71491	probable geranyl t
21	40	47.1	338	2 H84173	acetoin utilizatio
22	40	47.1	345	2 E90817	hypothetical prote
23	40	47.1	345	2 C90974	hypothetical prote
24	40	47.1	345	2 A85677	unknown protein en
25	40	47.1	345	2 E85821	unknown protein en
26	40	47.1	347	2 F90904	hypothetical prote
27	40	47.1	347	2 G85712	unknown protein en
28	40	47.1	473	2 JCI184	hypothetical 50.8K
29	40	47.1	478	1 I47154	transcription fact

30	40	47.1	544	2 S43058	cCteta protein eta
31	40	47.1	600	2 D84588	hypothetical prote
32	40	47.1	738	2 C97420	probable 3-hydroxy
33	40	47.1	738	2 AD2638	enoyl-CoA hydratase
34	40	47.1	784	2 T45697	hypothetical prote
35	39.5	46.5	285	2 B86687	conserved hypothet
36	39	45.9	163	2 T34604	hypothetical prote
37	39	45.9	237	2 A82607	hypothetical prote
38	39	45.9	260	2 C75454	hypothetical prote
39	39	45.9	312	2 T36986	probable ribosylgl
40	39	45.9	370	2 F86338	protein F2D10.2 li
41	39	45.9	386	2 S74778	hypothetical prote
42	39	45.9	418	2 S42031	LbJ2 protein - lee
43	39	45.9	434	1 S49457	pyrimidine-nucleos
44	39	45.9	518	2 S42387	MPP protein homol
45	39	45.9	524	2 S30575	glycoprotein precu

ALIGNMENTS

RESULT 1

A41319

C:3-oxosteroid 1-dehydrogenase (EC 1.3.99.4) - Comamonas testosteroni

C:Species: Comamonas testosteroni

C>Date: 05-Jun-1992 #sequence_revision 28-Apr-1993 #text_change 29-Sep-1999

C:Accession: A41319

R:Plesiat, P.; Grandguillot, M.; Harayama, S.; Vragar, S.; Michel-Briand, Y.

J. Bacteriol. 173, 7219-7227, 1991

A:Title: Cloning, sequencing, and expression of the pseudomonas testosterone gene enc

A:Reference number: A41319; MUID:92041619; PMID:1657885

A:Accession: A41319

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-573 <PLE>

A:CROSS-references: GB:M68488; NID:g485378; PIDN:AAA25679.1; PID:g485379

A>Note: the authors translated the codon ACC for residue 497 as Tyr

C:Superfamily: 3-oxosteroid 1-dehydrogenase; 3-oxosteroid 1-dehydrogenase homology

C:Keywords: oxidoreductase

F:450-548/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>

Query Match

Best Local Similarity 55.3%; Score 47; DB 2; Length 573;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGVWDPIDY 14

DB 47 SGGGIWIPLNY 57

:|||:|:|:|

RESULT 2

B97182

acyl-protein synthetase, luxE [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: B97182

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L

.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B97182

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-381 <KUR>

A:CROSS-references: GB:AB001437; PIDN:AAK80245.1; PID:g15025293; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC2288

Query Match

Best Local Similarity 52.9%; Score 45; DB 2; Length 381;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 3 HTGGGVWD 10
|||||
Db 223 HTGGGGWD 230

RESULT 3
B43825
angiotensin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29833; B43825
R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discernme
A:Reference number: S29833; MUID:93192291; PMID:8448182
A:Accession: S29833
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-125 <BON>
A:Note: submitted to the Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 51.8%; Score 44; DB 1; Length 125;
Best Local Similarity 53.8%; Pred. No. 8.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 2 KHTGGGVWDPIDY 14
|||||
Db 82 KHVGGSPWPCRY 94

RESULT 4
A34768
ORF1 protein - Orf virus (strain NZ2)
C:Species: Orf virus
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Oct-1999
C:Accession: A34768
R:Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.
Virology 176, 379-389, 1990
A:Title: Sequence analysis of the inverted terminal repetition in the genome of the para
A:Reference number: A34768; MUID:90266454; PMID:2129563
A:Accession: A34768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <FRA>
A:Cross-references: GB:M30023; EMBL:M37623; NID:g332561; PIDN:AAA46787.1; PID:g332563

Query Match 50.6%; Score 43; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 7.1; Mismatches 4; Indels 1; Gaps 0;
Matches 5; Conservative 4;

QY 4 TGGGVWDPID 13
|||||
Db 32 SGGGIWGPLE 41

RESULT 5
H82984
hypothetical protein PA5284 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H82984
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: H82950; MUID:20437337; PMID:10984043
A:Accession: H82984
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-304 <STO>
A:Cross-references: GB:AE004941; GB:AE004941; NID:g9951596; PIDN:AAG08669.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA5284

Query Match 50.6%; Score 43; DB 2; Length 304;
Best Local Similarity 75.0%; Pred. No. 31; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;

QY 6 GGVWDPID 13
|||||
Db 75 GSVWDPVD 82

RESULT 6
B87412
conserved hypothetical protein CC1313 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: B87412
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: B87412
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <STO>
A:Cross-references: GB:AE005673; NID:g13422654; PIDN:AAK23294.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC1313

Query Match 50.6%; Score 43; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 44; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 1;

QY 3 HTGGGVWDPI 12
|||||
Db 372 HNPGGFWDPL 381

RESULT 7
T08241
gas-vesicle operon protein gvpD - Halobacterium sp. (strain NRC-1) plasmid pNRC100
N:Alternate names: hypothetical protein H0263
C:Species: Halobacterium sp.
A:Variety: strain NRC-1
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000
C:Accession: T08241
R:Ng, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B
Genome Res. 8, 1131-1141, 1998
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid o
A:Reference number: Z16408; MUID:99063795; PMID:9847077
A:Accession: T08241
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-536 <NGW>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822302; HALOSP:H0263
A:Experimental source: strain NRC-1
C:Genetics:
A:Gene: gvpD; HALOSP:H0263
A:Genome: plasmid pNRC100

Query Match 50.6%; Score 43; DB 2; Length 536;
Best Local Similarity 66.7%; Pred. No. 54; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 1;

QY 4 TGGGVWDPI 12
|||||
```

Db 247 TGNGTWDPL 255

RESULT 8

S15183
gas-vesicle operon protein gvpD - Halobacterium salinarum plasmids pHH1 and pNRC100
C:Species: Halobacterium salinarum
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Jan-2000
C:Accession: S15183; S06185
R:Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.
Mol. Microbiol. 5, 1159-1174, 1991
A:Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in
A:Reference number: S15183; MUID:92065812; PMID:1956294
A:Accession: S15183
A:Molecule type: DNA
A:Residues: 1-536 <HOR>
A:Cross-references: EMBL:X55648; NID:g43516; PID:g43517
A:Experimental source: plasmid pHH1
A:Genetics: PHH
A:Note: the authors translated the codon ACG for residue 531 as Ile
R:Jones, J.G.; Hackett, N.R.; Halladay, J.T.; Scothorn, D.J.; Yang, C.F.; Ng, W.L.; Dass
Nucleic Acids Res. 17, 7785-7793, 1989
A:Title: Analysis of insertion mutants reveals two new genes in the pNRC100 gas vesicle
A:Reference number: S06184; MUID:90016863; PMID:2552415
A:Accession: S06185
A:Molecule type: DNA
A:Residues: 1-536 <JON>
A:Cross-references: EMBL:X15374; NID:g43502; PID:g43504
A:Experimental source: plasmid pNRC100
A:Genetics: NRC
A:Note: the source is designated as Halobacterium halobium
C:Genetics: <NRC>
A:Gene: gvpD
A:Genome: plasmid pNRC100
C:Genetics: <PHH>
A:Gene: gvpD
A:Genome: plasmid pHH1

Query Match 50.6%; Score 43; DB 2; Length 536;

Best Local Similarity 66.7%; Pred. No. 54; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGGGVWDPI 12
| | | | |

Db 247 TGNGTWDPL 255

RESULT 9

G75070
hypothetical protein PAB0644 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: G75070
R:anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: G75070
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-597 <KAW>
A:Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB49868.1; PID:g545836
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0644

Query Match

Best Local Similarity 50.0%; Score 42.5; DB 2; Length 597;

Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 HTGGGVWDPI 14
| | | | |

Db 21 HDGSG-WDPIKY 31

RESULT 10

B71095
hypothetical protein PH1023 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: B71095
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: B71095
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-598 <KAW>
A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30120.1; PID:g3257437
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
C:Genetics:
A:Gene: PH1023

Query Match 50.0%; Score 42.5; DB 2; Length 598;

Best Local Similarity 66.7%; Pred. No. 72; Mismatches 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 HTGGGVWDPI 14
| | | | |

Db 21 HDGSG-WDPIKY 31

RESULT 11

S26020
cytochrome-c oxidase (EC 1.9.3.1) chain III - pig roundworm mitochondrion
C:Species: mitochondrion Ascaris suum (pig roundworm)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 07-Dec-1999
C:Accession: S26020; S25793
R:Okamoto, R.; Macfarlane, J.L.; Clary, D.O.; Wolstenholme, D.R.
Genetics 130, 471-498, 1992
A:Title: The mitochondrial genomes of two nematodes, Caenorhabditis elegans and Ascar
A:Reference number: S26014; MUID:92201635; PMID:1551572
A:Accession: S26020
A:Molecule type: DNA
A:Residues: 1-255 <OKI>
A:Cross-references: EMBL:X54253; NID:g13971; PIDN:CAA38169.1; PID:g575347
A:Note: the authors translated the initiation codon GTG for residue 1 as Val
R:Okamoto, R.; Macfarlane, J.L.; Wolstenholme, D.R.
Nucleic Acids Res. 18, 6113-6118, 1990
A:Title: Evidence for the frequent use of TTG as the translation initiation codon of
A:Reference number: S13139; MUID:91045077; PMID:2235493
A:Accession: S25793
A:Molecule type: DNA
A:Residues: 1-25 <OK2>
A:Cross-references: EMBL:X54253
A:Note: the authors translated the initiation codon GTG for residue 1 as Val
C:Genetics:
A:Gene: COIII
A:Genome: mitochondrion
A:Genetic code: SGC4
A:Start codon: GTG
A:Superfamily: cytochrome-c oxidase chain III
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr

Query Match

Best Local Similarity 49.4%; Score 42; DB 2; Length 255;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 HTGGGVWDPI 12
| | | | |

Db 106 HDVGGVWSPI 115

RESULT 12

E95061
peptide pheromone B1pC [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95061
R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-42 <KUR>
A:Cross-references: GB:AF005672; PIDN:AAK74686.1; PID:g14972003; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0528

Query Match 48.2%; Score 41; DB 2; Length 42;
Best Local Similarity 54.5%; Pred. No. 8.6;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGGGVWDPIDY 14
|||||: : :
DB 22 TGGGLWEDLLY 32

RESULT 13

S17005
AHT1 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: activator of hexose transport; protein H9332.3; protein YHR093W
C:Species: Saccharomyces cerevisiae
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 29-Oct-1999
C:Accession: S17005; S46717
R:Oezcan, S.; Ciriacy, M.
submitted to the EMBL Data Library, May 1991
A:Reference number: S17005
A:Accession: S17005
A:Molecule type: DNA
A:Residues: 1-182 <ORZ>
A:Cross-references: EMBL:X59464; NID:g3354; PIDN:CAA42071.1; PID:g663230
A:Experimental source: strain MC 971 B
R:Vaudin, M.
submitted to The EMBL Data Library, May 1994
A:Description: The sequence of S. cerevisiae cosmid 9332.
A:Reference number: S46715
A:Accession: S46717
A:Molecule type: DNA
A:Residues: 1-182 <VAU>
A:Cross-references: EMBL:U00060; NID:g487928; PIDN:AA68925.1; PID:g487931; MIPS:YHR093W

A:Gene: SGD:AHT1
A:Cross-references: SGD:S0001135; MIPS:YHR093W
A:Map position: 8R
C:Superfamily: Saccharomyces AHT1 protein

Query Match 48.2%; Score 41; DB 2; Length 182;
Best Local Similarity 55.6%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPID 13
|||||: : :
DB 44 GGGWGPME 52

RESULT 14

F69997
hypothetical protein ytnm - Bacillus subtilis

C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: F69997
R:Kunster, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95061
R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <KUN>
A:Cross-references: GB:Z99118; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14906.1;
A:Experimental source: strain 168
C:Genetics:
A:Gene: ytnm

Query Match 48.2%; Score 41; DB 2; Length 300;
Best Local Similarity 58.3%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AKHTGGGVWDPI 12
| ||||| :
DB 148 ADATGGGGGVPV 159

RESULT 15

T08411
hypothetical protein F18B3.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Oct-1999
C:Accession: T08411
R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16409
A:Accession: T08411
A:Molecule type: DNA
A:Residues: 1-114 <QUE>
A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.180
A:Experimental source: cultivar Columbia; BAC clone F18B3
C:Genetics:
A:Gene: ATSP:F18B3.180
A:Map position: 3
C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match 47.1%; Score 40; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGVWDPI 11
|||||
DB 99 GGVWDPI 104

Search completed: March 13, 2003, 15:17:52
Job time : 4.42308 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:06:24 ; Search time 1.4 seconds
(without alignments)
414.763 Million cell updates/sec

Title: US-09-822-698A-3_COPY_97_110

Perfect score: 85

Sequence: 1 AKHTGGVWDPIDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	55.3	573	1 30LD_COMTE	Q06401 comamonas t
2	44	51.8	125	1 ANGI_RABIT	P31347 oryctolegus
3	43	50.6	536	1 GVDL_HALNI	P13043 halobacteri
4	43	50.6	1371	1 PUR2_CHITE	Q26255 c trifuncti
5	42	49.4	255	1 COX3_ASCSU	P24879 ascaris suu
6	41	48.2	182	1 AHT1_YEAST	P29589 saccharomyc
7	40	47.1	478	1 OCT2_PIG	Q29013 sus scrofa
8	40	47.1	544	1 TCPH_MOUSE	P80313 mus musculu
9	39	45.9	418	1 DNJ2_ALIPO	P42824 allium porr
10	39	45.9	434	1 PDP_BACSU	P39142 bacillus su
11	39	45.9	518	1 YNV6_CAEEL	P34569 caenorhabdi
12	39	45.9	543	1 TCPH_HUMAN	Q99832 homo sapien
13	39	45.9	579	1 YR47_CAEEL	Q09563 caenorhabdi
14	39	45.9	807	1 YAK1_YEAST	P14680 saccharomyc
15	39	45.9	868	1 PRTH_PORGI	P43158 porphyromon
16	39	45.9	983	1 4ET_MOUSE	Q9est3 mus musculu
17	39	45.9	985	1 4ET_HUMAN	Q9nra8 homo sapien
18	38	44.7	185	1 EFP_DEIRA	Q9ry33 deinococcus
19	38	44.7	256	1 YM56_YEAST	Q03691 saccharomyc
20	38	44.7	272	1 COX3_PYLII	Q37600 pylaiella 1
21	38	44.7	387	1 YB96_YEAST	P38332 saccharomyc
22	38	44.7	420	1 TABA_PSES2	P31851 pseudomonas
23	38	44.7	447	1 DHEA_CORGL	P31026 corynebacte
24	38	44.7	521	1 GLGA_METJA	Q59001 methanococc
25	38	44.7	534	1 AWT1_CAEEL	P54145 caenorhabdi
26	38	44.7	628	1 BGAL_LACAC	Q07684 lactobacill
27	38	44.7	637	1 TRGS_ECOLI	Q00184 escherichia
28	38	44.7	643	1 YK09_CAEEL	P34304 caenorhabdi
29	38	44.7	738	1 DHET_ACEPO	P28036 acetobacter
30	38	44.7	739	1 DHET_ACEEU	Q44002 acetobacter
31	38	44.7	943	1 LBPA_NEIMB	Q06379 neisseria m
32	38	44.7	944	1 LBPA_NEIMA	Q9JCK4 neisseria m
33	38	44.7	1276	1 PMP6_CHLPN	Q9z899 chlamydia p

34	37	43.5	32	1	GHR4_RAT	P33581 rattus norv
35	37	43.5	145	1	ANGI_MOUSE	P21570 mus musculu
36	37	43.5	204	1	ADEN_ADEP3	Q84177 porcine ade
37	37	43.5	238	1	PRRC_RAT	P33579 rattus norv
38	37	43.5	242	1	Y252_MYCGE	P47494 mycoplasma
39	37	43.5	319	1	TAL_RALSO	Q8Y014 ralstonia s
40	37	43.5	344	1	PUR5_ECOLI	P08178 escherichia
41	37	43.5	344	1	PUR5_HAEIN	P43848 haemophilus
42	37	43.5	357	1	YFOB_SCHPO	Q10170 schizosacch
43	37	43.5	382	1	SUC1_ARCFU	Q28732 archaeglob
44	37	43.5	408	1	HUT1_RALSO	Q8XW31 ralstonia s
45	37	43.5	497	1	ACCD_CUSRE	P31562 cuscuta ref

ALIGNMENTS

RESULT 1					
30LD_COMTE					
ID	30LD_COMTE	STANDARD;	PRT;	573 AA.	
AC	Q06401;				
DT	01-OCT-1994 (Rel. 30, Created)				
DT	01-OCT-1994 (Rel. 30, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	3-oxosteroid 1-dehydrogenase (EC 1.3.99.4)				
OS	Comamonas testosteroni (Pseudomonas testosteroni).				
OC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.				
OX	NCBI_TaxID=285;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 17410;				
RX	MEDLINE=92041619; PubMed=1657885;				
RA	Plesiat P., Grandguillot M., Hatayama S., Vragar S., Michel-Briand Y.;				
RT	"Cloning, sequencing, and expression of the Pseudomonas testosteroni				
RT	gene encoding 3-oxosteroid delta 1-dehydrogenase.";				
RL	J. Bacteriol. 173:7219-7227(1991).				
CC	-!- FUNCTION: DEHYDROGENATES STEROIDS BY INTRODUCING A DOUBLE				
CC	BOND IN STEROID RING A.				
CC	-!- CATALYTIC ACTIVITY: A 3-oxosteroid + acceptor = a 3-oxo-delta(1)-				
CC	steroid + reduced acceptor.				
CC	-!- COFACTOR: FAD.				
CC	-!- PATHWAY: FIRST STEP IN STEROID CATABOLISM.				
CC	-!- SUBCELLULAR LOCATION: Inner membrane.				
CC	-----				
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CC	-----				
DR	EMBL; M68488; AAA25679.1; -				
DR	EMBL; A22347; CAA01596.1; -				
DR	PIR; A41319; A41319.				
KW	Oxidoreductase; Flavoprotein; Inner membrane; Steroid metabolism;				
KW	FAD.				
FT	NP_BIND 7 36 FAD (BY SIMILARITY).				
SQ	SEQUENCE 573 AA; 62672 MW; 8E941AF569897734 CRC64;				
Query Match 55.3%; Score 47; DB 1; Length 573;					
Best Local Similarity 54.5%; Pred. No. 5.5;					
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;					

QY	4	TGGGVWDPIDY 14			
DB	47	SGGGWIPLNY 57			
RESULT 2					
ANGI_RABIT					
ID	ANGI_RABIT	STANDARD;	PRT;	125 AA.	
AC	P31347;				

Gaps 0;

QY 4 TGGGWDP1 12
 Db 247 TCGGTWDP1 255

RESULT 4

PUR2_CHITE
 ID PUR2_CHITE STANDARD; PRT; 1371 AA.
 AC Q26255;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Trifunctional purine biosynthetic protein adenosine-3 [Includes:
 DE Phosphoribosylamine-glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide
 DE ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase);
 DE Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1) (AIRS)
 DE (Phosphoribosyl-aminimidazole synthetase) (AIR synthetase);
 DE Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (GART) (GAR
 DE transformylase) (5'-phosphoribosylglycinamide transformylase)].
 GN GART.
 OS Chironomus tentans (Midge).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=7153;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92389366; PubMed=1518084;
 RA Clark D.V., Henikoff S.;
 RT "Unusual organizational features of the Drosophila Gart locus are not
 RT conserved within Diptera.";
 RL J. Mol. Evol. 35:51-59(1992).
 CC -|- CATALYTIC ACTIVITY: ATP + 5-phospho-D-riboseylamine + glycine = ADP
 CC + phosphate + N(1)-(5-phospho-D-riboseyl)glycinamide.
 CC -|- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1)-(5-phospho-D-
 CC ribosyl)glycinamide = tetrahydrofolate + N(2)-formyl-N(1)-(5-
 CC phospho-D-riboseyl)glycinamide.
 CC -|- CATALYTIC ACTIVITY: ATP + 2'-(formamido)-N(1)-(5-phospho-D-
 CC ribosyl)acetamide = ADP + phosphate + 5-amino-1-(5-phospho-D-
 CC ribosyl)imidazole.
 CC -|- PATHWAY: SECOND, THIRD AND FIFTH STEPS IN DE NOVO PURINE
 CC BIOSYNTHESIS.
 CC -|- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GARS FAMILY.
 CC -|- SIMILARITY: TO OTHER AIRS AND GART FROM BACTERIA AND EUKARYOTES.
 CC -----
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 CC -----
 CC EMBL; S43653; AAB23115.1; -.
 DR HSSP; P08178; 1CL1.
 DR InterPro: IPR000728; AIRS_related.
 DR InterPro: IPR001555; GART.
 DR InterPro: IPR001115; Gars.
 DR InterPro: IPR004733; PurM_cligase.
 DR InterPro: IPR004607; PurN.
 DR InterPro: IPR002376; formyl_transf.
 DR Pfam: PF00551; formyl_transf; 1.
 DR Pfam: PF00586; AIRS; 2.
 DR Pfam: PF01071; GARS; 1.
 DR Pfam: PF02769; AIRS_C; 2.
 DR Pfam: PF02842; GARS_B; 1.
 DR Pfam: PF02843; GARS_C; 1.
 DR Pfam: PF02844; GARS_N; 1.
 DR TIGRfams: TIGR00639; PurN; 1.
 DR TIGRfams: TIGR00877; purD; 1.
 DR TIGRfams: TIGR00878; purM; 2.
 DR PROSITE; PS00184; GARS; 1.
 DR PROSITE; PS00373; GART; 1.

KW Multifunctional enzyme; Purine biosynthesis; Ligase; Transferase.
 FT DOMAIN 1 433 GARS.
 FT DOMAIN 434 1171 AIRS.
 FT DOMAIN 1172 1371 GART.
 FT ACT_SITE 1315 1315 BY SIMILARITY.
 SQ SEQUENCE 1371 AA; 149103 MW; 7BF4664DB1538946 CRC64;

Query Match 50.6%; Score 43; DB 1; Length 1371;
 Best Local Similarity 77.8%; Pred. No. 54;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGWDP1 12
 Db 1057 TGGGLWDNI 1065

RESULT 5

COX3_ASCSU
 ID COX3_ASCSU STANDARD; PRT; 255 AA.
 AC P24879;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide III (EC 1.9.3.1).
 GN COIII.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Body wall muscle, and Egg;
 RX MEDLINE=92201635; PubMed=1551572;
 RA Okimoto R., Macfarlane J.L., Clary D.O., Wolstenholme D.R.;
 RT "The mitochondrial genomes of two nematodes, Caenorhabditis elegans
 RT and Ascaris suum.";
 RL Genetics 130:471-498(1992).
 CC -|- FUNCTION: Subunits I, II and III form the functional core of
 CC the enzyme complex.
 CC -|- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -|- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
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 CC -----
 CC EMBL; X54253; CAA38169.1; -.
 DR PIR; S26020; S26020.
 DR InterPro: IPR000298; Cytc_oxdse_III.
 DR Pfam: PF00510; COX3; 1.
 DR ProDom: PD000382; Cytc_oxdse_III; 1.
 DR PROSITE; PS00253; COX3; 1.
 DR Oxidoreductase; Mitochondrion; Transmembrane.
 KW SEQUENCE 255 AA; 29094 MW; 05A992684AC92755 CRC64;

Query Match 49.4%; Score 42; DB 1; Length 255;
 Best Local Similarity 70.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 HTGGGWDP1 12
 Db 106 HDVGVWSPI 115

RESULT 6

AHT1_YEAST
 ID AHT1_YEAST STANDARD; PRT; 182 AA.

```
AC P29589: P38807:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hexose transport activator protein.
GN AHT1 OR YHR093W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=MC 971 B.
RC Oezcan S., Cirilacy M.;
RA Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=S288C / AB972;
RC MEDLINE=94378003; PubMed=8091229;
RX Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
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CC -----
DR EMBL; X59464; CAA42071.1; -
DR EMBL; U00060; AB68925.1; -
DR PIR; S17005; S17005.
DR PIR; S46717; S46717.
DR SGD; S0001135; AHT1.
SQ SEQUENCE 182 AA; 19776 MW; 7B0723BAA1066713 CRC64;

Query Match 48.28; Score 41; DB 1; Length 182;
Best Local Similarity 55.68; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPID 13
DB 44 GGGINGPME 52
|||||
STANDARD; PRT; 478 AA.

RESULT 7
OCT2_PIG
ID OCT2_PIG STANDARD; PRT; 478 AA.
AC Q29013; Q29089;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-2002 (Rel. 41, Last annotation update)
DE Octamer-binding transcription factor 2 (OTF-2) (Lymphoid-restricted
DE immunoglobulin octamer binding protein NF-A2) (OCT-2 factor).
GN POU2F2 OR OTF2 OR OCT2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A.
RP Tissue=Spleen;
RC MEDLINE=95030552; PubMed=7943947;
RX Tuggie C.K., Helm J., Rothschild M.F.;
RA -----

RT "Cloning, sequencing and restriction fragment length polymorphism
RT analys. of a porcine cDNA for OCT2.";
RL Anim. Genet. 25:141-145(1994).
RN [2]
RN SEQUENCE OF 210-350 FROM N.A.
RC STRAIN=Duroc; PubMed=8270542;
RX MEDLINE=94095558; PubMed=8270542;
RA Tuggie C.K.;
RT "Cloning and sequence analysis of the swine Oct-2 POU-domain genomic
RT region.";
RL J. Anim. Sci. 71:3172-3172(1993).
CC -!- FUNCTION: THIS PROTEIN IS A TRANSCRIPTION FACTOR THAT SPECIFICALLY
CC BINDS TO THE OCTAMER MOTIF ('ATTGTCAT') AND PLAYS AN IMPORTANT
CC ROLE IN REGULATING TRANSCRIPTION IN A NUMBER OF TISSUES IN
CC ADDITION TO ACTIVATING IMMUNOGLOBULIN GENE EXPRESSION (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN B-CELLS (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
CC -!- CLASS-2 SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U00794; AAA80148.1; -
DR EMBL; L03842; AAA74657.1; -
DR HSSP; P09086; LHDP.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000972; Octamer-bind_TF.
DR InterPro; IPR000327; POU_domain.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00157; pou; 1.
DR PRINTS; PR00029; OCTAMER.
DR PRINTS; PR00028; POUDOMAIN.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000583; POU_domain; 1.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00352; POU; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00035; POU_1; 1.
DR PROSITE; PS00465; POU_2; 1.
KW Homeobox; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein.
FT DOMAIN 199 269 POU.
FT DNA_BIND 297 356 HOMEBOX.
FT DOMAIN 389 410 LEUCINE-ZIPPER.
FT DOMAIN 77 80 POLY-PRO.
FT DOMAIN 417 424 GLY-RICH.
FT DOMAIN 437 440 POLY-PRO.
FT CONFLICT 212 212 Q -> V (IN REF. 2).
FT CONFLICT 215 215 I -> M (IN REF. 2).
FT CONFLICT 222 222 G -> V (IN REF. 2).
FT CONFLICT 233 233 G -> A (IN REF. 2).
FT CONFLICT 238 238 Q -> K (IN REF. 2).
FT CONFLICT 285 285 R -> S (IN REF. 2).
SQ SEQUENCE 478 AA; 51098 MW; FD196758B603B718 CRC64;

Query Match 47.18; Score 40; DB 1; Length 478;
Best Local Similarity 54.58; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGGGVWDPIDY 14
DB 466 TGGGLWNPAPY 476
|||||
```

```
RESULT 8
TCPL_MOUSE
ID TCPL_MOUSE STANDARD; PRT; 544 AA.
AC P80313;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE T-complex protein 1, eta subunit (TCP-1-eta) (CCT-eta).
GN CCT7 OR COTH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=129/SV;
RX MEDLINE=9266022; PubMed=10336634;
RA Kubota H., Yokota S., Yanagi H., Yura T.;
RT "Structures and co-regulated expression of the genes encoding mouse
cytosolic chaperonin CCT subunits."
RL Eur. J. Biochem. 262:492-500(1999).
CC -!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
ACTIN AND TUBULIN.
CC -!- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
-----
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-----
EMBL: Z31399; CAA83274.1; -.
DR EMBL; AB022160; BA81878.1; -.
DR PIR; S43058; S43058.
DR HSP; P48424; 1A6D.
DR MGD; MGI:107184; Cct7.
DR InterPro; IPR002194; Chaperonin_TCP-1.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; Cpn60_TCP1; 1.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00750; TCP1_1; 1.
DR PROSITE; PS00751; TCP1_2; 1.
DR PROSITE; PS00995; TCP1_3; 1.
DR Chaperone; ATP-binding; Multigene family.
KW Chaperone; ATP-binding; Multigene family.
SQ SEQUENCE 544 AA; 59652 MW; 0BD7AD35456EE677 CRC64;

Query Match 47.1%; Score 40; DB 1; Length 544;
Best Local Similarity 46.2%; Pred. No. 65;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 AKHTGGVNDPID 13
Db 466 ARHAQGMWYVD 478

RESULT 9
DNJ2_ALLPO
ID DNJ2_ALLPO STANDARD; PRT; 418 AA.
AC P42824;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DnaJ protein homolog 2.
GN LDJ2.
OS Allium porrum (Leek).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=4681;
RN [1]
RP SEQUENCE FROM N.A.
RA Bessoule J.J., Testet E., Cassagne C.;
RT "Cloning of a new isoform of a DnaJ protein from Allium porrum
epidermal cells."
RL Plant Physiol. Biochem. 32:723-727(1994).
CC -!- FUNCTION: HAVE A CONTINUOUS ROLE IN PLANT DEVELOPMENT PROBABLY
IN THE STRUCTURAL ORGANIZATION OF COMPARTMENTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -!- SIMILARITY: CONTAINS 1 J DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 CR DOMAIN.
-----
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-----
EMBL: X77632; CAA54720.1; -.
DR HSP; P25685; 1HDJ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF00684; DnaJ_CXXCXXGXG; 1.
DR PRINTS; PR00625; DnaJ_C; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_CXXCXXGXG; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR Chaperone; Repeat; Prenylation; Lipoprotein; Multigene family.
KW Chaperone; Repeat; Prenylation; Lipoprotein; Multigene family.
FT DOMAIN 11 76 J-DOMAIN.
FT DOMAIN 83 88 POLY-GLY.
FT REPEAT 148 155 CXXCXXGXG MOTIF.
FT REPEAT 164 171 CXXCXXGXG MOTIF.
FT REPEAT 191 198 CXXCXXGXG MOTIF.
FT REPEAT 207 214 CXXCXXGXG MOTIF.
FT LIPID 415 415 FARNESYL (HY SIMILARITY).
SQ SEQUENCE 418 AA; 46584 MW; DCE2A4DF192329E6 CRC64;

Query Match 45.9%; Score 39; DB 1; Length 418;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGVGWDPID 13
Db 85 GGVGWDPID 93

RESULT 10
PDP_BACSU
ID PDP_BACSU STANDARD; PRT; 434 AA.
AC P39142;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
```

DE Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2) (PNP).
GN PDP.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96134975; PubMed=8550462;
RA Saxild H.H., Andersen L.N., Hammer K.;
RT "Dra-nupC-pdp operon of Bacillus subtilis: nucleotide sequence,
RT induction by deoxyribonucleosides, and transcriptional regulation by
RT the deOR-encoded DeOR repressor protein.";
RL J. Bacteriol. 178:424-434(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / HGSC1A1;
RX MEDLINE=97021444; PubMed=8867804;
RA Yoshida K.-I., Fujimura M., Yanai N., Fujita Y.;
RT "Cloning and sequencing of a 23-kb region of the Bacillus subtilis
RT genome between the tol and hut operons.";
RL DNA Res. 2:295-301(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bortner M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chol S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert B., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris H., Karamata D., Kasahara Y., Klearr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinol S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medique C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Portwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofione F., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seiror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
CC -!- CATALYTIC ACTIVITY: Pyrimidine nucleoside + phosphate = pyrimidine
CC + alpha-D-ribose 1-phosphate.
CC -!- SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE
CC PHOSPHORYLASES FAMILY.
CC -----
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CC -----
CC EMBL; X82174; CAA57664.1; -.
CC EMBL; D45912; BAA08339.1; -.
CC EMBL; 299124; CAB15976.1; -.
DR

HSSP; P77836; 1BRW.
DR Subtilist; BG10985; pdp.
DR InterPro; IPR000312; Glycos_transf_3.
DR InterPro; IPR000053; Thymid_phosphils.
DR Pfam; PF00591; Glycos_transf_3; 1.
DR Pfam; PF02885; Glycos_trans_3N; 1.
DR ProDom; PD005916; Thymid_phosphils; 1.
DR PROSITE; PS00647; Thymid_PHOSPHORYLASE; 1.
KW Transferase; Glycosyltransferase; Complete proteome.
SQ SEQUENCE 434 AA; 46532 MW; E451CF497ECr5B30 CRC64;
Query Match 45.9%; Score 39; DB 1; Length 434;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 KHTGGGVW 9
Db 81 KHTGGGVW 88
|||:||||
RESULT 11
YINV6_CAEEL STANDARD; PRT; 518 AA.
ID YINV6_CAEEL
AC P34569; P34570;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 59.0 kDa protein T16H12.6 in chromosome III.
GN T16H12.6
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smith A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC -----
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CC -----
CC EMBL; Z30662; CAA83141.1; -.
CC PIR; S42387; S42387.
DR Wormpep; T16H12.6; CE00627.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR001798; Kelch.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR PROSITE; PS50097; BTB; FALSE_NEG.
KW Hypothetical protein; Repeat.
FT DOMAIN 1 98 BTB
FT REPEAT 205 255 KELCH 1.
FT REPEAT 256 302 KELCH 2.
FT REPEAT 308 354 KELCH 3.
FT REPEAT 356 402 KELCH 4.
FT REPEAT 404 450 KELCH 5.
FT REPEAT 452 498 KELCH 6.
SQ SEQUENCE 518 AA; 59036 MW; 117A355F4EAD6A9F CRC64;
Query Match 45.9%; Score 39; DB 1; Length 518;
Best Local Similarity 60.0%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 HTGGGVWDP 12

```
Db 368 HQGGGVDPV 377
      ||| |||
Query Match 45.9%; Score 39; DB 1; Length 543;
Best Local Similarity 46.2%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 12
TCFH_HUMAN
ID TCPL_HUMAN STANDARD; PRT; 543 AA.
AC Q99832; O14871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-complex protein 1, eta subunit (TCP-1-eta) (CCT-eta) (HIV-1 Nef
DE interacting protein).
DE CC17 OR CCTH OR NIP1-1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99038262; PubMed=9819444;
RA Won K.-A., Schumacher R.J., Farr G.W., Horwich A.L., Reed S.I.;
RT "Maturation of human cyclin E requires the function of eukaryotic
RL chaperonin CCT.";
RL Mol. Cell. Biol. 18:7584-7589(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 13-424 FROM N.A.
RA Fukushi M., Kimura T., Yamamoto N.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
CC ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
CC ACTIN AND TUBULIN (BY SIMILARITY).
CC -!- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
CC
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CC
CC EMBL; AF026292; AAC96011.1; -
CC DR EMBL; BC019296; AAH19296.1; -
CC DR EMBL; U83843; AAB41437.1; -
CC DR HSSP; P48424; 1A6D.
CC DR Genew; HGNC:1622; CCT7.
CC MIM; 605140; -
CC DR InterPro; IPR002194; Chaperonin_TCP-1.
CC DR InterPro; IPR002423; Cpn60/TCP-1.
CC DR Pfam; PF00118; cpn60_TCP1.1.
CC DR PRINTS; PR00304; TCOMPLEXTCP1.
CC DR PROSITE; PS00750; TCP1_1; 1.
CC DR PROSITE; PS00751; TCP1_2; 1.
CC DR PROSITE; PS00995; TCP1_3; 1.
CC DR Chaperone; ATP-binding; Multigene family.
CC KW CONFLICT 282 283 HH -> RQ (IN REF. 3).
CC FT CONFLICT 293 293 L -> P (IN REF. 3).
CC FT CONFLICT 336 336 A -> P (IN REF. 3).
CC FT CONFLICT 364 364 C -> L (IN REF. 3).
CC FT CONFLICT 374 376 LRG -> SPC (IN REF. 3).
CC FT CONFLICT 407 407 A -> P (IN REF. 3).
CC FT CONFLICT 411 411 A -> P (IN REF. 3).
CC SQ SEQUENCE 543 AA; 59366 MW; 9F1E33FA80E6238E CRC64;

Query Match 45.9%; Score 39; DB 1; Length 579;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query Match 45.9%; Score 39; DB 1; Length 543;
Best Local Similarity 46.2%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AKHITGGVWDPI 13
      ||| |||
Db 466 ARHAQGGTWGYVD 478

RESULT 13
YR47_CAEEL STANDARD; PRT; 579 AA.
AC Q09563;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 66.0 kDa protein F47D12.7 in chromosome III.
GN F47D12.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Taich A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U22831; AAK20068.1; -
CC DR WormPep; F47D12.7; CE01951.
CC DR InterPro; IPR000210; BTB_POZ.
CC DR InterPro; IPR001798; Kelch.
CC DR Pfam; PF00651; BTB; 1.
CC DR Pfam; PF01344; Kelch; 6.
CC DR PRINTS; PR00501; KELCHREPEAT.
CC DR SMART; SM00225; BTB; 1.
CC DR PROSITE; PS00097; BTB; 1.
CC KW Hypothetical protein; Repeat.
CC FT DOMAIN 51 119 BTB.
CC FT REPEAT 266 316 KELCH 1.
CC FT REPEAT 317 363 KELCH 2.
CC FT REPEAT 369 415 KELCH 3.
CC FT REPEAT 417 463 KELCH 4.
CC FT REPEAT 465 511 KELCH 5.
CC FT REPEAT 513 559 KELCH 6.
CC SQ SEQUENCE 579 AA; 66042 MW; 3FE770B5E4C2D32F CRC64;

Query Match 45.9%; Score 39; DB 1; Length 579;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 HTGGGVWDPI 12
      ||| |||
Db 429 HQGGGVDPV 438

RESULT 14
YAKL_YEAST
ID YAKL_YEAST STANDARD; PRT; 807 AA.
AC P14680;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

DE Protein kinase YAK1 (EC 2.7.1.1.-).
GN YAK1 OR YJL141C OR J0652.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90108683; PubMed=2558053;
RA Garrett S., Broach J.;
RT "Loss of Ras activity in Saccharomyces cerevisiae is suppressed by
RT disruptions of a new kinase gene, YAK1, whose product may act
RT downstream of the cAMP-dependent protein kinase.";
RL Genes Dev. 3:1336-1348(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96408771; PubMed=8813765;
RA Katsoulou C., Ternita M., Tavernarakis N., Alexandraki D.;
RT "Sequence analysis of a 40.7 kb segment from the left arm of yeast
RT chromosome X reveals 14 known genes and 13 new open reading frames
RT including homologues of genes clustered on the right arm of
RT chromosome XI.";
RL Yeast 12:787-797(1996).
CC -!- FUNCTION: THIS PROTEIN OCCURS IN REVERTANT RAS/CAMP MUTANTS
CC YEAST AND MAY BE INVOLVED IN CELL-CYCLE REGULATION.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MNB/DRK SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X16056; CAA34192.1; -;
DR EMBL; X87371; CAA60814.1; -;
DR EMBL; 249417; CAA89437.1; -;
DR PIR; A32582; A32582.
DR HSP; P24941; IAO1.
DR SGD; S0003677; YAK1.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 56 85 GLN-RICH.
FT DOMAIN 369 704 PROTEIN KINASE.
FT NP_BIND 375 383 ATP (BY SIMILARITY).
FT BINDING 398 398 ATP (BY SIMILARITY).
FT ACT_SITE 496 496 BY SIMILARITY.
FT MOD_RES 127 127 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 206 206 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 240 240 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 295 295 PHOSPHORYLATION (PROBABLE).
SQ SEQUENCE 807 AA; 91245 MW; E0B7C56FAA35E056 CRC64;

Query Match 45.9%; Score 39; DB 1; Length 807;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 HTGGGVDP 11
| | | | |
DB 43 HMGRIWNP 51

RESULT 15
PRTT_PORGI
ID PRTT_PORGI STANDARD; PRT; 868 AA.
AC P43158;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Thiol protease/hemagglutinin prtr precursor (EC 3.4.22.-).
GN PRTT.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 53977;
RX MEDLINE=93114862; PubMed=8093357;
RA Ootogoto J.-I., Kuramitsu H.K.;
RT "Isolation and characterization of the Porphyromonas gingivalis prtr
RT gene, coding for protease activity.";
RL Infect. Immun. 61:1117-123(1993).
RN [2]
RP REVISIONS, SEQUENCE FROM N.A.
RX STRAIN=ATCC 53977;
RX MEDLINE=95105001; PubMed=7806362;
RA Madden T.E., Clark V.L., Kuramitsu H.K.;
RT "Revised sequence of the Porphyromonas gingivalis prtr cysteine
RT protease/hemagglutinin gene: homology with streptococcal pyrogenic
RT exotoxin B/streptococcal proteinase.";
RL Infect. Immun. 63:238-247(1995).
CC -!- FUNCTION: APPEARS TO BE SPECIFIC FOR ARGININE-CONTAINING PEPTIDE
CC BONDS. POSSESSES HEMAGGLUTININ ACTIVITY.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M83096; -; NOT_ANNOTATED_CDS.
DR MEROPS; C10.002; -;
DR InterPro; IPR000200; Peptidase_C10.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01640; Peptidase_C10; 1.
DR PRINTS; PR00757; STREPTOPAIN.
KW Hydrolase; Thiol protease; Signal; Hemagglutinin.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 ? POTENTIAL.
FT CHAIN ? 868 THIOI PROTEASE/HEMAGGLUTININ PRTT.
FT ACT_SITE 184 184 BY SIMILARITY.
FT ACT_SITE 327 327 BY SIMILARITY.
SQ SEQUENCE 868 AA; 96444 MW; 45436EFE32779323 CRC64;
Query Match 45.9%; Score 39; DB 1; Length 868;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GVWDPID 13
| | | | |
DB 736 GFWDPID 742

Search completed: March 13, 2003, 15:15:15
Job time : 3.4 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:11:14 ; Search time 5.06154 seconds
(without alignments)
569.918 Million cell updates/sec

Title: US-09-822-698a-3_COPY_97_110
Perfect score: 85
Sequence: 1 AKHTGGGWDPIDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	ID	Description
1	46	54.1	171	13	Q98U44	Q98U44 mantidactyl
2	46	54.1	177	13	Q98U43	Q98U43 aglyptodact
3	46	54.1	177	13	Q98U41	Q98U41 boophis tep
4	46	54.1	177	13	Q98U33	Q98U33 nyctibatrac
5	46	54.1	177	13	Q98U32	Q98U32 nyctibatrac
6	46	54.1	177	13	Q98U26	Q98U26 micrixalus
7	46	54.1	177	13	Q98U25	Q98U25 micrixalus
8	46	54.1	177	13	Q98U24	Q98U24 indirana sp
9	46	54.1	177	13	Q98U20	Q98U20 philautus m
10	46	54.1	177	13	Q98U19	Q98U19 philautus w
11	45	52.9	131	4	Q8WYX0	Q8WYX0 homo sapien
12	45	52.9	177	13	Q98U42	Q98U42 boophis xer
13	45	52.9	177	13	Q98U21	Q98U21 rhacophorus
14	45	52.9	381	16	Q97G57	Q97G57 clostridium
15	44	51.8	489	2	P72455	P72455 streptomyces
16	43.5	51.2	762	2	Q9RM63	Q9RM63 myroides od

17	43	50.6	51	2	Q9F2F8	Q9F2F8 streptococc
18	43	50.6	71	12	Q85298	Q85298 orf virus.
19	43	50.6	102	2	Q9LCA9	Q9LCA9 rhodocyclus
20	43	50.6	304	16	Q9HTS0	Q9HTS0 pseudomonas
21	43	50.6	435	16	Q9A8P0	Q9A8P0 caulobacter
22	43	50.6	762	2	Q9RQ15	Q9RQ15 neisseria d
23	42.5	50.0	597	17	Q9V038	Q9V038 pyrococcus
24	42.5	50.0	597	17	Q8U2G5	Q8U2G5 pyrococcus
25	42.5	50.0	598	17	Q58774	Q58774 pyrococcus
26	42	49.4	174	13	Q8U4U5	Q8U4U5 mantella ma
27	42	49.4	458	10	Q8RU64	Q8RU64 oryza sativ
28	42	49.4	502	16	Q8Y012	Q8Y012 raietonia s
29	41	48.2	42	16	Q9ETQ9	Q9ETQ9 streptococc
30	41	48.2	300	16	Q34430	Q34430 bacillus su
31	41	48.2	324	10	Q9LVM5	Q9LVM5 arabidopsis
32	41	48.2	399	4	Q9Y5P5	Q9Y5P5 homo sapien
33	41	48.2	420	4	Q9NWC3	Q9NWC3 homo sapien
34	41	48.2	420	4	Q961J6	Q961J6 homo sapien
35	41	48.2	695	2	Q934G0	Q934G0 pseudomonas
36	41	48.2	792	4	Q9H0D2	Q9H0D2 homo sapien
37	41	48.2	801	16	Q8XV55	Q8XV55 raietonia s
38	41	48.2	1022	2	Q9XG16	Q9XG16 bifidobacte
39	41	48.2	1023	2	Q9X6Y5	Q9X6Y5 bifidobacte
40	41	48.2	1044	2	Q9F4D6	Q9F4D6 bifidobacte
41	41	48.2	1456	2	Q9F636	Q9F636 stigmatella
42	40.5	47.6	181	10	Q9C5D5	Q9C5D5 arabidopsis
43	40.5	47.6	388	10	Q9M8R4	Q9M8R4 arabidopsis
44	40	47.1	56	2	Q9RMH8	Q9RMH8 lactobacilli
45	40	47.1	114	10	Q9SVK9	Q9SVK9 arabidopsis

ALIGNMENTS

RESULT 1

Q98U44 ID Q98U44 PRELIMINARY; PRT; 171 AA.
AC Q98U44;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Mantidactylus cf. ulcersus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rhacophoridae;
OC Mantidactylus.
OX NCBI_TaxID=129014;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249165; AAG49808.1; .
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; Tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 171
SQ SEQUENCE 171 AA; 19816 MW; 50CEEF8A130D2A7B CRC64;

Query Match 54.1%; Score 46; DB 13; Length 171;

Best Local Similarity 70.0%; Pred. No. 11;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGWDPIDY 14

|||||: ||:

Db 133 GGGWENIDF 142

```
RESULT 2
Q98043 ID Q98043 PRELIMINARY; PRT; 177 AA.
AC Q98043;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Tyrosinase (Fragment).
OS Aglyptodactylus madagascariensis (Madagascar jumping frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rhacophoridae;
OC Aglyptodactylus.
OX NCBI_TaxID=68424;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249166; AAG49809.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20410 MW; A4E5A34F90563FF1 CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
| | | | | : | |
DB 133 GGGVWENIDF 142

RESULT 3
Q98041 ID Q98041 PRELIMINARY; PRT; 177 AA.
AC Q98041;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Boophis tephraeomystax.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rhacophoridae;
OC Boophis.
OX NCBI_TaxID=68440;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249168; AAG49811.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20542 MW; 22C28DBB1217467B CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
```

```
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
| | | | | : | |
DB 133 GGGVWENIDF 142

RESULT 4
Q98U33 ID Q98U33 PRELIMINARY; PRT; 177 AA.
AC Q98U33;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Nyctibatrachus major.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Nyctibatrachus.
OX NCBI_TaxID=129023;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249176; AAG49819.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20589 MW; 1B647613316D7C42 CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
| | | | | : | |
DB 133 GGGVWENIDF 142

RESULT 5
Q98U32 ID Q98U32 PRELIMINARY; PRT; 177 AA.
AC Q98U32;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Nyctibatrachus aliciae.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Nyctibatrachus.
OX NCBI_TaxID=129021;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249177; AAG49820.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
```

DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; UNKNOWN_1.
 FT NON_TER 1 177
 SQ SEQUENCE 177 AA; 20556 MW; 2C67161CD96FB382 CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 5 GGGVWDPIDY 14
 |||||: ||:
 Db 133 GGGVWENIDF 142

RESULT 6

ID Q98U26 PRELIMINARY; PRT; 177 AA.
 AC Q98U26;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Micrixalus fuscus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Micrixalus.
 OX NCBI_TaxID=129016;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249183; AAC49826.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 FT NON_TER 1 177
 SQ SEQUENCE 177 AA; 20560 MW; A76738DA4102C9CE CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 5 GGGVWDPIDY 14
 |||||: ||:
 Db 133 GGGVWENIDF 142

RESULT 7

ID Q98U25 PRELIMINARY; PRT; 177 AA.
 AC Q98U25;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Micrixalus kottigeharensis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Micrixalus.
 OX NCBI_TaxID=130786;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs

RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249184; AAC49827.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 FT NON_TER 1 177
 SQ SEQUENCE 177 AA; 20574 MW; 05A658678D3BF9D4 CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 5 GGGVWDPIDY 14
 |||||: ||:
 Db 133 GGGVWENIDF 142

RESULT 8

ID Q98U24 PRELIMINARY; PRT; 177 AA.
 AC Q98U24;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Indirana sp. 1.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Indirana.
 OX NCBI_TaxID=147865;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249185; AAC49828.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 FT NON_TER 1 177
 SQ SEQUENCE 177 AA; 20434 MW; 29EB35222BA6D60B CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 5 GGGVWDPIDY 14
 |||||: ||:
 Db 133 GGGVWENIDF 142

RESULT 9

ID Q98U20 PRELIMINARY; PRT; 177 AA.
 AC Q98U20;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Philautus microlypanum.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Philautus.
OX NCBI_TaxID=129024;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249189; AAG49832.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR SMART; SM00001; EGF-like; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20464 MW; 4E2C1654EA212ADE CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
DB 133 GGGVWENIDF 142

RESULT 10
Q98U19 PRELIMINARY; PRT; 177 AA.
AC Q98U19;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Philautus wynaedensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Philautus.
OX NCBI_TaxID=130794;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249190; AAG49833.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20516 MW; 51214062A983B9DE CRC64;

Query Match 54.1%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
DB 133 GGGVWENIDF 142
```

```
ID Q8WY0 PRELIMINARY; PRT; 131 AA.
AC Q8WY0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 13.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289615; AAL55799.1; -.
KW Hypothetical protein.
SQ SEQUENCE 131 AA; 13879 MW; B1D6A5917F3608ED CRC64;

Query Match 52.9%; Score 45; DB 4; Length 131;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGVWDP 11
DB 40 TGGGVWQP 47

RESULT 12
Q98U42 PRELIMINARY; PRT; 177 AA.
AC Q98U42;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Boophis.
OX NCBI_TaxID=128996;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249167; AAG49810.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20587 MW; DB6493AF16D0F020 CRC64;

Query Match 52.9%; Score 45; DB 13; Length 177;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDPIDY 14
DB 133 GGGVWENIDF 142

RESULT 13
Q98U21 PRELIMINARY; PRT; 177 AA.
ID Q98U21
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AC Q98U21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (fragment).
OS Rhacophorus malabaricus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Rhacophorus.
OX NCBI_TaxID=129031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF249188; AAG49831.1; -.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR002227; Tyrosinase.
DR Pfam: PF00264; tyrosinase; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE: PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT 177
FT 177
SQ SEQUENCE 177 AA; 20426 MW; 16A9E9F4F1BE2035 CRC64;

Query Match 52.9%; Score 45; DB 13; Length 177;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGVWDFIDY 14
DB 133 GGGVWENVD 142
|||||:|:|

RESULT 14
Q97GS7 PRELIMINARY; PRT; 381 AA.
AC Q97GS7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Acyl-protein synthetase, luxE.
GN CAC2288.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007729; AAK80245.1; -.
KW Complete proteome.
SQ SEQUENCE 381 AA; 43104 MW; 68D07900AC06AA70 CRC64;

Query Match 52.9%; Score 45; DB 16; Length 381;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HTGGGVWD 10
DB 223 HTGGGGWD 230
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RESULT 15
P72455 PRELIMINARY; PRT; 489 AA.
AC P72455;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NADH:N-amidino-scylllo-inosamine oxidoreductase.
GN STSB.
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=97385085; PubMed=9238101;
RA Ahlert J., Distler J., Mansouri K., Piepersberg W.;
RT "Identification of stsc, the gene encoding the L-glutamine:scyllo-
RT inosose aminotransferase from streptomycin-producing Streptomyces.";
RL Arch. Microbiol. 168:102-113(1997).
DR EMBL: Y08763; CAA70011.1; -.
DR InterPro: IPR000205; NAD_binding.
SQ SEQUENCE 489 AA; 51575 MW; 73B6863C3FAA3C93 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 489;
Best Local Similarity 75.0%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGGGVWDP 11
DB 166 SGGGLWDP 173
|||||

Search completed: March 13, 2003, 15:17:00
Job time : 7.06154 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:59 ; Search time 29.0769 Seconds
(without alignments)
54.992 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110

Perfect score: 12

Sequence: 1 HTRGGVWDPIY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying Chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq.101002.*

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22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	14	22	AAE12770 Human PH1 Fab anti
2	12	100.0	121	22	AAE12706 Human PH1 Fab anti
3	12	100.0	381	22	AAE12707 Human b1vPH1-IL-2
4	12	100.0	451	22	AAE12715 Human recombinant
5	11	91.7	14	22	AAE12740 Human PH1 Fab anti
6	11	91.7	14	22	AAE12762 Human PH1 Fab anti
7	11	91.7	16	22	AAE12734 Human PH1 Fab anti
8	10	83.3	14	22	AAE12718 Human PH1 Fab anti
9	10	83.3	14	22	AAE12719 Human PH1 Fab anti
10	10	83.3	14	22	AAE12720 Human PH1 Fab anti

11	10	83.3	14	22	AAE12741 Human PH1 Fab anti
12	10	83.3	14	22	AAE12742 Human PH1 Fab anti
13	10	83.3	14	22	AAE12743 Human PH1 Fab anti
14	10	83.3	14	22	AAE12744 Human PH1 Fab anti
15	10	83.3	14	22	AAE12748 Human PH1 Fab anti
16	10	83.3	14	22	AAE12749 Human PH1 Fab anti
17	10	83.3	14	22	AAE12751 Human PH1 Fab anti
18	10	83.3	14	22	AAE12753 Human PH1 Fab anti
19	10	83.3	14	22	AAE12754 Human PH1 Fab anti
20	10	83.3	14	22	AAE12755 Human PH1 Fab anti
21	10	83.3	14	22	AAE12759 Human PH1 Fab anti
22	10	83.3	14	22	AAE12761 Human PH1 Fab anti
23	10	83.3	14	22	AAE12763 Human PH1 Fab anti
24	10	83.3	14	22	AAE12765 Human PH1 Fab anti
25	10	83.3	14	22	AAE12766 Human PH1 Fab anti
26	10	83.3	14	22	AAE12767 Human PH1 Fab anti
27	10	83.3	14	22	AAE12772 Human PH1 Fab anti
28	10	83.3	14	22	AAE12774 Human PH1 Fab anti
29	10	83.3	16	22	AAE12735 Human PH1 Fab anti
30	9	75.0	14	22	AAE12746 Human PH1 Fab anti
31	9	75.0	14	22	AAE12747 Human PH1 Fab anti
32	9	75.0	14	22	AAE12756 Human PH1 Fab anti
33	9	75.0	14	22	AAE12757 Human PH1 Fab anti
34	9	75.0	14	22	AAE12758 Human PH1 Fab anti
35	9	75.0	14	22	AAE12764 Human PH1 Fab anti
36	9	75.0	14	22	AAE12768 Human PH1 Fab anti
37	8	66.7	14	22	AAE12771 Human PH1 Fab anti
38	8	66.7	14	22	AAE12773 Human PH1 Fab anti
39	7	58.3	14	22	AAE12745 Human PH1 Fab anti
40	7	58.3	14	22	AAE12769 Human PH1 Fab anti
41	7	58.3	16	22	AAE12722 Human PH1 Fab anti
42	7	58.3	16	22	AAE12723 Human PH1 Fab anti
43	7	58.3	16	22	AAE12724 Human PH1 Fab anti
44	7	58.3	16	22	AAE12725 Human PH1 Fab anti
45	7	58.3	16	22	AAE12726 Human PH1 Fab anti

ALIGNMENTS

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RESULT 1
AAE12770
ID AAE12770 standard; peptide; 14 AA.
XX
AC AAE12770;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody VH region FR3-CDR3 variant #37.
XX
KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody; variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..2
FT FT /label= Framework_region_3
FT FT 3..14
FT FT /label= Complementarity_determining_region_3
XX
PN WO200175110-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10589.
XX
PR 30-MAR-2000; 2000US-0538913.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Henderikx MPG;

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XX WPI; 2001-626437/72.
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -
XX
XX Example 2; Page 125; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human PH1 Fab antibody VH
CC region FR (framework region)3-CDR3 variant.
XX

XX Sequence 14 AA;

Query Match 100.0%; Score 12; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.1e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

|||||

3 HTGGGVWDPIDY 14

RESULT 2

AAE12706

ID AAE12706 standard; Protein; 121 AA.

XX

AC AAE12706;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody variable heavy chain region (VH).

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX cytostatic; therapy; PH1 antibody.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 31..35

XX /label= CDR1

XX /note= "Complementarity determining region 1"

XX 50..66

XX /label= CDR2

XX /note= "Complementarity determining region 2"

XX 97..99

XX /label= FR3

XX /note= "Framework region 3"

XX 97..112

XX /note= "VH domain"

XX 99..110

XX /label= CDR3

XX /note= "Complementarity determining region 3"

XX 111..112

XX /label= FR4

XX /note= "Framework region 4"

XX

PN WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

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PA (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.
 DR N-PSDB; AAD20732.
 XX
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Claim 9; Page 95-97; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human bivPH1-1L-2
 CC immunocytokine protein. bivPH1 is mucin specific binding portion.
 XX
 XX Sequence 381 AA;
 SQ
 Query Match 100.0%; Score 12; DB 22; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPIDY 12
 DB 99 HTGGGVWDPIDY 110
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 RESULT 4
 AAE12715
 ID AAE12715 standard; Protein; 451 AA.
 XX
 AC AAE12715;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human recombinant immunoglobulin (Ig) heavy chain region.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
 KW heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; immunoglobulin; Ig.
 XX
 OS Homo sapiens.
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 DR N-PSDB; AAD20745.
 XX

PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Claim 12; Page 106-108; 126pp; English.
 XX
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human recombinant immunoglobulin
 CC (Ig) heavy chain region (variable VH and CH constant heavy chain).
 XX
 XX Sequence 451 AA;
 SQ
 Query Match 100.0%; Score 12; DB 22; Length 451;
 Best Local Similarity 100.0%; Pred. No. 5.7e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPIDY 12
 DB 99 HTGGGVWDPIDY 110
 |||||
 RESULT 5
 AAE12740
 ID AAE12740 standard; peptide; 14 AA.
 XX
 AC AAE12740;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #7.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT Region /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1
XX
PS Example 2; Page 119; 126pp; English.
XX
CC The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human PH1 Fab antibody VH
CC region FR (framework region)3-CDR3 variant.
XX
SQ Sequence 14 AA;

Query Match 91.7%; Score 11; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HTGGGVNDPID 11
Db 3 HTGGGVNDPID 13
|||||

RESULT 6
AAE12762
ID AAE12762 standard; peptide; 14 AA.

XX AAE12762;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #29.

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
XX variable heavy chain region; cancer; breast; ovary; lung; bladder;
XX cytosstatic; therapy; PH1 antibody; variant.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..2

XX /label= Framework_region_3

XX Region 3..14

XX /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX its portion for binding to an epitope of the protein core of mucin-1

Example 2; Page 123; 126pp; English.

PS The invention relates to an isolated tumour-associated antigen mucin-1
XX (MUC-1)-specific binding member comprising an antigen binding domain
XX region having an antibody variable light (VL) or heavy (VH) region,
XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX The binding of MUC1-specific binding member to MUC1 is detected by a
XX detection method selected from enzyme-linked immunosorbent assay,
XX magnetic resonance imaging, scintillation counting, and X-ray film.
XX MUC1-specific binding member is useful for treating cancer, preferably
XX adenocarcinoma, in an individual, where the cancer is present in tissue
XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX binding member is useful for diagnosing and imaging MUC1-expressing
XX cancer cells and tissues, for purifying or isolating non-glycosylated,
XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX containing molecules, and for therapeutically or prophylactically
XX treating cancer. The present sequence is human PH1 Fab antibody VH
XX region FR (framework region)3-CDR3 variant.
XX
SQ Sequence 14 AA;

Query Match 91.7%; Score 11; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.4e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HTGGGVNDPID 11
Db 3 HTGGGVNDPID 13
|||||

RESULT 7

AAE12734
ID AAE12734 standard; peptide; 16 AA.

XX AAE12734;

XX 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody variable heavy chain domain (VH) #13.

XX Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
XX variable heavy chain region; cancer; breast; ovary; lung; bladder;
XX cytosstatic; therapy; PH1 antibody.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..2

XX /label= FR3

XX /note= "Framework region 3"

XX Region 3..14

XX /label= CDR3

XX /note= "Complementarity determining region 3"

XX Region 15..16

XX /label= FR4

XX /note= "Framework region 4"

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX N-PSDB; AAD20765.

PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 XX Example 2; Page 52; 126pp; English.
 PS
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC domain.
 XX
 SQ Sequence 16 AA;

Query Match 91.7%; Score 11; DB 22; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGGGVWDPIDY 12
 |||||
 Db 4 TGGGVWDPIDY 14

RESULT 8
 AAEL12718
 ID AAEL12718 standard; peptide; 14 AA.
 XX
 AC AAEL12718;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #2.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -

PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Claim 2; Page 75; 126pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

RESULT 9
 AAEL12719
 ID AAEL12719 standard; peptide; 14 AA.
 XX
 AC AAEL12719;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #3.
 XX
 KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10589.
 XX
 PR 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

RESULT 12

AAE12742
 ID AAE12742 standard; peptide; 14 AA.

XX AC AAE12742;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #9.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX Homo sapiens.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..2

XX FT FT /label= Framework_region_3

XX FT FT 3..14

XX FT FT /label= Complementarity_determining_region_3

XX PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX DR WPI; 2001-626437/72.

XX DR Novel isolated tumor-associated antigen mucin-1-specific binding member

XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX PT its portion for binding to an epitope of the protein core of mucin-1 -

XX PS Example 2; Page 119; 126pp; English.

XX CC The invention relates to an isolated tumour-associated antigen mucin-1

XX CC (MUC-1)-specific binding member comprising an antigen binding domain

XX CC region having an antibody variable light (VL) or heavy (VH) region,

XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

RESULT 13

AAE12743
 ID AAE12743 standard; peptide; 14 AA.

XX AC AAE12743;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #10.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX Homo sapiens.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..2

XX FT FT /label= Framework_region_3

XX FT FT 3..14

XX FT FT /label= Complementarity_determining_region_3

XX PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX DR WPI; 2001-626437/72.

XX DR Novel isolated tumor-associated antigen mucin-1-specific binding member

XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX PT its portion for binding to an epitope of the protein core of mucin-1 -

XX PS Example 2; Page 119; 126pp; English.

XX CC The invention relates to an isolated tumour-associated antigen mucin-1

XX CC (MUC-1)-specific binding member comprising an antigen binding domain

XX CC region having an antibody variable light (VL) or heavy (VH) region,

XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVNDPI 10
 |||||
 Db 3 HTGGGVNDPI 12

RESULT 14
 AAEL2744
 ID AAEL2744 standard; peptide; 14 AA.
 XX
 AC AAEL2744;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #11.
 XX
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 XX variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 XX 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 119; 136pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX
 SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVNDPI 10
 |||||
 Db 3 HTGGGVNDPI 12

RESULT 15
 AAEL2748
 ID AAEL2748 standard; peptide; 14 AA.
 XX
 AC AAEL2748;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #15.
 XX
 DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotatic; therapy; PH1 antibody; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 FT
 PN WO200175110-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10589.
 XX
 XX 30-MAR-2000; 2000US-0538913.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Hoogenboom HRJM, Henderikx MPG;
 XX
 DR WPI; 2001-626437/72.
 XX
 PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX
 PS Example 2; Page 120; 126pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX

SQ Sequence 14 AA;

Query Match 83.3%; Score 10; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
 |||||
 Db 3 HTGGGVWDPI 12

Search completed: March 13, 2003, 15:31:41
 Job time : 29.0769 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:30:39 ; Search time 10.6154 Seconds
(without alignments)
33.261 Million cell updates/sec

Title: US-09-822-698a-3_COPY_99_110

Perfect score: 12
Sequence: 1 HTGGVWDPIDY 12

Scoring Table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5	41.7	8	4	US-08-637-732A-34
3	5	41.7	8	4	US-08-637-732A-36
4	5	41.7	14	4	US-08-973-131-75
5	5	41.7	20	1	US-08-103-742-12
6	5	41.7	20	1	US-08-189-508-5
7	5	41.7	22	1	US-07-791-930C-9
8	5	41.7	22	1	US-08-173-515B-12
9	5	41.7	22	3	US-08-329-799-40
10	5	41.7	33	2	US-08-415-788-28
11	5	41.7	34	2	US-08-415-788-11
12	5	41.7	34	2	US-08-415-788-14
13	5	41.7	34	2	US-08-415-788-18
14	5	41.7	34	2	US-08-415-788-24
15	5	41.7	41	2	US-08-415-788-5
16	5	41.7	41	2	US-08-415-788-41
17	5	41.7	56	4	US-07-741-453A-47
18	5	41.7	58	4	US-09-605-785-553
19	5	41.7	116	2	US-08-428-197-10
20	5	41.7	116	5	PCT-US93-10555-10
21	5	41.7	187	4	US-09-117-257-23
22	5	41.7	187	4	US-08-945-476-23
23	5	41.7	187	4	US-09-489-352-23
24	5	41.7	188	4	US-09-117-257-44
25	5	41.7	188	4	US-09-489-352-44
26	5	41.7	264	4	US-08-856-841-14
27	5	41.7	325	1	US-08-118-270-30

Sequence 18, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921el Cossackievirus and Adenovirus
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-928-383B-18

ALIGNMENTS

RESULT 1

US-08-928-383B-18
Sequence 18, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921el Cossackievirus and Adenovirus
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-928-383B-18

Query Match 50.0%; Score 6; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6

Db 88 HTGGGV 93
|||||

RESULT 2

US-08-637-732A-34
; Sequence 34, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant pILC Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/637,732A

; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-732A-34

Query Match 41.7%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
|||||

Db 1 HTGGG 5

RESULT 3

US-08-637-732A-36
; Sequence 36, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant pILC Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia

; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/637,732A
; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-732A-36

Query Match 41.7%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
|||||

Db 1 HTGGG 5

RESULT 4

US-08-973-131-75
; Sequence 75, Application US/08973131
; Patent No. 6326166
; GENERAL INFORMATION:
; APPLICANT: Pomerantz, Joel L.
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Pabo, Carl O.
; TITLE OF INVENTION: Chimeric DNA-binding proteins
; FILE REFERENCE: APV-022.02
; CURRENT APPLICATION NUMBER: US/08/973,131
; CURRENT FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: PCT/US95/16982
; EARLIER FILING DATE: 1995-12-29
; EARLIER APPLICATION NUMBER: 08/366,083
; EARLIER FILING DATE: 1994-12-29
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chimeric motif
US-08-973-131-75

Query Match 41.7%; Score 5; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
|||||

Db 3 HTGGG 7

RESULT 5

US-08-103-742-12
; Sequence 12, Application 08/103742

```
; Patent No. 5420244
; GENERAL INFORMATION:
; APPLICANT: RUDOLPH, DONNA L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: DIAGNOSING HTLV-I ASSOCIATED MYELOPATHY AND ADULT T-CELL LEUKA
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/103,742
; FILING DATE: 06 AUG 1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: SPRATT, GWENDOLYN D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-103-742-12

Query Match 41.7%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WDPID 11
Db 11 WDPID 15

RESULT 6
US-08-199-508-5
; Sequence 5, Application US/08199508
; Patent No. 5717058
; GENERAL INFORMATION:
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Stetler, Gary L.
; APPLICANT: Anthony-Cahill, Spencer J.
; APPLICANT: Anderson, David C.
; TITLE OF INVENTION: Modulators of Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,508
; FILING DATE: February 18, 1994
```

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,536
; FILING DATE: February 23, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5717058ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 121 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; TOPOLOGY: unknown to applicant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
US-08-199-508-5

Query Match 41.7%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WDPID 11
Db 8 WDPID 12

RESULT 7
US-07-791-930C-9
; Sequence 9, Application US/07791930C
; Patent No. 5360726
; GENERAL INFORMATION:
; APPLICANT: Natasha V. Raikhel
; TITLE OF INVENTION: Polypeptides Enabling Sorting
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,930C
; FILING DATE: 1991 No. 5360726ember 12
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/612,200
; FILING DATE: No. 5360726ember 13, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Peptide
```

;;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Tobacco -1,3-glucanase
; ORIGINAL SOURCE:
; ORGANISM: N. tabacum
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: -glucanase peptide
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
; US-07-791-930C-9

Query Match 41.7%; Score 5; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGWVD 8
Db 3 GGWVD 7

RESULT 8
US-08-173-515B-12
; Sequence 12, Application US/08173515B
; Patent No. 5525713
; GENERAL INFORMATION:
; APPLICANT: Natasha V. Raikhel
; TITLE OF INVENTION: DNA Encoding Polypeptides
; TITLE OF INVENTION: Enabling Sorting of proteins to
; TITLE OF INVENTION: vacuoles of plants.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,515B
; FILING DATE: 1993 December 23
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/791,930
; FILING DATE: 1991 No. 5525713ember 12
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5525713e
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22

;;
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Tobacco -1,3-glucanase
; ORIGINAL SOURCE:
; ORGANISM: N. tabacum
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: -glucanase peptide
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
; US-08-173-515B-12

Query Match 41.7%; Score 5; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGWVD 8
Db 3 GGWVD 7

RESULT 9
US-08-329-799-40
; Sequence 40, Application US/08329799
; Patent No. 6054637
; GENERAL INFORMATION:
; APPLICANT: Boller, Thomas
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Ryals, John
; TITLE OF INVENTION: No. 6054637el Signal Sequences
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,799
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,521
; FILING DATE: 13-JUN-1991
; APPLICATION NUMBER: CH 2007/90-9
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: GA/5-18123/A
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-329-799-40

Query Match 41.7%; Score 5; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGWD 8
Db 3 GGWD 7

RESULT 10

US-08-415-788-28
Sequence 28, Application US/08415788
Patent No. 5834591

GENERAL INFORMATION:
APPLICANT: NORMARK, STAFFAN
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,788
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,465
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SCHWENNING, LYNN E.
REGISTRATION NUMBER: 37,233
REFERENCE/DOCKET NUMBER: 29500-20046.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-415-788-28

Query Match 41.7%; Score 5; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
Db 13 HTGGG 17

RESULT 11
US-08-415-788-11
Sequence 11, Application US/08415788
Patent No. 5834591

GENERAL INFORMATION:
APPLICANT: NORMARK, STAFFAN
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,788
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,465
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SCHWENNING, LYNN E.
REGISTRATION NUMBER: 37,233
REFERENCE/DOCKET NUMBER: 29500-20046.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-415-788-11

Query Match 41.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGG 5
Db 13 HTGGG 17

RESULT 12

US-08-415-788-14
Sequence 14, Application US/08415788
Patent No. 5834591

GENERAL INFORMATION:
APPLICANT: NORMARK, STAFFAN
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/415,788
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/829,465
;; FILING DATE: 31-JAN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SCHWENNING, LYNN E.
;; REGISTRATION NUMBER: 37,233
;; REFERENCE/DOCKET NUMBER: 29500-20046.20
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-415-788-14

Query Match 41.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGG 5
|
|
|
|
|
Db 13 HTGGG 17

RESULT 13
US-08-415-788-18
; Sequence 18, Application US/08415788
; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-415-788-18

Query Match 41.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGG 5
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|
|
|
Db 13 HTGGG 17

RESULT 14
US-08-415-788-24
; Sequence 24, Application US/08415788
; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-415-788-24

Query Match 41.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGG 5
|
|
|
|
|
Db 13 HTGGG 17

RESULT 15
US-08-415-788-5
; Sequence 5, Application US/08415788

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; Patent No. 5834591
; GENERAL INFORMATION:
; APPLICANT: NORMARK, STAFFAN
; APPLICANT: JONSSON, ANN-BETH
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES USEFUL
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF PATHOGENIC NEISSERIA
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,465
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHWENNING, LYNN E.
; REGISTRATION NUMBER: 37,233
; REFERENCE/DOCKET NUMBER: 29500-20046.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-415-788-5

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Query Match      41.7%; Score 5; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGG 5
Db 24 HTGGG 28

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Search completed: March 13, 2003, 15:34:10
Job time : 10.6154 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 15:33:09 ; Search time 9.69231 Seconds
(without alignments)
57.066 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110

Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	14	10	US-09-822-698A-105
2	12	100.0	121	10	US-09-822-698A-3
3	12	100.0	381	10	US-09-822-698A-5
4	12	100.0	451	10	US-09-822-698A-26
5	11	91.7	14	10	US-09-822-698A-75
6	11	91.7	14	10	US-09-822-698A-97
7	11	91.7	16	10	US-09-822-698A-65
8	10	83.3	14	10	US-09-822-698A-30
9	10	83.3	14	10	US-09-822-698A-31
10	10	83.3	14	10	US-09-822-698A-32
11	10	83.3	14	10	US-09-822-698A-76
12	10	83.3	14	10	US-09-822-698A-77
13	10	83.3	14	10	US-09-822-698A-78
14	10	83.3	14	10	US-09-822-698A-79
15	10	83.3	14	10	US-09-822-698A-83
16	10	83.3	14	10	US-09-822-698A-84
17	10	83.3	14	10	US-09-822-698A-86
18	10	83.3	14	10	US-09-822-698A-88
19	10	83.3	14	10	US-09-822-698A-89

20 10 83.3 14 10 US-09-822-698A-90 Sequence 90, Appl
21 10 83.3 14 10 US-09-822-698A-94 Sequence 94, Appl
22 10 83.3 14 10 US-09-822-698A-96 Sequence 96, Appl
23 10 83.3 14 10 US-09-822-698A-98 Sequence 98, Appl
24 10 83.3 14 10 US-09-822-698A-100 Sequence 100, Appl
25 10 83.3 14 10 US-09-822-698A-101 Sequence 101, Appl
26 10 83.3 14 10 US-09-822-698A-102 Sequence 102, Appl
27 10 83.3 14 10 US-09-822-698A-107 Sequence 107, Appl
28 10 83.3 14 10 US-09-822-698A-109 Sequence 109, Appl
29 10 83.3 16 10 US-09-822-698A-67 Sequence 67, Appl
30 9 75.0 14 10 US-09-822-698A-81 Sequence 81, Appl
31 9 75.0 14 10 US-09-822-698A-82 Sequence 82, Appl
32 9 75.0 14 10 US-09-822-698A-91 Sequence 91, Appl
33 9 75.0 14 10 US-09-822-698A-92 Sequence 92, Appl
34 9 75.0 14 10 US-09-822-698A-93 Sequence 93, Appl
35 9 75.0 14 10 US-09-822-698A-99 Sequence 99, Appl
36 9 75.0 14 10 US-09-822-698A-103 Sequence 103, Appl
37 8 66.7 14 10 US-09-822-698A-106 Sequence 106, Appl
38 8 66.7 14 10 US-09-822-698A-108 Sequence 108, Appl
39 7 58.3 14 10 US-09-822-698A-80 Sequence 80, Appl
40 7 58.3 14 10 US-09-822-698A-104 Sequence 104, Appl
41 7 58.3 16 10 US-09-822-698A-41 Sequence 41, Appl
42 7 58.3 16 10 US-09-822-698A-43 Sequence 43, Appl
43 7 58.3 16 10 US-09-822-698A-45 Sequence 45, Appl
44 7 58.3 16 10 US-09-822-698A-47 Sequence 47, Appl
45 7 58.3 16 10 US-09-822-698A-49 Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-09-822-698A-105

; Sequence 105, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 105

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-105

Query Match 100.0%; Score 12; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.2e+06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

Db 3 HTGGGVWDPIDY 14

RESULT 2

US-09-822-698A-3

; Sequence 3, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

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; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 12; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 3
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bIVPH1-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 12; DB 10; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 4
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT

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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PHI-IgG1
US-09-822-698A-26

Query Match      100.0%; Score 12; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 5
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

Query Match      91.7%; Score 11; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPID 11
Db 3 HTGGGVWDPID 13

RESULT 6
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match      91.7%; Score 11; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 HTGGGVWDPI 11
|1111111111|
Db 3 HTGGGVWDPI 13

RESULT 7

US-09-822-698A-65
; Sequence 65, Application US/09822698A
; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 65

; LENGTH: 16

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region

US-09-822-698A-65

Query Match

Best Local Similarity 91.7%; Score 11; DB 10; Length 16;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVWDPI 12

Db 4 TGGGVWDPI 14

RESULT 8

US-09-822-698A-30

; Sequence 30, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 30

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: region of a MUC1-specific binding member

US-09-822-698A-30

Query Match

Best Local Similarity 83.3%; Score 10; DB 10; Length 14;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10

Db 3 HTGGGVWDPI 12

RESULT 9

US-09-822-698A-31

; Sequence 31, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 31

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: region of a MUC1-specific binding member

US-09-822-698A-31

Query Match

Best Local Similarity 83.3%; Score 10; DB 10; Length 14;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10

Db 3 HTGGGVWDPI 12

RESULT 10

US-09-822-698A-32

; Sequence 32, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 32

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member

US-09-822-698A-32

Query Match

Best Local Similarity 83.3%; Score 10; DB 10; Length 14;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10

Db 3 HTGGGVWDPI 12

RESULT 11

US-09-822-698A-76

; Sequence 76, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
   |||||
Db 3 HTGGGVWDPI 12

```

```

RESULT 12
US-09-822-698A-77
; Sequence 77, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 77
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-77

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
   |||||
Db 3 HTGGGVWDPI 12

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RESULT 13
US-09-822-698A-78
; Sequence 78, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 78
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-78

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
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Db 3 HTGGGVWDPI 12

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RESULT 14
US-09-822-698A-79
; Sequence 79, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 79
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-79

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Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
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Db 3 HTGGGVWDPI 12

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RESULT 15
US-09-822-698A-83
; Sequence 83, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

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```

Query Match      83.3%; Score 10; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HTGGGVWDPI 10
   |||||
Db 3 HTGGGVWDPI 12

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Search completed: March 13, 2003, 15:40:23
Job time : 9.69231 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 15:31:49 ; Search time 130.154 Seconds
(without alignments)
59.443 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110

Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
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- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
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- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	12	100.0	14	22	US-09-822-698A-105
2	12	100.0	121	19	US-09-538-913-3
3	12	100.0	121	22	US-09-822-698A-3
4	12	100.0	381	19	US-09-538-913-5
5	12	100.0	381	22	US-09-822-698A-5
6	12	100.0	451	22	US-09-822-698A-26

7	11	91.7	14	22	US-09-822-698A-75	Sequence 75, Appl
8	11	91.7	14	22	US-09-822-698A-97	Sequence 97, Appl
9	11	91.7	16	22	US-09-822-698A-65	Sequence 65, Appl
10	10	83.3	14	22	US-09-822-698A-30	Sequence 30, Appl
11	10	83.3	14	22	US-09-822-698A-31	Sequence 31, Appl
12	10	83.3	14	22	US-09-822-698A-32	Sequence 32, Appl
13	10	83.3	14	22	US-09-822-698A-76	Sequence 76, Appl
14	10	83.3	14	22	US-09-822-698A-77	Sequence 77, Appl
15	10	83.3	14	22	US-09-822-698A-78	Sequence 78, Appl
16	10	83.3	14	22	US-09-822-698A-79	Sequence 79, Appl
17	10	83.3	14	22	US-09-822-698A-83	Sequence 83, Appl
18	10	83.3	14	22	US-09-822-698A-84	Sequence 84, Appl
19	10	83.3	14	22	US-09-822-698A-86	Sequence 86, Appl
20	10	83.3	14	22	US-09-822-698A-88	Sequence 88, Appl
21	10	83.3	14	22	US-09-822-698A-89	Sequence 89, Appl
22	10	83.3	14	22	US-09-822-698A-90	Sequence 90, Appl
23	10	83.3	14	22	US-09-822-698A-94	Sequence 94, Appl
24	10	83.3	14	22	US-09-822-698A-96	Sequence 96, Appl
25	10	83.3	14	22	US-09-822-698A-98	Sequence 98, Appl
26	10	83.3	14	22	US-09-822-698A-100	Sequence 100, App
27	10	83.3	14	22	US-09-822-698A-101	Sequence 101, App
28	10	83.3	14	22	US-09-822-698A-102	Sequence 102, App
29	10	83.3	14	22	US-09-822-698A-107	Sequence 107, App
30	10	83.3	14	22	US-09-822-698A-109	Sequence 109, App
31	10	83.3	16	22	US-09-822-698A-67	Sequence 67, Appl
32	9	75.0	14	22	US-09-822-698A-81	Sequence 81, Appl
33	9	75.0	14	22	US-09-822-698A-82	Sequence 82, Appl
34	9	75.0	14	22	US-09-822-698A-91	Sequence 91, Appl
35	9	75.0	14	22	US-09-822-698A-92	Sequence 92, Appl
36	9	75.0	14	22	US-09-822-698A-93	Sequence 93, Appl
37	9	75.0	14	22	US-09-822-698A-99	Sequence 99, Appl
38	9	75.0	14	22	US-09-822-698A-103	Sequence 103, App
39	8	66.7	14	22	US-09-822-698A-106	Sequence 106, App
40	8	66.7	14	22	US-09-822-698A-108	Sequence 108, App
41	7	58.3	14	22	US-09-822-698A-80	Sequence 80, Appl
42	7	58.3	14	22	US-09-822-698A-104	Sequence 104, App
43	7	58.3	16	22	US-09-822-698A-41	Sequence 41, Appl
44	7	58.3	16	22	US-09-822-698A-43	Sequence 43, Appl
45	7	58.3	16	22	US-09-822-698A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendriks, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DXX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match 100.0%; Score 12; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14

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RESULT 2
US-09-538-913-3
; Sequence 3, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-3

Query Match      100.0%; Score 12; DB 19; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 3
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 12; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 4
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPHI-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match      100.0%; Score 12; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 5
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPHI-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 12; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 6
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26
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Query Match      100.0%; Score 12; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 12
   |||||
Db 99 HTGGGVWDPI 110

RESULT 7
US-09-822-698A-75
; Sequence 75, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75

Query Match      91.7%; Score 11; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 11
   |||||
Db 3 HTGGGVWDPI 13

RESULT 8
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match      91.7%; Score 11; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 11
   |||||
Db 3 HTGGGVWDPI 13

RESULT 9
US-09-822-698A-97
; Sequence 97, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-97

Query Match      91.7%; Score 11; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 11
   |||||
Db 3 HTGGGVWDPI 13

RESULT 9
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US-09-822-698A-65
; Sequence 65, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 65
; LENGTH: 16
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-65

Query Match      91.7%; Score 11; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVWDPI 12
   |||||
Db 4 TGGGVWDPI 14

RESULT 10
US-09-822-698A-30
; Sequence 30, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 30
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-30

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
   |||||
Db 3 HTGGGVWDPI 12

RESULT 11
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 12
US-09-822-698A-32
; Sequence 32, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 32
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member
US-09-822-698A-32

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 13
US-09-822-698A-76
; Sequence 76, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 14
US-09-822-698A-77
; Sequence 77, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 77
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-77

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

RESULT 15
US-09-822-698A-78
; Sequence 78, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 78
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-78

Query Match      83.3%; Score 10; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 10
Db 3 HTGGGVWDPI 12

Search completed: March 13, 2003, 15:39:00
Job time : 130.154 secs
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 15:32:14 ; Search time 20.7692 Seconds
(without alignments)
75.113 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 596842 seqs, 130003698 residues

Word size : 0

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_New : *
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	50.0	55	1	PCT-US02-32727-11588
2	6	50.0	55	5	US-09-978-825-11588
3	6	50.0	55	6	US-10-057-498-11588
4	6	50.0	93	1	PCT-US02-32727-9150
5	6	50.0	93	5	US-09-978-825-9150
6	6	50.0	93	6	US-10-057-498-9150
7	6	50.0	330	6	US-10-366-683-23794
8	6	50.0	701	6	US-10-282-122A-62129
9	6	50.0	1583	1	PCT-US02-32727-15149
10	6	50.0	1583	5	US-09-978-825-15149
11	6	50.0	1583	6	US-10-057-498-15149
12	5	41.7	38	6	US-10-156-761-15030
13	5	41.7	51	5	US-09-724-676-87689
14	5	41.7	51	5	US-09-724-676A-87689
15	5	41.7	56	1	PCT-US02-32727-26391
16	5	41.7	56	5	US-09-978-825-26391
17	5	41.7	56	6	US-10-057-498-26391
18	5	41.7	58	5	US-09-593-793A-553
19	5	41.7	58	6	US-10-294-025-553
20	5	41.7	66	1	PCT-US02-32727-28218
21	5	41.7	66	5	US-09-978-825-28218
22	5	41.7	66	6	US-10-057-498-28218
23	5	41.7	67	1	PCT-US02-32727-9117
24	5	41.7	67	5	US-09-978-825-9117
25	5	41.7	67	6	US-10-057-498-9117
26	5	41.7	68	1	PCT-US02-32727-28689

ALIGNMENTS

RESULT 1
PCT-US02-32727-11588
; Sequence 11588, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyan
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darlick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propionl acnes
PCT-US02-32727-11588

Query Match 50.0%; Score 6; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 37 HTGGGV 42

RESULT 2
US-09-978-825-11588
; Sequence 11588, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing

Sequence 28689, A
Sequence 28689, A
Sequence 87695, A
Sequence 87695, A
Sequence 21401, A
Sequence 21401, A
Sequence 21401, A
Sequence 21401, A
Sequence 87694, A
Sequence 87694, A
Sequence 16769, A
Sequence 16769, A
Sequence 159, App
Sequence 9048, Ap
Sequence 9048, Ap
Sequence 9048, Ap
Sequence 25439, A
Sequence 25439, A
Sequence 25439, A

5 US-09-978-825-28689
6 US-10-057-498-28689
5 US-09-724-676-87695
5 US-09-724-676A-87695
1 PCT-US02-32727-21401
5 US-09-978-825-21401
6 US-10-057-498-21401
5 US-09-724-676-87694
5 US-09-724-676A-87694
1 PCT-US02-32727-16769
5 US-09-978-825-16769
6 US-10-057-498-16769
5 US-10-263-929-159
1 PCT-US02-32727-9048
5 US-09-978-825-9048
6 US-10-057-498-9048
1 PCT-US02-32727-25439
5 US-09-978-825-25439
6 US-10-057-498-25439

27 5 41.7 68 5
28 5 41.7 68 6
29 5 41.7 77 5
30 5 41.7 77 5
31 5 41.7 78 1
32 5 41.7 78 5
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34 5 41.7 84 5
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36 5 41.7 93 1
37 5 41.7 93 5
38 5 41.7 93 6
39 5 41.7 94 6
40 5 41.7 97 1
41 5 41.7 97 5
42 5 41.7 97 6
43 5 41.7 102 1
44 5 41.7 102 5
45 5 41.7 102 6

```
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-11588

Query Match          50.0%; Score 6; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 37 HTGGGV 42

RESULT 3
US-10-057-498-11588
; Sequence 11588, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 11588
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-11588

Query Match          50.0%; Score 6; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 37 HTGGGV 42

RESULT 4
PCT-US02-32727-9150
; Sequence 9150, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-9150

Query Match          50.0%; Score 6; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVWD 8
Db 10 GGGVWD 15

RESULT 5
US-09-978-825-9150
; Sequence 9150, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
US-09-978-825-9150

Query Match          50.0%; Score 6; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVWD 8
Db 10 GGGVWD 15

RESULT 6
US-10-057-498-9150
; Sequence 9150, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 9150
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Propioni acnes
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US-10-057-498-9150

Query Match 50.0%; Score 6; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVWD 8
Db 10 GGGVWD 15

RESULT 7

US-10-366-683-23794
; Sequence 23794, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nolling, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: PATH03-04
; CURRENT APPLICATION NUMBER: US/10/366,683
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23794
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-23794

Query Match 50.0%; Score 6; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VWDPID 11
Db 103 VWDPID 108

RESULT 8

US-10-282-122A-62129
; Sequence 62129, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62129
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-62129

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QY 1 HTGGGV 6
Db 75 HTGGGV 80

RESULT 9

PCT-US02-32727-15149
; Sequence 15149, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 15149
; LENGTH: 1583
; TYPE: PRT
; ORGANISM: Propionibacterium acnes
PCT-US02-32727-15149

Query Match 50.0%; Score 6; DB 1; Length 1583;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVWD 8
Db 1039 GGGVWD 1044

RESULT 10

US-09-978-825-15149
; Sequence 15149, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay


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; Sequence 26391, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes v
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 26391
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-26391
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Best Local Similarity 100.0%; Pred. No. 3.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 HTGGG 5
    |||||
Db 25 HTGGG 29
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Search completed: March 13, 2003, 15:39:55
Job time : 21.7692 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:29:54 ; Search time 12,4615 Seconds
(without alignments)
92.574 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	50.0	114	2 T08411	hypothetical prote
2	6	50.0	193	2 C82683	disulfide oxidore
3	6	50.0	436	2 H84121	NADH oxidase (nox)
4	6	50.0	1123	2 S20497	phytochrome A - po
5	5	41.7	10	2 H60787	sperm-activating p
6	5	41.7	10	2 D60788	sperm-activating p
7	5	41.7	10	2 B60787	sperm-activating p
8	5	41.7	10	2 A60788	sperm-activating p
9	5	41.7	10	2 C60589	sperm-activating p
10	5	41.7	10	2 D60588	sperm-activating p
11	5	41.7	71	2 T26663	hypothetical prote
12	5	41.7	72	2 T48971	hypothetical prote
13	5	41.7	75	2 A69147	hypothetical prote
14	5	41.7	101	2 S22454	ribosomal protein
15	5	41.7	107	2 S58218	hypothetical prote
16	5	41.7	113	2 S25575	Ig heavy chain V r
17	5	41.7	119	2 D83723	hypothetical prote
18	5	41.7	119	2 T48745	hypothetical prote
19	5	41.7	120	2 C53482	transcription regu
20	5	41.7	133	2 C97301	uncharacterized co
21	5	41.7	144	2 F64094	ribosomal protein
22	5	41.7	145	2 D70938	hypothetical prote
23	5	41.7	150	2 A53482	exsF protein [limpo
24	5	41.7	155	2 C86206	hypothetical prote
25	5	41.7	158	2 C95159	shikimate kinase [
26	5	41.7	158	2 C98025	shikimate kinase (
27	5	41.7	160	2 G69376	conserved hypothet
28	5	41.7	163	2 A70847	hypothetical prote
29	5	41.7	168	2 D82310	CiNA-related prote

30	5	41.7	169	2 A40522	plasmin (EC 3.4.21
31	5	41.7	175	2 A71680	cytochrome C (cycM
32	5	41.7	175	2 A97742	cytochrome c limpo
33	5	41.7	181	1 I41314	K88 fibrial prote
34	5	41.7	185	2 F95008	acetyltransferase,
35	5	41.7	188	2 B95365	probable oxidoredu
36	5	41.7	189	1 S74659	shikimate kinase (
37	5	41.7	189	2 D69128	conserved hypothet
38	5	41.7	189	2 A87254	hypothetical prote
39	5	41.7	194	2 JCA4589	immunoreactive pro
40	5	41.7	197	2 S25106	capsid protein - b
41	5	41.7	198	2 S30968	major tail protein
42	5	41.7	198	2 E72802	major tail subunit
43	5	41.7	198	2 S31937	coat protein - Myc
44	5	41.7	203	2 F70601	probable rimJ prot
45	5	41.7	205	2 C90140	conserved hypothet

ALIGNMENTS

RESULT 1

T08411
hypothetical protein F18B3.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C:Accession: T08411
R:Quetier, F.; Krieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16409
A:Accession: T08411
A:Molecule type: DNA
A:Residues: 1-114 <QUE>
A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.180
A:Experimental source: cultivar Columbia; BAC clone F18B3
C:Genetics:
A:Gene: ATSP:F18B3.180
A:Map position: 3
C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match 50.0%; Score 6; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGWVDP 9
Db 99 GGWVDP 104

RESULT 2

C82683
disulfide oxidoreductase XF1436 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: C82683
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82683
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <SUM>
A:Cross-references: GB:AE003973; GB:AE003849; NID:g9106438; PIDN:AAF84245.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorrry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XFL436

Query Match 50.0%; Score 6; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGVDP 9
Db 68 GGVDP 73

RESULT 3
RH4121
NADH oxidase (nox) BH3776 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84121
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H84121
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-436 <STO>
A:Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAR07495.1; GSPDB:GN00 A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3776
C:Superfamily: NADH peroxidase; dihydrolipoamide dehydrogenase homology

Query Match 50.0%; Score 6; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GWDPI 10
Db 424 GWDPI 429

RESULT 4
S20497
phytochrome A - potato
C:Species: Solanum tuberosum (potato)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 30-Apr-1999
C:Accession: S20497
R:Heyer, A.; Gatz, C.
Plant Mol. Biol. 18, 535-544, 1992
A:Title: Isolation and characterization of a cDNA-clone coding for potato type A phytoch A:Reference number: S20497; MUID:92163018; PMID:11536928
A:Accession: S20497
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1123 <HEY>
C:Genetics:
A:Gene: phyA
C:Superfamily: phytochrome; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation F:67-582/Domain: phytochrome homology <PHYT>
F:323/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 50.0%; Score 6; DB 2; Length 1123;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 1058 HTGGGV 1063

RESULT 5
H60787

sperm-activating peptide (Thr-5 speract) - sea urchin (Anthocidaris crassispina)
C:Species: Anthocidaris crassispina
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: H60787
R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocen A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: H60787
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 41.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
Db 5 TGGGV 9

RESULT 6
D60788

sperm-activating peptide (Thr-5 speract) - sea urchin (Pseudocentrotus depressus)
C:Species: Pseudocentrotus depressus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C:Accession: D60788
R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocen A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: D60788
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 41.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
Db 5 TGGGV 9

RESULT 7
B60787

sperm-activating peptide (Thr-5 speract) - sea urchin (Hemicentrotus pulcherrimus)
C:Species: Hemicentrotus pulcherrimus
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: B60787
R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocen A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: B60787
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 41.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
Db 5 TGGGV 9

RESULT 8

A60788
sperm-activating peptide (Thr-5 speract) - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: A60788
R: Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus nodosus, Echinometra mathaei and Heterocentrotus mammillatus.
A:Reference number: A60787; PMID:88242184; PMID:3378407
A:Accession: A60788
A:Molecule type: protein
A:Residues: 1-10 <SUS>
A:Comment: This oligopeptide from egg jelly is one of several from this species. Unlike of the repeats in the known precursor (see PIR:A34543).
C:Superfamily: unassigned animal peptides

Query Match 41.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
Db 5 TGGGV 9

RESULT 9

C60589
sperm-activating peptide (Thr-5 SAP-I) - Echinometra mathaei
C:Species: Echinometra mathaei
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: C60589
R: Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, K.
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptides, Echinometra mathaei and Heterocentrotus mammillatus.
A:Reference number: A60527
A:Accession: C60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Note: an identical peptide was isolated from Echinometra mathaei type A and type B
C:Superfamily: unassigned animal peptides

Query Match 41.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
Db 5 TGGGV 9

RESULT 10

D60588
sperm-activating peptide (Thr-5 SAP-I) - sea urchin (Strongylocentrotus nodosus)
N: Alternate names: speract homolog
C:Species: Strongylocentrotus nodosus
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: D60588
R: Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, K.
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptides, Echinometra mathaei and Heterocentrotus mammillatus.

A:Reference number: A60527
A:Accession: D60588
A:Molecule type: protein
A:Residues: 1-10 <YOS>
C:Superfamily: unassigned animal peptides

Query Match 41.7%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
Db 5 TGGGV 9

RESULT 11

T26663
hypothetical protein Y38E10A.m - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26663
R: Wallis, J.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20252
A:Accession: T26663
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-71 <WIL>
A:Cross-references: EMBL:AL110484; NID:el542205; PIDN:CAB54404.1; CESP:Y38E10A.m
A:Experimental source: clone Y38E10A
C:Genetics:
A:Gene: CESP:Y38E10A.m

Query Match 41.7%; Score 5; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
Db 32 TGGGV 36

RESULT 12

T48971
hypothetical protein F14D17.20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T48971
R: Jordan, N.; Bangerter, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25008
A:Accession: T48971
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-72 <JOR>
A:Cross-references: EMBL:AL353992; GSPDB:GN000061; ATSP:F14D17.20
A:Experimental source: cultivar Columbia; BAC clone F14D17
C:Genetics:
A:Gene: ATSP:F14D17.20
A:Map position: 3
A:Introns: 42/3

Query Match 41.7%; Score 5; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVW 7
Db 66 GGGVW 70

RESULT 13

A69147

hypothetical protein MTH364 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: A69147
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: A69147
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-75 <MTH>
A:CROSS-references: GB:AE000822; GB:AE000666; NID:g2621420; PIDN:AAB84870.1; PID:g262142
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH364
A:Start codon: TTG

Query Match 41.7%; Score 5; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGGGV 6
|
|
|
|
|
Db 23 TGGGV 27

RESULT 14

S22454
ribosomal protein L2 REP - wood tobacco mitochondrion (fragment)
C:Species: mitochondrion Nicotiana sylvestris (wood tobacco)
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 21-Jul-2000
C:Accession: S22454
R:Vitart, V.; de Paepe, R.; Mathieu, C.; Chetrit, P.; Vedel, F.
Mol. Gen. Genet. 233, 193-200, 1992
A:Title: Amplification of substoichiometric recombinant mitochondrial DNA sequences in a
A:Reference number: S22454; MUID:92293115; PMID:1376403
A:Accession: S22454
A:Molecule type: DNA
A:Residues: 1-101 <VIT>
A:CROSS-references: EMBL:X66519; NID:g396185; PIDN:CAA47138.1; PID:g396186
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: Escherichia coli ribosomal protein L2
C:Keywords: mitochondrion

Query Match 41.7%; Score 5; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGGGV 6
|
|
|
|
|
Db 73 TGGGV 77

RESULT 15

S58218
hypothetical protein 3 - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
C:Accession: S58218
R:Lim, A.; de Vos, D.; Brauns, M.; Gaballa, A.; Hamers, R.; Cornelis, P.
submitted to the EMBL Data Library, August 1995
A:Description: Molecular cloning, nucleotide sequence, and characterization of OprL, a m
A:Reference number: S58216
A:Accession: S58218
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <LIM>
A:CROSS-references: EMBL:Z50191; NID:g2251191; PIDN:CAA90572.1; PID:g929777

Query Match 41.7%; Score 5; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGGGV 6
|
|
|
|
|
Db 52 TGGGV 56

Search completed: March 13, 2003, 15:33:40
Job time : 12.4615 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:18:49 ; Search time 6.46154 Seconds
(without alignments)
77.027 Million cell updates/sec

Title: us-09-822-698a-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Description
1	6	50.0	1123	PHYA_SOLTU P30733 solanum tub
2	5	50.0	1124	PHY1_TOBAC P33530 nicotiana t
3	5	41.7	144	RL15_HAEIN P44353 haemophilus
4	5	41.7	169	PLMN_RAT Q01177 rattus norv
5	5	41.7	181	FMKA_ECOLI P04738 escherichia
6	5	41.7	184	VP50_BPADS Q91198 bacterioph
7	5	41.7	189	AROK_SYNY3 P72796 synecocyst
8	5	41.7	197	VG23_BPMD2 Q38362 mycobacteri
9	5	41.7	197	VG23_BPMD5 Q05229 mycobacteri
10	5	41.7	223	RL4_MYCBO Q06045 mycobacteri
11	5	41.7	223	RL4_MYCTU P95050 mycobacteri
12	5	41.7	229	H1S4_PYRAE Q82Y14 pyrobaculum
13	5	41.7	238	MOTB_TREPA Q07887 treponema p
14	5	41.7	241	PYRF_THETH P96076 thermus the
15	5	41.7	245	PELA_HAEIN P43751 haemophilus
16	5	41.7	245	T2M4_METJA Q38723 methanococc
17	5	41.7	262	RS2_THEME Q9WZM1 thermotoga
18	5	41.7	265	H1S4_XYLEA Q9PBC9 xylella fas
19	5	41.7	270	L181_CHLEU Q03965 chlamydomon
20	5	41.7	270	URED_SYNY3 P73047 synecocyst
21	5	41.7	285	NADC_MYCTU Q06594 mycobacteri
22	5	41.7	296	SAPR_STRPU P11761 strongyloce
23	5	41.7	297	EY3_CHLRE Q08336 chlamydomon
24	5	41.7	303	L722_SYNY3 P72667 synecocyst
25	5	41.7	304	LST_HAEIN Q48211 haemophilus
26	5	41.7	319	AES_ECOLI P23872 escherichia
27	5	41.7	325	YC83_MYCTU Q10611 mycobacteri
28	5	41.7	337	TAT_HTLV2 P03410 human t-cel
29	5	41.7	343	SLAM_MOUSE Q9QUM4 mus musculu
30	5	41.7	344	JUNB_MOUSE P04450 mus musculu
31	5	41.7	349	JUNB_RAT P24898 rattus norv
32	5	41.7	349	MRAY_CHLPN Q92706 chlamydia p
33	5	41.7	350	REDD_STRCO P16922 streptomyce

34	5	41.7	358	1	TAT_HTLIA	P03409 human t-cel
35	5	41.7	358	1	TAT_HTLIC	P14079 human t-cel
36	5	41.7	370	1	EL3E_TOBAC	P23546 nicotiana t
37	5	41.7	370	1	EL3E_TOBAC	P27666 nicotiana t
38	5	41.7	371	1	EL3B_TOBAC	P15797 nicotiana t
39	5	41.7	374	1	ADH1_ALLMI	P80222 alligator m
40	5	41.7	387	1	YB96_YEAST	P38332 saccharomyc
41	5	41.7	406	1	METK_AERPE	Q9YBK2 aeropyrum p
42	5	41.7	417	1	ARCA_PSEAE	P13981 pseudomonas
43	5	41.7	420	1	ARCA_PSEPU	P41142 pseudomonas
44	5	41.7	421	1	SHIA_MOUSE	Q64264 mus musculu
45	5	41.7	422	1	SHIA_HUMAN	P08908 homo sapien

ALIGNMENTS

RESULT 1
PHYA_SOLTU STANDARD; PRT; 1123 AA.
ID AC P30733;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome A.
GN PHYA.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree;
RX MEDLINE=92163018; PubMed=1536928;
RA Heyer A., Gatz C.;
RT "Isolation and characterization of a cDNA-clone coding for potato
type A phytochrome.";
RL Plant Mol. Biol. 18:535-544(1992).
CC -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC -!- SUBUNIT: HOMODIMER.
CC -!- PFM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC -!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC -----
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CC -----
CC EMBL; S84872; AAB21533.2; -.
CC PIR; S20497; S20497.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR004359; HIS_KIN_sig.
CC InterPro; IPR003661; His_KinA.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000700; PAS-assoc_C.

InterPro: IPR000014; PAS_domain.
InterPro: IPR001294; Phytochrome.
Pfam: PF00360; phytochrome; 1.
Pfam: PF00512; signal; 1.
Pfam: PF00989; PAS; 2.
Pfam: PF01590; GAF; 1.
Pfam: PF02318; HATPase_C; 1.
PRINTS: PR01033; PHYTOCHROME.
SMART: SM00065; GAF; 1.
SMART: SM00387; HATPase_C; 1.
SMART: SM00388; His_KinA.
SMART: SM00086; PAC; 1.
SMART: SM00091; PAS; 2.
SMART: SM00091; PAS; 2.
TIGRFAMs: TIGR00229; sensory_box; 1.
PROSITE: PS50109; HIS_KIN; 1.
PROSITE: PS50113; PAC; 1.
PROSITE: PS50112; PAS; 2.
PROSITE: PS00245; PHYTOCHROME_1; 1.
PROSITE: PS50046; PHYTOCHROME_2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
Repeat; Multigene family.
FT DOMAIN 617 687
FT DOMAIN 690 746
FT DOMAIN 747 821
FT DOMAIN 901 1118
FT BINDING 323 323
SQ SEQUENCE 1123 AA; 124689 MW; 3A97062A5DFB29EA CRC64;

Query Match 50.0%; Score 6; DB 1; Length 1123;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGV 6
|||||
Db 1058 HTGGGV 1063

RESULT 2
PHYLL_TOBAC ID PHYL_TOBAC STANDARD; PRT; 1124 AA.
AC P33530;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome A1.
GN PHYA1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
RN [1]
RX MEDLINE=94143494; PubMed=8310074;
RA Adam E., Deak M., Key S., Chua N.H., Nagy F.;
RT "Sequence of a tobacco (Nicotiana glauca) gene coding for type A
Plant Physiol. 101:1407-1408(1993)."
RL CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT
CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC BISPHOSPHATE CARBOXYLASE, CHLOROPLAST A/B BINDING PROTEIN,
CC PROTOCHLOROPHYLLIDE REDUCTASE, RNAP, ETC. IT ALSO CONTROLS
CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC -1- SUBUNIT: ROMODIMER.
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARN-T-SIM) DIMERIZATION DOMAINS.

--!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAS) DOMAIN.
--!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.

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EMBL: X66784; CA947284.1; --
InterPro: IPR003594; ATPbind_ATPase.
InterPro: IPR003018; GAF.
InterPro: IPR004359; HIS_KIN_sig.
InterPro: IPR003661; His_KinA.
InterPro: IPR001610; PAC.
InterPro: IPR000700; PAS-assoc.C.
InterPro: IPR000014; PAS_domain.
InterPro: IPR001294; Phytochrome.
Pfam: PF00360; phytochrome; 1.
Pfam: PF00512; signal; 1.
Pfam: PF00989; PAS; 2.
Pfam: PF01590; GAF; 1.
Pfam: PF02518; HATPase_C; 1.
PRINTS: PR01033; PHYTOCHROME.
SMART: SM00065; GAF; 1.
SMART: SM00387; HATPase_C; 1.
SMART: SM00388; His_KinA; 1.
SMART: SM00086; PAC; 1.
SMART: SM00091; PAS; 2.
TIGRFAMs: TIGR00229; sensory_box; 1.
PROSITE: PS50109; HIS_KIN; 1.
PROSITE: PS50113; PAC; 1.
PROSITE: PS50112; PAS; 2.
PROSITE: PS00245; PHYTOCHROME_1; 1.
PROSITE: PS50046; PHYTOCHROME_2; 1.
KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
KW Repeat; Multigene family.
FT DOMAIN 617 687
FT DOMAIN 690 746
FT DOMAIN 747 821
FT DOMAIN 901 1118
FT BINDING 323 323
SQ SEQUENCE 1124 AA; 124296 MW; 4C2938CFE9A5F130 CRC64;

Query Match 50.0%; Score 6; DB 1; Length 1124;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGV 6
|||||
Db 1058 HTGGGV 1063

RESULT 3
RL15_HAEIN ID RL15_HAEIN STANDARD; PRT; 144 AA.
AC P44353;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L15.
GN RPLO OR RPL15 OR HI0797.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
OC Haemophilus.
NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

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RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RA Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U32762; AAC22455.1; -.
DR TIGR: HI0797; -.
DR InterPro: IPR001196; Ribosomal_L15.
DR Pfam: PF00256; L15; 1.
DR Pfam: PF01305; Ribosomal_L15; 1.
DR TIGRFAMs: TIGR01071; rplO_bact; 1.
DR PROSITE: PS00475; RIBOSOMAL_L15; 1.
DR Ribosomal protein; rRNA-binding; Complete proteome.
KW RIBOSOMAL 144 AA; 15072 MW; FOCPC80684DC64C5 CRC64;
SQ
SEQUENCE 144 AA: 15072 MW; FOCPC80684DC64C5 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
| | | | |
DB 42 TGGGV 46

RESULT 4
PLMN_RAT
ID PLMN_RAT STANDARD; PRT; 169 AA.
AC Q01177;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN Plg.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanalas J.J., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen."
RL J. Biol. Chem. 266:10825-10829(1991).
CC -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-I-Xaa > Arg-I-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble

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CC -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
CC -----
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CC -----
DR EMBL: M62832; AAA41884.1; -.
DR PIR: A40522; A40522.
DR HSP: P00747; 1PMK.
DR MEROPS: S01.233; -.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00051; kringle; 2.
DR ProDom: PD000395; Kringle; 2.
DR SMART: SM00130; KR; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS50070; KRINGLE_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; PARTIAL.
DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
DR Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Repeat.
FT NON_TER 1
FT DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
FT DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
FT DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
FT DISULFID 34 112 BY SIMILARITY.
FT DISULFID 55 95 BY SIMILARITY.
FT DISULFID 83 107 BY SIMILARITY.
FT NON_TER 169
SQ SEQUENCE 169 AA: 18401 MW; 77A54214C49D010C CRC64;

Query Match 41.7%; Score 5; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
| | | | |
DB 115 TGGGV 119

RESULT 5
EMKA_ECOLI
ID EMKA_ECOLI STANDARD; PRT; 181 AA.
AC P04738;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE K88 fimbrial protein A precursor.
GN FAPC.
OS Escherichia coli.
OG Plasmid pF205.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=84264326; PubMed=6086572;
RA Mool F.R., van Buuren M., Koopman G., Roosendaal B., de Graaf F.K.;
RT "K88ab gene of Escherichia coli encodes a fimbria-like protein
RT distinct from the K88ab fimbrial adhesin."

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ID VG23_BPMD2 STANDARD; PRT; 197 AA.
AC Q38362; O64217;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Major tail protein GP23 (Major coat protein).
GN 23.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC unclassified Siphoviridae.
OX NCBI_TaxID=28369;
RN [1]
RP SEQUENCE FROM N.A.
RA Schramm Y., Wyse J., Mink S., Suissa M., Kuhn J.;
RT "Cloning, sequence and expression of the gene coding for the major
RT coat protein of Mycobacteriophage D29.";
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: Implications for phage
RT evolution.";
RL J. Mol. Biol. 279:143-164 (1998).
CC -----
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CC -----
DR EMBL; X70353; CAA49811.1; -.
DR EMBL; AF022214; AAC18464.1; -.
KW Coat protein.
FT INIT_MET 0 BY SIMILARITY.
FT CONFLICT 25 25 H -> P (IN REF. 1).
FT CONFLICT 176 176 K -> E (IN REF. 1).
SQ SEQUENCE 197 AA; 21183 MW; 548580298149564D CRC64;

Query Match 41.7%; Score 5; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DPIDY 12
DB 86 DPIDY 90
|||||

RESULT 9
VG23_BPML5 STANDARD; PRT; 197 AA.
AC O05229;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Major tail protein GP23 (Major coat protein).
GN 23.
OS Mycobacteriophage L5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC L5-like viruses.
OX NCBI_TaxID=31757;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-16.
RX MEDLINE=93211282; PubMed=8459766;
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -----
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CC -----
DR EMBL; Z18946; CAA79399.1; -.
DR PIR; S30968; S30968.
KW Coat protein.
FT INIT_MET 0
SQ SEQUENCE 197 AA; 21395 MW; 2151C128687EF239 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DPIDY 12
DB 86 DPIDY 90
|||||

RESULT 10
RL4_MYCBO STANDARD; PRT; 223 AA.
ID RL4_MYCBO
AC O06045;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 50S ribosomal protein L4.
GN RPLD.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCG;
RX MEDLINE=98065585; PubMed=9402018;
RA Sander P., Pramananan T., Meier A., Frischkorn K., Bottger E.C.;
RT "The role of ribosomal RNAs in macrolide resistance.";
RL Mol. Microbiol. 26:469-480(1997).
CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY AND SPECIFICALLY TO 23S
CC RNA (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE L4P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y13228; CAA73673.1; -.
DR InterPro; IPR002136; Ribosomal_L4/L1E.
DR Pfam; PF00573; Ribosomal_L4; 1.
KW Ribosomal protein; rRNA-binding.
SQ SEQUENCE 223 AA; 23942 MW; 43229717543F23E5 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGV 6
DB 91 TGGGV 95
|||||

RESULT 11
RL4_MYCTU STANDARD; PRT; 223 AA.
ID RL4_MYCTU
AC P95050;
DT 30-MAY-2000 (Rel. 39, Created)

```

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L4.
 GN RPLD OR RV0702 OR MT0729 OR MTCY210.21.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=96344230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY AND SPECIFICALLY TO 23S
 CC RRNA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE L4P FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL; Z84395; CAB06465.1; -;
 DR EMBL; AE006966; AAK4960.1; -;
 DR TIGR; MT0729; -;
 DR TubercuList; RV0702; -;
 DR InterPro; IPR002136; Ribosomal_L4/L1E.
 DR Pfam; PF00573; Ribosomal_L4; 1.
 KW Ribosomal protein; rRNA-binding; Complete proteome.
 SQ SEQUENCE 223 AA; 23743 MW; E9AF8F30E35A66AB CRC64;

 Query Match 41.7%; Score 5; DB 1; Length 223;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 TGGGV 6
 Db 91 TGGGV 95
 |||||

 RESULT 12
 HIS4_PYRAE
 ID HIS4_PYRAE STANDARD; PRT; 229 AA.
 AC Q8ZX14;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)
 DE Imidazole-4-carboxamide isomerase

DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
 DE isomerase).
 GN HISA OR PAE0991.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 RT aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 CC -!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
 CC phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-
 CC [(5-phospho-1-deoxyribose-1-ylamino)methylideneamino]-1-(5-
 CC phosphoribosyl)imidazole-4-carboxamide.
 CC -!- PATHWAY: Histidine biosynthesis; fourth step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
 CC -----
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 CC -----
 DR EMBL; AE009797; AAL63182.1; -;
 KW Isomerase; Histidine biosynthesis; Complete proteome.
 SQ SEQUENCE 229 AA; 24830 MW; F064FDBEC3B0B7FA CRC64;

 Query Match 41.7%; Score 5; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 TGGGV 6
 Db 168 TGGGV 172
 |||||

 RESULT 13
 MOTB_TREPA
 ID MOTB_TREPA STANDARD; PRT; 238 AA.
 AC O07887;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chemotaxis motB protein (Motility protein B).
 GN MOTB OR TP0724.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96345631; PubMed=8755894;
 RA Limberger R.J., Slivinski L.L., El-Afandi M.C.T., Dantuono L.A.;
 RT "Organization, transcription, and expression of the 5' region of the
 RL fla operon of Treponema phagedenis and Treponema pallidum.";
 RL J. Bacteriol. 178:4628-4634(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,

RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RL spirochete."
 CC Science 281:375-388(1998).
 CC -!- FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR. MIGHT
 CC BE A LINKER THAT FASTENS THE TORQUE-GENERATING MACHINERY TO THE
 CC CELL WALL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE MOTB FAMILY.
 CC -----
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 CC -----
 CC EMBL; U28219; AAB61254.1; -.
 CC EMBL; AE001244; AAC65689.1; -.
 DR TIGR; TP0724; -.
 DR InterPro: IPR001145; Bac_OmpA.
 DR Pfam; PF00691; OmpA; 1.
 DR ProDom; PD000930; Bac_OmpA; 1.
 KW Chemotaxis; Flagella; Transmembrane; Inner membrane;
 KW Flagellar rotation; Complete proteome.
 FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 15 34 POTENTIAL.
 FT DOMAIN 35 238 PERIPLASMIC (POTENTIAL).
 SQ SEQUENCE 238 AA; 26050 MW; 0AB5FCD8E9852E1F CRC64;
 Query Match 41.7%; Score 5; DB 1; Length 238;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGGGV 6
 Db 56 TGGGV 60
 RESULT 14
 PYRF_THETH
 ID PYRF_THETH STANDARD; PRT; 241 AA.
 AC P96076;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
 DE (OMPDCase) (OMPDecase) (Fragment).
 GN PYRF.
 OS Thermus thermophilus.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
 OC Thermaceae; Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB27;
 RX MEDLINE=96236211; PubMed=8787418;
 RA Yamagishi A., Tanimoto T., Suzuki T., Oshima T.;
 RT "Pyrimidine biosynthetic genes (pyrE and pyrF) of an extreme
 RT thermophile, Thermus thermophilus."
 RL Appl. Environ. Microbiol. 62:2191-2194(1996).
 CC -!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).
 CC -!- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
 CC -!- SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY. SUBFAMILY 2.
 CC -----
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 CC -----

CC or send an email to license@isb-sib.ch.
 CC -----
 CC EMBL; D83330; BAA11885.1; -.
 DR HSP; O26232; IDVJ.
 DR InterPro: IPR001734; OMPDecase.
 DR Pfam; PF00215; OMPDecase; 1.
 DR PROSITE; PS00156; OMPDECASE; 1.
 KW Lyase; Decarboxylase; Pyrimidine biosynthesis.
 FT NON_TER 1 1
 FT ACT_SITE 70 70 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 241 AA; 25696 MW; 03AB5721A21F60F4 CRC64;
 Query Match 41.7%; Score 5; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGGGV 6
 Db 115 TGGGV 119
 RESULT 15
 PFLA_HAEIN
 ID PFLA_HAEIN STANDARD; PRT; 245 AA.
 AC P43751;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pyruvate formate-lyase 1 activating enzyme (EC 1.97.1.4) (PFL-
 DE activating enzyme).
 GN PFLA OR ACT OR HI0179.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uiterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd."
 RL Science 269:496-512(1995).
 CC -!- FUNCTION: ACTIVATION OF PYRUVATE FORMATE-LYASE 1 UNDER ANAEROBIC
 CC CONDITIONS BY GENERATION OF AN ORGANIC FREE RADICAL, USING
 CC S-ADENOSYLMETHIONINE AND REDUCED FLAVODOXIN AS COSUBSTRATES TO
 CC PRODUCE 5'-DEOXY-ADENOSINE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + dihydroflavodoxin +
 CC [formate acetyltransferase]-glycine = 5'-deoxyadenosine +
 CC methionine + flavodoxin + [formate acetyltransferase]-glycine-2-yl
 CC radical.
 CC -!- COFACTOR: BINDS 1 4FE-4S CLUSTER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE ORGANIC RADICAL ACTIVATING ENZYMES
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; U32703; AAC21848.1; -.

DR TIGR; H10179; -.
DR InterPro; IPR001989; Radical_activat.
DR Pfam; PF02143; Radical_activat; 1.
DR ProDom; PD004758; Radical_activat; 1.
DR PROSITE; PS01087; RADICAL_ACTIVATING; 1.
KW Oxidoreductase; Iron-sulfur; 4Fe-4S; Glucose metabolism;
KW Complete proteome.
FT INIT_MET 0 0 BY SIMILARITY.
FT METAL 29 29 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 33 33 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 36 36 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 245 AA; 28104 MW; E868E3BD5B9BE3FD CRC64;
Query Match 41.7%; Score 5; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TGGGV 6
DB 69 TGGGV 73

Search completed: March 13, 2003, 15:32:06
Job time : 6.46154 secs

GenCore version 5.1.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:28:09 ; Search time 23.0769 Seconds
(without alignments)
107.144 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 12
Sequence: 1 HTGGGVMDPIDY 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_prodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bactexiap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	50.0	114	10 Q9SVK9	Q9svk9 arabidopsis
2	6	50.0	131	4 Q8WY0	Q8wy0 homo sapien
3	6	50.0	181	13 Q91665	Q91665 xenopus lae
4	6	50.0	192	5 Q9N6S3	Q9n6s3 leishmania
5	6	50.0	193	16 Q9PDE3	Q9pde3 xylella fas
6	6	50.0	381	16 Q98C19	Q98c19 rhizobium l
7	6	50.0	436	16 Q9K6F3	Q9k6f3 bacillus ha
8	6	50.0	502	16 Q8Y012	Q8y012 raistonia s
9	6	50.0	614	16 Q982I2	Q982i2 rhizobium l
10	6	50.0	1068	10 Q9FF3	Q9fff3 arabidopsis
11	6	50.0	1123	10 Q41331	Q41331 lycopersico
12	5	41.7	46	15 Q80812	Q80812 human t-lym
13	5	41.7	52	12 Q98809	Q98809 yam mosaic
14	5	41.7	53	15 Q992L1	Q992l1 human t-cel
15	5	41.7	57	10 Q9SAT4	Q9sat4 nicotiana t
16	5	41.7	71	5 Q9NAJ8	Q9naj8 caenorhabdi

17	5	41.7	72	10 Q9LX10	Q9lx10 arabidopsis
18	5	41.7	75	17 Q26464	Q26464 methanobact
19	5	41.7	77	15 Q39198	Q39198 human t-lym
20	5	41.7	78	5 Q8WR25	Q8wr25 anopheles g
21	5	41.7	85	11 Q91HY3	Q91hy3 mus musculu
22	5	41.7	90	16 Q931P1	Q931p1 staphylococ
23	5	41.7	94	5 Q9VM00	Q9vm00 drosophila
24	5	41.7	101	8 Q08712	Q08712 nicotiana s
25	5	41.7	102	2 Q9LCA9	Q9lca9 rhodocyclu
26	5	41.7	103	16 Q9KJ66	Q9rj66 streptomyce
27	5	41.7	107	2 Q51490	Q51490 pseudomonas
28	5	41.7	109	10 Q9EJZ0	Q9ejz0 arabidopsis
29	5	41.7	110	11 Q9D9U5	Q9d9u5 mus musculu
30	5	41.7	117	2 Q9RH52	Q9rns2 streptomyce
31	5	41.7	117	11 Q9D466	Q9d466 mus musculu
32	5	41.7	118	6 Q95JT4	Q95jtt4 macaca fasc
33	5	41.7	119	16 Q9KF97	Q9kf97 bacillus ha
34	5	41.7	122	10 Q9LW24	Q9lw24 arabidopsis
35	5	41.7	124	8 Q35862	Q35862 schistosoma
36	5	41.7	128	8 Q95AT6	Q95at6 dugesia pol
37	5	41.7	133	16 Q97ES2	Q97es2 clostridium
38	5	41.7	136	10 Q94GS2	Q94gs2 oryza sativ
39	5	41.7	139	2 Q9JMX1	Q9jmx1 bradyrhizob
40	5	41.7	140	16 Q9EWE4	Q9ewe4 streptomyce
41	5	41.7	143	10 Q944U8	Q944u8 kokia dryna
42	5	41.7	144	10 Q944V1	Q944v1 gossypium a
43	5	41.7	144	10 Q944V0	Q944v0 gossypium l
44	5	41.7	144	10 Q944U9	Q944u9 gossypium b
45	5	41.7	144	15 O41286	O41286 primate t-1

ALIGNMENTS

RESULT 1

Q9SVK9 ID Q9SVK9 PRELIMINARY; PRT; 114 AA.
AC Q9SVK9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Hypothetical 12.9 kDa protein.
GN F18B3.180.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetier F.,
RA Salanoubat M.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049862; CAB42919.1; -
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12923 MW; F8156E1465887DBB CRC64;

Query Match 50.0%; Score 6; DB 10; Length 114;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGVWDP 9
|||||
Db 99 GGVWDP 104

RESULT 2

Q8WY0

```
ID Q8WY0 PRELIMINARY; PRT; 131 AA.
AC Q8WY0;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical 13.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289615; AAL55799.1; -.
KW Hypothetical protein.
SQ SEQUENCE 131 AA; 13879 MW; B1D6A5917F3608ED CRC64;

Query Match 50.0%; Score 6; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVW 7
Db 29 TGGGVW 34

RESULT 3
Q91665 PRELIMINARY; PRT; 181 AA.
ID Q91665;
AC Q91665;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CTX (Fragment).
DE CTX (Fragment).
OS Xanopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FP;
RX MEDLINE=96210130; PubMed=8625968;
RA Chretien I., Robert J., Marcuz A., Garcia-Sanz J.A., Courtet M.,
RA Du Pasquier L.;
RT "CTX, a novel molecule specifically expressed on the surface of
RT cortical thymocytes in Xenopus.";
RL Eur. J. Immunol. 26:780-791(1996).
DR EMBL; U43393; AAC59860.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG-like; 1.
FT NON_TER
SQ SEQUENCE 181 AA; 19380 MW; 6A58F6C824EDC16 CRC64;

Query Match 50.0%; Score 6; DB 13; Length 181;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 154 HTGGGV 159

RESULT 4
```

```
Q9N6S3 PRELIMINARY; PRT; 192 AA.
ID Q9N6S3;
AC Q9N6S3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE L7535.14.
DE L822.2 OR L7535.14.
GN L822.2 OR L7535.14.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Myler P.J.;
RA Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,
RA Cawthra J., Marsolini F., Sunkin S., Stuart K.D.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Myler P.J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005893; AAF31031.1; -.
DR EMBL; AC005767; AAF27953.1; -.
DR EMBL; AC005766; AAF28379.1; -.
SQ SEQUENCE 192 AA; 19650 MW; 0CE9460B1FB5A9C4 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 192;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 129 HTGGGV 134

RESULT 5
Q9PDE3 PRELIMINARY; PRT; 193 AA.
ID Q9PDE3;
AC Q9PDE3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Disulfide oxidoreductase.
GN XF1436.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Artuda P., Abreu F.A., Ascencio M.,
RA Alvares A.J.G., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carver H.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.N., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.W.,
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de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
"Complete genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003973; AAF84245.1; -.
DR InterPro; IPR001853; DSBA.
DR InterPro; IPR000063; ThioRed.
DR Pfam; PF01323; DSBA; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 193 AA; 21305 MW; 552DC6D86B4F555D CRC64;

Query Match 50.0%; Score 6; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGVWDP 9
Db 68 GGVWDP 73
|||||

RESULT 6
Q98C19 ID Q98C19 PRELIMINARY; PRT; 381 AA.
AC Q98C19;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein mlf5331.
GN Mlf5331.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF30309; PubMed=11214968;
RX MEDLINE=2108930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Tateuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003006; BAB51802.1; -.
DR InterPro; IPR000160; GGDEF.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc.C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00990; GGDEF; 1.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00267; DUF1; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 1.
DR TIGRfams; TIGR00254; GGDEF; 1.
DR TIGRfams; TIGR00229; sensory_box; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 381 AA; 41817 MW; 7CDACE8F8F6E32B4 CRC64;

Query Match 50.0%; Score 6; DB 16; Length 381;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVWDP 8
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Db 138 GGVWDP 143

RESULT 7
Q9K6F3 ID Q9K6F3 PRELIMINARY; PRT; 436 AA.
AC Q9K6F3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH oxidase (nox).
GN BH3776.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -!- COFACTOR: FAD (BY SIMILARITY).
DR EMBL; AP001519; BAB07495.1; -.
DR HSP; P37062; 1NHP.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR000103; Pyridine_redox_2.
DR InterPro; IPR001100; Pyr_redox_dim.
DR InterPro; IPR004099; Pyr_redox_dim.
DR Pfam; PF00070; Pyr_redox; 1.
DR Pfam; PF02852; Pyr_redox_dim; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDPDTASEI.
DR PRINTS; PR00469; PNDPDTASEII.
DR ProDom; PD000139; FAD_pyr_redox; 1.
KW FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SQ SEQUENCE 436 AA; 47376 MW; 6B7997FD763FF732 CRC64;

Query Match 50.0%; Score 6; DB 16; Length 436;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGVWDP 10
|||||
Db 424 GGVWDP 429

RESULT 8
Q8Y012 ID Q8Y012 PRELIMINARY; PRT; 502 AA.
AC Q8Y012;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable transporter transmembrane protein.
GN RSC1233 OR RS02740.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salenouat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,

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RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646063; CAD14935.1; -.
DR InterPro: IPR001248; Cyt_pur_permease.
DR Pfam: PF02133; Transp_cyt_pur; 1.
DR TIGRFAMs: TIGR00800; ncs1; 1.
KW Complete proteome.
SQ SEQUENCE 502 AA; 53783 MW; 7F72D191E74030C0 CRC64;

Query Match 50.0%; Score 6; DB 16; Length 502;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VWDPID 11
Db 304 VWDPID 309

RESULT 9
Q98212 ID Q98212 PRELIMINARY; PRT; 614 AA.
AC Q98212;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE DNA methyltransferase.
GN MLL9056.
OS Rhizobium loti (Mesorhizobium loti).
OC Plasmid pMLa.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003015; BAB54474.1; -.
DR InterPro: IPR001091; CM4_Mettransf.
DR InterPro: IPR002295; D21N6_mtfase.
DR InterPro: IPR002941; N6/N4_Mtase.
DR InterPro: IPR002052; N6_Mtase.
DR Pfam: PF01555; N6_N4_Mtase; 1.
DR PRINTS; PR00506; D21N6MTFRASE.
DR PRINTS; PR00508; S21N4MTFRASE.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Transferrase; Methyltransferase; Plasmid; Complete proteome.
SQ SEQUENCE 614 AA; 69230 MW; 14507EDDAE0FBFCE CRC64;

Query Match 50.0%; Score 6; DB 16; Length 614;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 116 HTGGGV 121

RESULT 10
Q9FFF3 ID Q9FFF3 PRELIMINARY; PRT; 1068 AA.
AC Q9FFF3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Low density lipoprotein B-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT P1 clones.";
RL DNA Res. 4:215-230(1997).
DR EMBL; AB005242; BAB09597.1; -.
KW Lipoprotein.
SQ SEQUENCE 1068 AA; 118802 MW; D696E592DD4B991C CRC64;

Query Match 50.0%; Score 6; DB 10; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVW 7
Db 484 TGGGVW 489

RESULT 11
Q41331 ID Q41331 PRELIMINARY; PRT; 1123 AA.
AC Q41331;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE PHYA protein (Phytochrome A).
GN PHYA.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. UC82B;
RX MEDLINE=98346008; PubMed=9681030;
RA Lazarova G.I., Cordonnier-Pratt M.M., Kerckhoffs L.J.,
RA Brandstatter J., Matsui M., Pratt L.H., Kendrick R.E.;
RT "Molecular analysis of PHYA in wild-type and phytochrome A-deficient
RT mutants of tomato.";
RL Plant J. 14:653-662(1998).
RN [2]
RP SEQUENCE OF 165-277 FROM N.A.
RC STRAIN=UC-82B;
RX MEDLINE=96191281; PubMed=8616214;
RA Hauser B.A., Cordonnier-Pratt M.M., Daniel-Vedele F., Pratt L.H.;
RT "The phytochrome gene family in tomato includes a novel subfamily.";
RL Plant Mol. Biol. 29:1143-1155(1995).
DR EMBL; AJ001916; CAA05089.1; -.
DR EMBL; U32345; AAC49297.1; -.
DR EMBL; AJ001915; CAA05088.1; -.
DR EMBL; AJ001913; CAA05086.1; -.
DR EMBL; AJ001914; CAA05087.1; -.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR004359; HIS_KIN_sig.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000700; PAS-associat.
DR InterPro: IPR000014; PAS_domain.
DR InterPro: IPR001294; Phytochrome.

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DR InterPro; IPR001680; WD40.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF00360; phytochrome; 1.
DR Pfam; PF00512; signal; 1.
DR PRINTS; PR01033; PHYTOCHROME.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR TIGRFSMS; TIGR00229; sensory_box; 1.
DR PROSITE; PS00245; PHYTOCHROME_1; 1.
DR PROSITE; PS00046; PHYTOCHROME_2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Phytochrome.
SQ SEQUENCE 1123 AA; 124659 MW; 0432ADCCCFDF0FB1 CRC64;

Query Match 50.0%; Score 6; DB 10; Length 1123;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGV 6
Db 1058 HTGGGV 1063
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RESULT 12
Q80812 PRELIMINARY; PRT; 46 AA.
AC Q80812;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tax protein (Fragment).
GN PX.
OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=93124579; PubMed=8093491;
RA Bastian I., Gardner J.F., Webb D., Gardner I.;
RT "Isolation of a human T-lymphotropic virus type I from Australian
RT Aborigines.";
RL J. Virol. 67:843-851(1993).
DR EMBL; M92819; AAA45401.1; -.
DR InterPro; IPR004120; Tax.
DR Pfam; PF02959; Tax; 1.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5031 MW; 52BB1E8188659FF0 CRC64;

Query Match 41.7%; Score 5; DB 15; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WDPID 11
Db 27 WDPID 31
|||||

RESULT 13
Q98809 PRELIMINARY; PRT; 52 AA.
AC Q98809;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Putative 6K2 protein (Fragment).
OS Yam mosaic virus.

Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=41460;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN-IVORY COAST;
RX MEDLINE=96370790; PubMed=8774686;
RA Aleman M.E., Marcos J.F., Brugidou C., Beachy R.N., Fauquet C.;
RT "The complete nucleotide sequence of yam mosaic virus (Ivory Coast
RT isolate) genomic RNA.";
RL Arch. Virol. 141:1259-1278(1996).
DR EMBL; U42596; AAC5552.1; -.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 6022 MW; 43EC15F948548287 CRC64;

Query Match 41.7%; Score 5; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGVW 7
Db 32 GGGVW 36
|||||

RESULT 14
Q992L1 PRELIMINARY; PRT; 53 AA.
ID Q992L1;
AC Q992L1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tax protein (Fragment).
OS Human T-cell leukemia virus type II (HTLV-II).
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11909;
RN [1]
RC SEQUENCE FROM N.A.
RA Glaser J.B., Dube S., Polesz B.J.;
RT "HTLV-II coinfection among HIV-1 infected prison inmates.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF327515; AAK19304.1; -.
DR InterPro; IPR004120; Tax.
DR Pfam; PF02959; Tax; 1.
FT NON_TER 1
FT NON_TER 53
SQ SEQUENCE 53 AA; 5815 MW; 416E03EF077132E7 CRC64;

Query Match 41.7%; Score 5; DB 15; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WDPID 11
Db 43 WDPID 47
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RESULT 15
Q9SAT4 PRELIMINARY; PRT; 57 AA.
ID Q9SAT4;
AC Q9SAT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Basic beta-1,3-glucanase (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=92404740; PubMed=2152343;

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RA Neale A.D., Wahleithner J.A., Lund M., Bonnett H.T., Kelly A.,
 RT Meeks-Wagner D.R., Peacock W.J., Dennis E.S.;
 RT "Chitinase, beta-1,3-glucanase, osmotin, and extensin are expressed in
 RT tobacco explants during flower formation.";
 RL Plant Cell 2:673-684(1990).
 DR EMBL; S44870; AAB23376.1; -.
 DR HSSP; F15737; IGHS.
 DR InterPro; IPR000490; Glyco_hydro_17.
 DR Pfam; PF00332; Glyco_hydro_17; 1.
 FT NON_TER 1
 SQ SEQUENCE 57 AA; 6401 MW; 64DFB8C1DB17E472 CRC64;

 Query Match 41.7%; Score 5; DB 10; Length 57;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 GGWWD 8
 Db 38 GGWWD 42

 Search completed: March 13, 2003, 15:33:05
 Job time : 23.0769 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:05:54 ; Search time 5.49231 seconds
(without alignments)
291.136 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	14	AAE12770	Human PH1 Fab anti
2	76	100.0	121	AAE12706	Human PH1 Fab anti
3	76	100.0	381	AAE12707	Human b1vPH1-IL-2
4	76	100.0	451	AAE12715	Human recombinant
5	75	98.7	14	AAE12764	Human PH1 Fab anti
6	73	96.1	14	AAE12758	Human PH1 Fab anti
7	71	93.4	14	AAE12748	Human PH1 Fab anti
8	71	93.4	14	AAE12749	Human PH1 Fab anti
9	71	93.4	14	AAE12753	Human PH1 Fab anti
10	71	93.4	14	AAE12769	Human PH1 Fab anti

11	70	92.1	14	AAE12771	Human PH1 Fab anti
12	69	90.8	14	AAE12719	Human PH1 Fab anti
13	69	90.8	14	AAE12720	Human PH1 Fab anti
14	69	90.8	14	AAE12740	Human PH1 Fab anti
15	69	90.8	14	AAE12741	Human PH1 Fab anti
16	69	90.8	14	AAE12742	Human PH1 Fab anti
17	69	90.8	14	AAE12743	Human PH1 Fab anti
18	69	90.8	14	AAE12743	Human PH1 Fab anti
19	69	90.8	14	AAE12759	Human PH1 Fab anti
20	69	90.8	14	AAE12762	Human PH1 Fab anti
21	68	89.5	14	AAE12772	Human PH1 Fab anti
22	68	89.5	14	AAE12754	Human PH1 Fab anti
23	68	89.5	14	AAE12766	Human PH1 Fab anti
24	68	89.5	14	AAE12773	Human PH1 Fab anti
25	67	88.2	14	AAE12734	Human PH1 Fab anti
26	67	88.2	14	AAE12746	Human PH1 Fab anti
27	67	88.2	14	AAE12747	Human PH1 Fab anti
28	67	88.2	14	AAE12763	Human PH1 Fab anti
29	67	88.2	14	AAE12774	Human PH1 Fab anti
30	66	86.8	14	AAE12735	Human PH1 Fab anti
31	65	85.5	14	AAE12768	Human PH1 Fab anti
32	64	84.2	14	AAE12750	Human PH1 Fab anti
33	64	84.2	14	AAE12718	Human PH1 Fab anti
34	64	84.2	14	AAE12744	Human PH1 Fab anti
35	64	84.2	14	AAE12751	Human PH1 Fab anti
36	64	84.2	14	AAE12756	Human PH1 Fab anti
37	63	82.9	14	AAE12736	Human PH1 Fab anti
38	63	82.9	14	AAE12755	Human PH1 Fab anti
39	63	82.9	14	AAE12761	Human PH1 Fab anti
40	63	82.9	14	AAE12765	Human PH1 Fab anti
41	62	81.6	14	AAE12767	Human PH1 Fab anti
42	61	80.3	14	AAE12760	Human PH1 Fab anti
43	61	80.3	14	AAE12717	Human PH1 Fab anti
44	61	80.3	14	AAE12739	Human PH1 Fab anti
45	60	78.9	14	AAE12733	Human PH1 Fab anti
			14	AAE12738	Human PH1 Fab anti

ALIGNMENTS

RESULT 1
AAE12770
ID AAE12770 standard; peptide; 14 AA.
XX
AC AAE12770;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human PH1 Fab antibody VH region FR3-CDR3 variant #37.
XX
KW Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody; variant.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT Location/Qualifiers
FT 1..2
FT /label= Framework_region_3
FT 3..14
FT /label= Complementarity_determining_region_3
XX
PN WO200175110-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10589.
XX
PR 30-MAR-2000; 2000US-0538913.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Henderikx MFC;

XX WPI: 2001-626437/72.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1
XX
XX Example 2; Page 125; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma,
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human PH1 Fab antibody VH
CC region FR (framework region)3-CDR3 variant.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 76; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14
|||||
RESULT 2
ID AAE12706
XX AAE12706 standard; Protein; 121 AA.
AC AAE12706;
XX
XX 04-JAN-2002 (first entry)
DT Human PH1 Fab antibody variable heavy chain region (VH).
DE
DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; PH1 antibody.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 31..35
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT Region 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT Region 97..99
FT /label= FR3
FT /note= "Framework region 3"
FT Region 97..112
FT /note= "VH domain"
FT Region 99..110
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT Region 111..112
FT /label= FR4
FT /note= "Framework region 4"
XX

PN WO200175110-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
PF
XX
XX 30-MAR-2000; 2000US-0538913.
PR
XX
XX (DYAX-) DYAX CORP.
PA
XX
XX Hoogenboom HRJM, Henderikx MPG;
PI
XX WPI: 2001-626437/72.
DR
XX N-PSDB; AAD20731.
DR
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1
XX
XX Claim 2; Page 94-95; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
CC antibody VH region.
XX
XX Sequence 121 AA;
SQ
Query Match 100.0%; Score 76; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110
|||||
RESULT 3
ID AAE12707
XX AAE12707 standard; Protein; 381 AA.
AC AAE12707;
XX
XX 04-JAN-2002 (first entry)
DT Human biVPH1-IL-2 immunocytokine protein.
DE
DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
KW
XX Homo sapiens.
XX
XX WO200175110-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10589.
PF
XX
XX 30-MAR-2000; 2000US-0538913.
PR
XX
XX 30-MAR-2000; 2000US-0538913.
PR
XX

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PA (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX N-PSDB; AAD20732.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX its portion for binding to an epitope of the protein core of mucin-1 -
XX
XX Claim 9; Page 95-97; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
XX (MUC-1)-specific binding member comprising an antigen binding domain
XX region having an antibody variable light (VL) or heavy (VH) region,
XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX The binding of MUC1-specific binding member to MUC1 is detected by a
XX detection method selected from enzyme-linked immunosorbent assay,
XX magnetic resonance imaging, scintillation counting, and X-ray film.
XX MUC1-specific binding member is useful for treating cancer, preferably
XX adenocarcinoma, in an individual, where the cancer is present in tissue
XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX binding member is useful for diagnosing and imaging MUC1-expressing
XX cancer cells and tissues, for purifying or isolating non-glycosylated,
XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX containing molecules, and for therapeutically or prophylactically
XX treating cancer. The present sequence is human bivPHI-1L-2
XX immunocytokine protein. bivPHI is mucin specific binding portion.
XX
XX Sequence 381 AA;
SQ
Query Match 100.0%; Score 76; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
DB 99 HTGGGVWDPIDY 110
|||||
RESULT 4
AAE12715
ID AAE12715 standard; Protein: 451 AA.
XX
XX AAE12715;
XX
XX 04-JAN-2002 (first entry)
XX
XX Human recombinant immunoglobulin (Ig) heavy chain region.
XX
XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX heavy chain region; cancer; breast; ovary; lung; bladder;
XX cytostatic; therapy; immunoglobulin; Ig.
XX
XX Homo sapiens.
XX
XX WO200175110-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
XX
XX 30-MAR-2000; 2000US-0538913.
XX
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX N-PSDB; AAD20745.
XX
PT

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PT Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -
XX
XX Claim 12; Page 106-108; 126pp; English.
XX
XX The invention relates to an isolated tumour-associated antigen mucin-1
XX (MUC-1)-specific binding member comprising an antigen binding domain
XX region having an antibody variable light (VL) or heavy (VH) region,
XX or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX The binding of MUC1-specific binding member to MUC1 is detected by a
XX detection method selected from enzyme-linked immunosorbent assay,
XX magnetic resonance imaging, scintillation counting, and X-ray film.
XX MUC1-specific binding member is useful for treating cancer, preferably
XX adenocarcinoma, in an individual, where the cancer is present in tissue
XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX binding member is useful for diagnosing and imaging MUC1-expressing
XX cancer cells and tissues, for purifying or isolating non-glycosylated,
XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX containing molecules, and for therapeutically or prophylactically
XX treating cancer. The present sequence is human recombinant immunoglobulin
XX (Ig) heavy chain region (variable VH and CH constant heavy chain).
XX
XX Sequence 451 AA;
SQ
Query Match 100.0%; Score 76; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
DB 99 HTGGGVWDPIDY 110
|||||
RESULT 5
AAE12764
ID AAE12764 standard; peptide: 14 AA.
XX
XX AAE12764;
XX
XX 04-JAN-2002 (first entry)
XX
XX Human PH1 Fab antibody VH region FR3-CDR3 variant #31.
XX
XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
XX variable heavy chain region; cancer; breast; ovary; lung; bladder;
XX cytostatic; therapy; PH1 antibody; variant.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Region 1..2
XX FT Region /label= Framework_region_3
XX FT Region 3..14
XX FT /label= Complementarity_determining_region_3
XX
XX WO200175110-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
XX
XX 30-MAR-2000; 2000US-0538913.
XX
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI; 2001-626437/72.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX its portion for binding to an epitope of the protein core of mucin-1 binding domain or
XX
XX
XX
PT

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PT its portion for binding to an epitope of the protein core of mucin-1 -

XX Example 2; Page 123; 126pp; English.

PS The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 98.7%; Score 75; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 2e-05;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVNDPIDY 12

Db 3 HTGGGVNDPVDY 14

|||||||:|

RESULT 6

AAEL2758

ID AAE12758 standard; peptide; 14 AA.

XX AC AAE12758;

XX DT 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #25.

DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

FT WO200175110-A2.

XX PN 11-OCT-2001.

XX PD 30-MAR-2001; 2001WO-US10589.

XX PF 30-MAR-2000; 2000US-0538913.

XX PR (DYAX-) DYAX CORP.

XX PA Hoogenboom HRJM, Henderikx MPG;

XX PI WPI; 2001-626437/72.

XX DR Novel isolated tumor-associated antigen mucin-1-specific binding member

XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

PS Example 2; Page 122; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX SQ Sequence 14 AA;

Query Match 96.1%; Score 73; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 4.3e-05;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVNDPIDY 12

Db 3 HTGGGVNDPMDY 14

|||||||:|

RESULT 7

AAEL2748

ID AAE12748 standard; peptide; 14 AA.

XX AC AAE12748;

XX DT 04-JAN-2002 (first entry)

XX Human PH1 Fab antibody VH region FR3-CDR3 variant #15.

DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..2

FT /label= Framework_region_3

FT Region 3..14

FT /label= Complementarity_determining_region_3

FT WO200175110-A2.

XX PN 11-OCT-2001.

XX PD 30-MAR-2001; 2001WO-US10589.

XX PF 30-MAR-2000; 2000US-0538913.

XX PR (DYAX-) DYAX CORP.

XX PA Hoogenboom HRJM, Henderikx MPG;

XX PI WPI; 2001-626437/72.

XX DR Novel isolated tumor-associated antigen mucin-1-specific binding member

XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX PT its portion for binding to an epitope of the protein core of mucin-1 -

XX

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;
 Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPIDY 12
 DQ 3 HTGGGVWDPINV 14
 |||||
 |||||

RESULT 8
 AAE12749
 ID AAE12749 standard; peptide; 14 AA.
 AC AAE12749;
 XX AAE12749;
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #16.
 XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT 3..14
 FT /label= Complementarity_determining_region_3
 PN WO200175110-A2.
 PD 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 PF 30-MAR-2000; 2000US-0538913.
 PR (DYAX-) DYAX CORP.
 PA Hoogenboom HRJM, Henderikx MPG;
 PI WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 120; 126pp; English.
 PS The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;
 Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HTGGGVWDPIDY 12
 DQ 3 HTGGGVWDPINV 14
 |||||
 |||||

RESULT 9
 AAE12753
 ID AAE12753 standard; peptide; 14 AA.
 AC AAE12753;
 XX AAE12753;
 DT 04-JAN-2002 (first entry)
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #20.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT 3..14
 FT /label= Complementarity_determining_region_3
 PN WO200175110-A2.
 PD 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 PF 30-MAR-2000; 2000US-0538913.
 PR (DYAX-) DYAX CORP.
 PA Hoogenboom HRJM, Henderikx MPG;
 PI WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 121; 126pp; English.
 PS The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
 |||||
 DB 3 HTGGGVWDPIY 14

RESULT 10

AAE12769
 ID AAE12769 standard; peptide; 14 AA.

XX AC AAE12769;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #36.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 124; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC magnetic resonance imaging, scintillation counting, and x-ray film.

CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.

XX Sequence 14 AA;

Query Match 93.4%; Score 71; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
 |||||
 DB 3 HTGGGVWNPIDY 14

RESULT 11

AAE12771
 ID AAE12771 standard; peptide; 14 AA.

XX AC AAE12771;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #38.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 125; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and x-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 92.1%; Score 70; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00013; Mismatches 1; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12

Db 3 HTGGGVDPIDY 14

RESULT 12

AAE12719
 ID AAE12719 standard; peptide: 14 AA.

XX AC AAE12719;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #3.

XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX KW cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key

XX FT Region

XX FT 1..2 Location/Qualifiers

XX FT /label= Framework_region_3

XX FT 3..14

XX FT /label= Complementarity_determining_region_3

XX PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX DR WPI; 2001-626437/72.

XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member

XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX PT its portion for binding to an epitope of the protein core of mucin-1 -

XX PS Claim 2; Page 75; 126pp; English.

XX CC The invention relates to an isolated tumour-associated antigen mucin-1

XX CC (MUC-1)-specific binding member comprising an antigen binding domain

XX CC region having an antibody variable light (VL) or heavy (VH) region,

XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX CC The binding of MUC1-specific binding member to MUC1 is detected by a

XX CC detection method selected from enzyme-linked immunosorbent assay,

XX CC magnetic resonance imaging, scintillation counting, and X-ray film.

XX CC MUC1-specific binding member is useful for treating cancer, preferably

XX CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 90.8%; Score 69; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00018; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12

Db 3 HTGGGVDPIDY 14

RESULT 13

AAE12720
 ID AAE12720 standard; peptide: 14 AA.

XX AC AAE12720;

XX DT 04-JAN-2002 (first entry)

XX DE Human PH1 Fab antibody VH region FR3-CDR3 variant #4.

XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;

XX KW variable heavy chain region; cancer; breast; ovary; lung; bladder;

XX KW cytostatic; therapy; PH1 antibody; variant.

XX OS Homo sapiens.

XX FH Key

XX FT Region

XX FT 1..2 Location/Qualifiers

XX FT /label= Framework_region_3

XX FT 3..14

XX FT /label= Complementarity_determining_region_3

XX PN WO200175110-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10589.

XX PR 30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.

XX PI Hoogenboom HRJM, Henderikx MPG;

XX DR WPI; 2001-626437/72.

XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member

XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

XX PT its portion for binding to an epitope of the protein core of mucin-1 -

XX PS Claim 2; Page 75; 126pp; English.

XX CC The invention relates to an isolated tumour-associated antigen mucin-1

XX CC (MUC-1)-specific binding member comprising an antigen binding domain

XX CC region having an antibody variable light (VL) or heavy (VH) region,

XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX CC The binding of MUC1-specific binding member to MUC1 is detected by a

XX CC detection method selected from enzyme-linked immunosorbent assay,

XX CC magnetic resonance imaging, scintillation counting, and X-ray film.

XX CC MUC1-specific binding member is useful for treating cancer, preferably

XX CC adenocarcinoma, in an individual, where the cancer is present in tissue

XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

XX CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 90.8%; Score 69; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00018;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
 |||||
 Db 3 HTGGGVWDPIKY 14

RESULT 14
 AAE12740
 ID AAE12740 standard; peptide; 14 AA.
 XX
 AC AAE12740;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #7.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotatic; therapy; PH1 antibody; variant.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX WO200175110-A2.

XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 119; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope

CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH
 CC region FR (framework region)3-CDR3 variant.
 XX
 SQ Sequence 14 AA;

Query Match 90.8%; Score 69; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11
 |||||
 Db 3 HTGGGVWDPID 13

RESULT 15
 AAE12741
 ID AAE12741 standard; peptide; 14 AA.
 XX
 AC AAE12741;
 XX
 DT 04-JAN-2002 (first entry)
 XX
 DE Human PH1 Fab antibody VH region FR3-CDR3 variant #8.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VH;
 KW variable heavy chain region; cancer; breast; ovary; lung; bladder;
 KW cytotatic; therapy; PH1 antibody; variant.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..2
 FT /label= Framework_region_3
 FT Region 3..14
 FT /label= Complementarity_determining_region_3
 XX WO200175110-A2.

XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 2; Page 119; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human PH1 Fab antibody VH

CC region FR (framework region)3-CDR3 variant.

XX

SQ Sequence 14 AA;

Query Match 90.8%; Score 69; DB 22; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00018;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12

|||||||

Db 3 HTGGGVDPIGY 14

Search completed: March 13, 2003, 15:14:42

Job time : 6.49231 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:44 ; Search time 1.84615 seconds
(without alignments)
191.249 Million cell updates/sec

Title: US-09-822-698a-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	47	61.8	573	1 US-08-200-512-2	Sequence 2, Appli
2	43.5	57.2	774	4 US-09-346-237-8	Sequence 8, Appli
3	40	52.6	123	6 5171845-1	Patent No. 5171845
4	38	50.0	28	3 US-08-978-741-14	Sequence 14, Appl
5	38	50.0	28	4 US-09-333-729A-14	Sequence 14, Appl
6	38	50.0	109	4 US-09-134-001C-3523	Sequence 3523, Ap
7	38	50.0	328	4 US-09-300-672-2	Sequence 2, Appli
8	38	50.0	397	3 US-08-978-741-6	Sequence 6, Appli
9	38	50.0	397	4 US-09-333-729A-7	Sequence 7, Appli
10	38	50.0	447	3 US-08-508-761B-6	Sequence 6, Appli
11	38	50.0	738	1 US-07-985-458-3	Sequence 3, Appli
12	38	50.0	941	4 US-09-074-658-3	Sequence 75, Appl
13	38	50.0	944	2 US-08-867-941-23	Sequence 23, Appl
14	38	50.0	944	2 US-08-867-941-24	Sequence 24, Appl
15	38	50.0	944	4 US-09-074-658-23	Sequence 23, Appl
16	38	50.0	944	4 US-09-074-658-24	Sequence 24, Appl
17	37	48.7	848	4 US-08-976-255-10	Sequence 10, Appl
18	36	47.4	20	4 US-08-992-877-65	Sequence 65, Appl
19	36	47.4	79	2 US-08-499-676A-13	Sequence 13, Appl
20	36	47.4	152	3 US-08-916-043-2	Sequence 2, Appli
21	36	47.4	152	6 5212286-6	Patent No. 5212286
22	36	47.4	300	4 US-09-134-001C-4385	Sequence 4385, Ap
23	36	47.4	384	3 US-09-071-434-3	Sequence 3, Appli
24	36	47.4	627	2 US-08-466-589-6	Sequence 6, Appli
25	36	47.4	627	2 US-08-700-636-6	Sequence 6, Appli
26	36	47.4	627	3 US-08-467-574-6	Sequence 6, Appli
27	36	47.4	627	4 US-09-217-345-6	Sequence 6, Appli

28	36	47.4	627	4 US-08-487-596-6	Sequence 6, Appli
29	36	47.4	720	4 US-09-296-284-25	Sequence 25, Appl
30	36	47.4	754	4 US-09-296-284-4	Sequence 4, Appli
31	35.5	46.7	659	1 US-08-240-049B-16	Sequence 16, Appl
32	35.5	46.7	659	1 US-08-259-148A-20	Sequence 20, Appl
33	35.5	46.7	659	1 US-08-484-054-20	Sequence 20, Appl
34	35.5	46.7	659	2 US-07-876-941A-20	Sequence 20, Appl
35	35.5	46.7	659	4 US-08-477-232-14	Sequence 14, Appl
36	35.5	46.7	659	4 US-07-870-985A-20	Sequence 20, Appl
37	35.5	46.7	660	4 US-08-542-634-14	Sequence 14, Appl
38	35.5	46.7	660	4 US-09-462-606-48	Sequence 48, Appl
39	35.5	46.7	660	5 PCT-US95-13703-14	Sequence 14, Appl
40	35.5	46.7	970	1 US-08-375-709-7	Sequence 7, Appli
41	35.5	46.7	970	1 US-08-752-929-7	Sequence 7, Appli
42	35.5	46.7	970	4 US-09-090-793-5	Sequence 5, Appli
43	35	46.1	13	3 US-08-525-716-2	Sequence 2, Appli
44	35	46.1	95	4 US-08-928-383B-18	Sequence 18, Appl
45	35	46.1	112	4 US-08-469-260A-222	Sequence 222, App

ALIGNMENTS

RESULT 1
US-08-200-512-2
; Sequence 2, Application US/08200512
; Patent No. 5674718
; GENERAL INFORMATION:
; APPLICANT: BRIAND, MICHELLE
; APPLICANT: PLESIAT, PATRICK
; TITLE OF INVENTION: DNA SEGMENTS AND TRANS-
; TITLE OF INVENTION: FORMED MICROORGANISMS COMPRISING THE DELTA'-
; TITLE OF INVENTION: DEHYDROGENASE GENE, AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,512
; FILING DATE: 17-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,660
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR91/00094
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MUSERLIAN, CHARLES A.
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1116-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: (212) 661-8002
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PROTEIN
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: PSEUDOMONAS TESTOSTERONI
FEATURE: (R, repeat if necessary)
NAME/KEY: PROTEIN
LOCATION: 1..573
OTHER INFORMATION: /note = Delta
OTHER INFORMATION: dehydrogenase protein of Pseudomonas
OTHER INFORMATION: testosterone
US-08-200-512-2

Query Match 61.8%; Score 47; DB 1; Length 573;
Best Local Similarity 54.5%; Pred. No. 8.4;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGVWDPIDY 12
:||||:|:|:
Db 47 SGGGIWIPLY 57

RESULT 2
US-09-346-237-8
Sequence 8, Application US/09346237A
Patent No. 6265197
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629-200-US
CURRENT APPLICATION NUMBER: US/09/346.237A
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: PA 1998 00868
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: 60/094.353
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 774
TYPE: PRT
ORGANISM: Favobacterium odoratum
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(774)
OTHER INFORMATION: Isoamylase
US-09-346-237-8

Query Match 57.2%; Score 43.5; DB 4; Length 774;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 HTGGGVWDPID 11
|||||:
Db 329 HTGEGGANSPTD 340

RESULT 3
5171845-1
Patent No. 5171845
APPLICANT: SPIK, GENEVIEVE-TARTAR, ANDRE; MONTREUIL, JEAN
TITLE OF INVENTION: PROTEIN HOMOLOGUE OF HUMAN ANGIOGENIN
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/392.977
FILING DATE: 18-NOV-1988
SEQ ID NO: 1
LENGTH: 123
5171845-1

Query Match 52.6%; Score 40; DB 6; Length 123;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12

Db 85 GGSPWDPQY 94
||| |

RESULT 4
US-08-978-741-14
Sequence 14, Application US/08978741
Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978.741
FILING DATE: 26-NO. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/223-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-978-741-14

Query Match 50.0%; Score 38; DB 3; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
| | | | |
Db 8 HMPAGSWDPAGY 19

RESULT 5
US-09-333-729A-14
Sequence 14, Application US/09333729A
Patent No. 6270987
GENERAL INFORMATION:
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1-Substitute
CURRENT APPLICATION NUMBER: US/09/333.729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798.741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 14
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

; OTHER INFORMATION: Plasmid insert encoded protein.

; NAME/KEY: unsure

; LOCATION: 23, 25

; OTHER INFORMATION: unknown amino acid

US-09-333-729A-14

Query Match 50.0%; Score 38; DB 4; Length 28;

Best Local Similarity 50.0%; Pred. No. 9.8;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

 | | | | |

Db 8 HMPAGSWDPAGY 19

RESULT 6

US-09-134-001C-3523

; Sequence 3523, Application US/091344001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3523

; LENGTH: 109

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3523

Query Match 50.0%; Score 38; DB 4; Length 109;

Best Local Similarity 45.5%; Pred. No. 39;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11

 | | | | |

Db 27 HTLEGHWHPVE 37

RESULT 7

US-09-300-672-2

; Sequence 2, Application US/09300672

; Patent No. 6248937

; GENERAL INFORMATION:

; APPLICANT: Finkelstein, Ruth R.

; APPLICANT: Lynch, Tim

; APPLICANT: Goodman, Howard M.

; APPLICANT: Wang, Ming-Li

; TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,

; FILE REFERENCE: QUALITY AND COLD-TOLERANCE

; CURRENT APPLICATION NUMBER: US/09/300,672

; CURRENT FILING DATE: 1999-04-27

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Arabidopsis

US-09-300-672-2

Query Match 50.0%; Score 38; DB 4; Length 328;

Best Local Similarity 54.5%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11

Db 311 HNWGSIWDFID 321

RESULT 8

US-08-978-741-6

; Sequence 6, Application US/08978741

; Patent No. 6100076

; GENERAL INFORMATION:

; APPLICANT: Yang Wang, Michael W. Spellman

; TITLE OF INVENTION: O-Fucosyltransferase

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/978,741

; FILING DATE: 26-No. 6100076-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/792498

; FILING DATE: 31

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1041P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 397 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-978-741-6

Query Match 50.0%; Score 38; DB 3; Length 397;

Best Local Similarity 50.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12

 | | | | |

Db 32 HMPAGSWDPAGY 43

RESULT 9

US-09-333-729A-7

; Sequence 7, Application US/09333729A

; Patent No. 6270987

; GENERAL INFORMATION:

; APPLICANT: Wang, Yang

; APPLICANT: Spellman, Michael W.

; TITLE OF INVENTION: O-Fucosyltransferase

; FILE REFERENCE: P1041P1-Substitute

; CURRENT APPLICATION NUMBER: US/09/333,729A

; CURRENT FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: US 08/798,741

; PRIOR FILING DATE: 1997-11-26

; NUMBER OF SEQ ID NOS: 21

; SEQ ID NO 7

; LENGTH: 397

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Plasmid insert encoded protein.
US-09-333-729A-7

Query Match 50.0%; Score 38; DB 4; Length 397;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIY 12
| | | | |
DB 32 HMPAGSWDPAGY 43

RESULT 10

US-08-508-761B-6
; Sequence 6, Application US/08508761B
; Patent No. 6027920
; GENERAL INFORMATION:
; APPLICANT: Joliff, Gwennael
; APPLICANT: Guyonvarch, Arnel
; APPLICANT: Purification, Relano
; APPLICANT: Duchiron, Francis
; APPLICANT: Renaud, Michel
; TITLE OF INVENTION: System for Protein Expression and
; TITLE OF INVENTION: Secretion Especially in Corynebacteria
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,761B
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09652
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09870
; FILING DATE: 02-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58525NA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-508-761B-6

Query Match 50.0%; Score 38; DB 3; Length 447;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HTGGGVWD 8
| | | | |
DB 304 HTDGSIMD 311

RESULT 11

US-07-985-458-3
; Sequence 3, Application US/07985458
; Patent No. 5344777

; GENERAL INFORMATION:
; APPLICANT: Tamaki, Toshihimi;
; APPLICANT: Takemura, Hiroshi;
; APPLICANT: Tayama, Kenji;
; APPLICANT: Fukaya, Masahiro;
; APPLICANT: Okumura, Hajime and
; APPLICANT: Kawamura, Yoshiya
; TITLE OF INVENTION: Structural Gene of Membrane-Bound
; TITLE OF INVENTION: Alcohol Dehydrogenase Complex, Plasmid
; TITLE OF INVENTION: Containing The Same And Transformed Acetic Acid
; TITLE OF INVENTION: Bacteria
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frishauf, Holtz, Goodman & Woodward, P.C.
; STREET: 600 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2088
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.72 mb
; COMPUTER: IBM PC compatible (NEC PC-9801 ES)
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII Form
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/985,458
; FILING DATE: 19921203
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,221
; FILING DATE: 20-FEB-1991
; APPLICATION NUMBER: 73440/1990
; FILING DATE: 26-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Herbert
; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 910134/HG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)972-1400
; TELEFAX: (212)370-1622
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: MATURE PEPTIDE
; LOCATION: 36 to 738
; IDENTIFICATION METHOD: N-terminal sequences of the
; IDENTIFICATION METHOD: purified protein having a molecular weight of about
; IDENTIFICATION METHOD: 72,000
; ORIGINAL SOURCE:
; ORGANISM: Acetobacter altoacetigenes
; STRAIN: MH-24
; PUBLICATION INFORMATION:
; AUTHORS: Tamaki, Toshihimi;
; AUTHORS: Fukaya, Masahiro;
; AUTHORS: Takemura, Hiroshi;
; AUTHORS: Tayama, Kenji;
; AUTHORS: Okumura, Hajime;
; AUTHORS: Kawamura, Yoshiya;
; AUTHORS: Nishiyama, Makoto;
; AUTHORS: Horinouchi, Sueharu and
; AUTHORS: Beppu, Teruhiko
; TITLE: Cloning and Sequencing of the Gene Cluster
; TITLE: Encoding two Subunits of Membrane-Bound
; TITLE: Alcohol Dehydrogenase from Acetobacter
; TITLE: polyoxogenes
; JOURNAL: Biochimica et Biophysica Acta.
; VOLUME: 1088
; PAGES: 292-300

DATE: 1991
US-07-985-458-3

Query Match 50.0%; Score 38; DB 1; Length 738;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGVWDPIDY 12
|| ||| |
Db 276 GGTWDSIVY 285

RESULT 12

US-09-074-658-75
Sequence 75, Application US/09074658
Patent No. 6184371

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M
APPLICANT: Run-Pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-074-658-75

Query Match 50.0%; Score 38; DB 4; Length 941;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 HTGGG--VWDPIDY 12
:|||| : ||:|
Db 326 YTGGRILPDPMDY 339

RESULT 13

US-08-867-941-23
Sequence 23, Application US/08867941
Patent No. 5977337

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping

APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 944 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-867-941-23

Query Match 50.0%; Score 38; DB 2; Length 944;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 HTGGG--VWDPIDY 12
:|||| : ||:|
Db 331 YTGGRILPDPMDY 344

RESULT 14

US-08-867-941-24
Sequence 24, Application US/08867941
Patent No. 5977337

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H

TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I

Search completed: March 13, 2003, 15:18:42
Job time : 2.84615 secs

REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 944 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-867-941-24

Query Match 50.0%; Score 38; DB 2; Length 944;
Best Local Similarity 57.1%; Pred. No. 3 6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 HTGGG--VWDPIDY 12
Db 330 YTGGRILPDPMDY 343

RESULT 15

US-09-074-658-23
Sequence 23, Application US/09074658
Patent No. 6184371
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Run-Pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 944 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-074-658-23

Query Match 50.0%; Score 38; DB 4; Length 944;
Best Local Similarity 57.1%; Pred. No. 3 6e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 HTGGG--VWDPIDY 12
Db 331 YTGGRILPDPMDY 344

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:17:09 ; Search time 1.70769 Seconds
(without alignments)
323.890 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVNDPIDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues 199416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	76	100.0	14	10	US-09-822-698A-105
2	76	100.0	121	10	US-09-822-698A-3
3	76	100.0	381	10	US-09-822-698A-5
4	76	100.0	451	10	US-09-822-698A-26
5	75	98.7	14	10	US-09-822-698A-99
6	73	96.1	14	10	US-09-822-698A-93
7	71	93.4	14	10	US-09-822-698A-83
8	71	93.4	14	10	US-09-822-698A-84
9	71	93.4	14	10	US-09-822-698A-88
10	71	93.4	14	10	US-09-822-698A-104
11	70	92.1	14	10	US-09-822-698A-106
12	69	90.8	14	10	US-09-822-698A-31
13	69	90.8	14	10	US-09-822-698A-32
14	69	90.8	14	10	US-09-822-698A-75
15	69	90.8	14	10	US-09-822-698A-76
16	69	90.8	14	10	US-09-822-698A-77
17	69	90.8	14	10	US-09-822-698A-78
18	69	90.8	14	10	US-09-822-698A-94
19	69	90.8	14	10	US-09-822-698A-97

20	69	90.8	14	10	US-09-822-698A-107
21	68	89.5	14	10	US-09-822-698A-89
22	68	89.5	14	10	US-09-822-698A-101
23	68	89.5	14	10	US-09-822-698A-108
24	68	89.5	16	10	US-09-822-698A-65
25	67	88.2	14	10	US-09-822-698A-81
26	67	88.2	14	10	US-09-822-698A-82
27	67	88.2	14	10	US-09-822-698A-98
28	67	88.2	14	10	US-09-822-698A-109
29	67	88.2	16	10	US-09-822-698A-67
30	66	86.8	14	10	US-09-822-698A-103
31	65	85.5	14	10	US-09-822-698A-85
32	64	84.2	14	10	US-09-822-698A-30
33	64	84.2	14	10	US-09-822-698A-79
34	64	84.2	14	10	US-09-822-698A-86
35	64	84.2	14	10	US-09-822-698A-91
36	64	84.2	16	10	US-09-822-698A-69
37	63	82.9	14	10	US-09-822-698A-90
38	63	82.9	14	10	US-09-822-698A-96
39	63	82.9	14	10	US-09-822-698A-100
40	63	82.9	14	10	US-09-822-698A-102
41	62	81.6	14	10	US-09-822-698A-95
42	61	80.3	14	10	US-09-822-698A-29
43	61	80.3	14	10	US-09-822-698A-74
44	61	80.3	16	10	US-09-822-698A-63
45	60	78.9	14	10	US-09-822-698A-73

ALIGNMENTS

RESULT 1

US-09-822-698A-105

; Sequence 105, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hooenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DXX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 105

; LENGTH: 14

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match 100.0%; Score 76; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVNDPIDY 12

Db 3 HTGGGVNDPIDY 14

RESULT 2

US-09-822-698A-3

; Sequence 3, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hooenboom, Hendricus R.J.M.

; APPLICANT: Henderikx, Maria P.G.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DXX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

```

; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PH1 Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 76; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 3
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPH1-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 76; DB 10; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 4
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT

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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-igG1
US-09-822-698A-26

Query Match      100.0%; Score 76; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 5
US-09-822-698A-99
; Sequence 99, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-99

Query Match      98.7%; Score 75; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 1.6e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPIDY 14

RESULT 6
US-09-822-698A-93
; Sequence 93, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 93
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-93

Query Match      96.1%; Score 73; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.3e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPMDY 14

RESULT 7
US-09-822-698A-83
; Sequence 83, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPINY 14

RESULT 8
US-09-822-698A-84
; Sequence 84, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 84
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-84

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPINY 14

RESULT 9
US-09-822-698A-88
; Sequence 88, Application US/09822698A
; Patent No. US20020146750A1
```

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; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 88
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-88

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWDPINY 14

RESULT 10
US-09-822-698A-104
; Sequence 104, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 104
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-104

Query Match 93.4%; Score 71; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVWDPIDY 12
Db 3 HTGGGVWNPIDY 14

RESULT 11
US-09-822-698A-106
; Sequence 106, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
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```
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 106
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-106
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```
Query Match          92.1%; Score 70; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 9.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 HTGGGVWDPIDY 12
    ||| ||||| |
Db 3 HTGAGVWDPIDY 14
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RESULT 12

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US-09-822-698A-31
; Sequence 31, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31
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```
Query Match          90.8%; Score 69; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 HTGGGVWDPIDY 12
    ||| ||||| |
Db 3 HTGGGVWDPIGY 14
```

RESULT 13

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US-09-822-698A-32
; Sequence 32, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 32
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member
US-09-822-698A-32
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```
Query Match          90.8%; Score 69; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 HTGGGVWDPIDY 12
    ||| ||||| |
Db 3 HTGGGVWDPIKY 14
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RESULT 14

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US-09-822-698A-75
; Sequence 75, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-75
```

```
Query Match          90.8%; Score 69; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HTGGGVWDPID 11
    ||| ||||| |
Db 3 HTGGGVWDPID 13
```

RESULT 15

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US-09-822-698A-76
; Sequence 76, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 76
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-76
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Query Match          90.8%; Score 69; DB 10; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 HTGGGVWDPIDY 12
    ||| ||||| |
Db 3 HTGGGVWDPIGY 14
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Fri Mar 14 09:40:02 2003

us-09-822-698a-3_copy_99_110_1.rapb

Page 5

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Job time : 1.70769 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:14:49 ; Search time 25.5692 Seconds
(without alignments)
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Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/paa/US06 COMB.pcp.*
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- 4: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
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- 10: /cgn2_6/ptodata/2/paa/US086 COMB.pcp.*
- 11: /cgn2_6/ptodata/2/paa/US087 COMB.pcp.*
- 12: /cgn2_6/ptodata/2/paa/US088 COMB.pcp.*
- 13: /cgn2_6/ptodata/2/paa/US089 COMB.pcp.*
- 14: /cgn2_6/ptodata/2/paa/US090 COMB.pcp.*
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- 23: /cgn2_6/ptodata/2/paa/US099 COMB.pcp.*
- 24: /cgn2_6/ptodata/2/paa/US100 COMB.pcp.*
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- 27: /cgn2_6/ptodata/2/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	14	22	US-09-822-698A-105
2	76	100.0	121	19	US-09-538-913-3
3	76	100.0	121	22	US-09-822-698A-3
4	76	100.0	381	19	US-09-538-913-5
5	76	100.0	381	22	US-09-822-698A-5
6	76	100.0	451	22	US-09-822-698A-26

7	75	98.7	14	22	US-09-822-698A-99	Sequence 99, Appl
8	73	96.1	14	22	US-09-822-698A-93	Sequence 93, Appl
9	71	93.4	14	22	US-09-822-698A-83	Sequence 83, Appl
10	71	93.4	14	22	US-09-822-698A-84	Sequence 84, Appl
11	71	93.4	14	22	US-09-822-698A-88	Sequence 88, Appl
12	71	93.4	14	22	US-09-822-698A-104	Sequence 104, App
13	70	92.1	14	22	US-09-822-698A-106	Sequence 106, App
14	69	90.8	14	22	US-09-822-698A-31	Sequence 31, Appl
15	69	90.8	14	22	US-09-822-698A-32	Sequence 32, Appl
16	69	90.8	14	22	US-09-822-698A-75	Sequence 75, Appl
17	69	90.8	14	22	US-09-822-698A-76	Sequence 76, Appl
18	69	90.8	14	22	US-09-822-698A-77	Sequence 77, Appl
19	69	90.8	14	22	US-09-822-698A-78	Sequence 78, Appl
20	69	90.8	14	22	US-09-822-698A-94	Sequence 94, Appl
21	69	90.8	14	22	US-09-822-698A-97	Sequence 97, Appl
22	68	89.5	14	22	US-09-822-698A-107	Sequence 107, App
23	68	89.5	14	22	US-09-822-698A-89	Sequence 89, Appl
24	68	89.5	14	22	US-09-822-698A-101	Sequence 101, App
25	68	89.5	14	22	US-09-822-698A-108	Sequence 108, App
26	68	89.5	16	22	US-09-822-698A-65	Sequence 65, Appl
27	67	88.2	14	22	US-09-822-698A-81	Sequence 81, Appl
28	67	88.2	14	22	US-09-822-698A-82	Sequence 82, Appl
29	67	88.2	14	22	US-09-822-698A-98	Sequence 98, Appl
30	67	88.2	14	22	US-09-822-698A-109	Sequence 109, App
31	67	88.2	16	22	US-09-822-698A-67	Sequence 67, Appl
32	66	86.8	14	22	US-09-822-698A-103	Sequence 103, App
33	65	85.5	14	22	US-09-822-698A-85	Sequence 85, Appl
34	64	84.2	14	22	US-09-822-698A-30	Sequence 30, Appl
35	64	84.2	14	22	US-09-822-698A-79	Sequence 79, Appl
36	64	84.2	14	22	US-09-822-698A-86	Sequence 86, Appl
37	64	84.2	14	22	US-09-822-698A-91	Sequence 91, Appl
38	64	84.2	16	22	US-09-822-698A-69	Sequence 69, Appl
39	63	82.9	14	22	US-09-822-698A-90	Sequence 90, Appl
40	63	82.9	14	22	US-09-822-698A-96	Sequence 96, Appl
41	63	82.9	14	22	US-09-822-698A-100	Sequence 100, App
42	62	81.6	14	22	US-09-822-698A-102	Sequence 102, App
43	62	81.6	14	22	US-09-822-698A-95	Sequence 95, Appl
44	61	80.3	14	22	US-09-822-698A-29	Sequence 29, Appl
45	61	80.3	14	22	US-09-822-698A-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-105
; Sequence 105, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DXX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 105
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-105

Query Match 100.0%; Score 76; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
|||||
Db 3 HTGGGVWDPIDY 14

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RESULT 2
US-09-538-913-3
; Sequence 3, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-3

Query Match      100.0%; Score 76; DB 19; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 3
US-09-822-698A-3
; Sequence 3, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of the PHL Fab antibody
US-09-822-698A-3

Query Match      100.0%; Score 76; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 4
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for bivPH1-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5

Query Match      100.0%; Score 76; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 5
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPH1-IL-2
US-09-822-698A-5

Query Match      100.0%; Score 76; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPIDY 12
Db 99 HTGGGVWDPIDY 110

RESULT 6
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PHL-IgG1
US-09-822-698A-26
```

```

Query Match          100.0%; Score 76; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 99 HTGGGVDPIDY 110

RESULT 7
US-09-822-698A-99
; Sequence 99, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-99

Query Match          98.7%; Score 75; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 3 HTGGGVDPIDY 14

RESULT 8
US-09-822-698A-93
; Sequence 93, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 93
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-93

Query Match          96.1%; Score 73; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 3 HTGGGVDPIDY 14

RESULT 9
US-09-822-698A-93

```

```

US-09-822-698A-83
; Sequence 83, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-83

Query Match          93.4%; Score 71; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 3 HTGGGVDPIDY 14

RESULT 10
US-09-822-698A-84
; Sequence 84, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 84
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-84

Query Match          93.4%; Score 71; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HTGGGVDPIDY 12
   |||||
Db 3 HTGGGVDPIDY 14

RESULT 11
US-09-822-698A-88
; Sequence 88, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30

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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 88
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-88

Query Match          93.4%; Score 71; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPTDY 12
Db 3 HTGGGVWDPINY 14

RESULT 12
US-09-822-698A-104
; Sequence 104, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 104
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-104

Query Match          93.4%; Score 71; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPTDY 12
Db 3 HTGGGVWNPIDY 14

RESULT 13
US-09-822-698A-106
; Sequence 106, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 106
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant CDR3 region of an antibody heavy chain variable region
US-09-822-698A-106

Query Match          92.1%; Score 70; DB 22; Length 14;

```

```

Best Local Similarity 91.7%; Pred. No. 0.00063;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPTDY 12
Db 3 HTGGGVWDPTDY 14

RESULT 14
US-09-822-698A-31
; Sequence 31, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: region of a MUC1-specific binding member
US-09-822-698A-31

Query Match          90.8%; Score 69; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00091;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPTDY 12
Db 3 HTGGGVWDPIGY 14

RESULT 15
US-09-822-698A-32
; Sequence 32, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 32
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence in a MUC1-specific binding member
US-09-822-698A-32

Query Match          90.8%; Score 69; DB 22; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00091;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPTDY 12
Db 3 HTGGGVWDPIKY 14

Search completed: March 13, 2003, 15:28:04
Job time : 25.8192 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:15:24 ; Search time 4.38462 seconds
(without alignments)
355.800 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/ptodata1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	57.9	218	6	US-10-282-122A-50009
2	44	57.9	330	6	US-10-366-683-23794
3	41	53.9	57	1	PCT-US02-32727-17567
4	41	53.9	57	5	US-09-978-825-17567
5	41	53.9	57	6	US-10-057-498-17567
6	41	53.9	251	6	US-10-282-122A-46525
7	41	53.9	264	1	PCT-US02-40225-3079
8	41	53.9	264	6	US-10-320-797-3079
9	41	53.9	300	6	US-10-282-122A-46309
10	41	53.9	710	6	US-10-156-761-14284
11	40	52.6	34	6	US-10-203-138A-13646
12	40	52.6	93	1	PCT-US02-32727-9150
13	40	52.6	93	5	US-09-978-825-9150
14	40	52.6	93	6	US-10-057-498-9150
15	40	52.6	152	6	US-10-156-761-10926
16	40	52.6	158	6	US-10-282-122A-54884
17	40	52.6	717	6	US-10-369-493-10840
18	40	52.6	799	6	US-10-282-122A-49879
19	39.5	52.0	473	1	PCT-US02-32727-17396
20	39.5	52.0	473	5	US-09-978-825-17396
21	39.5	52.0	473	6	US-10-057-498-17396
22	39	51.3	351	6	US-10-156-761-13617
23	39	51.3	480	6	US-10-369-493-9063
24	39	51.3	687	6	US-10-369-493-7152
25	39	51.3	692	6	US-10-369-493-4397
26	39	51.3	807	6	US-10-369-493-22143

27	39	51.3	1583	1	PCT-US02-32727-15149
28	39	51.3	1583	5	US-09-978-825-15149
29	39	51.3	1583	6	US-10-057-498-15149
30	38.5	50.7	101	1	PCT-US02-32727-5698
31	38.5	50.7	101	5	US-09-978-825-5698
32	38.5	50.7	101	6	US-10-057-498-5698
33	38.5	50.7	327	6	US-10-369-493-634
34	38	50.0	76	1	PCT-US02-32727-2924
35	38	50.0	76	5	US-09-978-825-2924
36	38	50.0	76	6	US-10-057-498-2924
37	38	50.0	108	6	US-10-366-683-19965
38	38	50.0	107	6	US-10-092-411A-3523
39	38	50.0	217	6	US-10-282-122A-47986
40	38	50.0	250	5	US-09-724-676-96838
41	38	50.0	250	5	US-09-724-676A-96838
42	38	50.0	304	1	PCT-US03-01363-179
43	38	50.0	327	6	US-10-156-761-12586
44	38	50.0	328	1	PCT-US02-25805A-542
45	38	50.0	328	6	US-10-171-404A-32

ALIGNMENTS

RESULT 1

US-10-282-122A-50009
; Sequence 50009, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50009
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-10-282-122A-50009

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Query Match          57.9%; Score 44; DB 6; Length 218;
Best Local Similarity 63.6%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HTGGGVNDPID 11
   | | | | | | | |
Db 80 HGGGGLYQPID 90

RESULT 2
US-10-366-683-23794
; Sequence 23794, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nolling, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/10/366,683
; PRIOR FILING DATE: 2003-02-13
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23794
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-23794

Query Match          57.9%; Score 44; DB 6; Length 330;
Best Local Similarity 87.5%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGVNDPID 11
   | | | | | |
Db 101 GSVNDPID 108

RESULT 3
PCT-US02-32727-17567
; Sequence 17567, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Shiyang
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514c1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propionibacterium acnes
PCT-US02-32727-17567

Query Match          53.9%; Score 41; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 HTGGGVNDPID 9
   | | | | | | | |
Db 18 HSGGGRWPP 26

RESULT 4
US-09-978-825-17567
; Sequence 17567, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Shiyang
; APPLICANT: Jen, Shiyang
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514c1
; CURRENT APPLICATION NUMBER: US/09/978,825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propionibacterium acnes
US-09-978-825-17567

Query Match          53.9%; Score 41; DB 5; Length 57;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HTGGGVNDPID 9
   | | | | | | | |
Db 18 HSGGGRWPP 26

RESULT 5
US-10-057-498-17567
; Sequence 17567, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Shiyang
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 17567
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propionibacterium acnes
US-10-057-498-17567

Query Match          53.9%; Score 41; DB 6; Length 57;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HTGGGVNDPID 9
   | | | | | | | |
Db 18 HSGGGRWPP 26

RESULT 6
US-10-282-122A-46525
; Sequence 46525, Application US/10282122A
```

```

; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46525
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46525

Query Match          53.9%; Score 41; DB 6; Length 251;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGGGWDPI 10
      : | | | | |
Db      152 TGGGWDGPI 160

RESULT 7
PCT-US02-40225-3079
; Sequence 3079, Application PC/TUS0240225
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: METHODS OF USE
; FILE REFERENCE: 10182-021-228
; CURRENT APPLICATION NUMBER: PCT/US02/40225
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3079
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3079

Query Match          53.9%; Score 41; DB 6; Length 264;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 HTGGGVWDPI 11
      : | | | | |
Db      233 YKGTGVWTPVD 243

RESULT 8
US-10-320-797-3079
; Sequence 3079, Application US/10320797
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS A
; FILE REFERENCE: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3079
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3079

Query Match          53.9%; Score 41; DB 6; Length 264;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 HTGGGVWDPI 11
      : | | | | |
Db      233 YKGTGVWTPVD 243

RESULT 9
US-10-282-122A-46309
; Sequence 46309, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09

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;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 46309
;; LENGTH: 300
;; TYPE: PRT
;; ORGANISM: Bacillus anthracis
US-10-282-122A-46309

Query Match 53.9%; Score 41; DB 6; Length 300;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGGVWDPI 10
|||||
Db 149 TGGGGWGPI 157

RESULT 10
US-10-156-761-14284
;; Sequence 14284, Application US/10156761
;; GENERAL INFORMATION:
;; APPLICANT: OMURA, SATOSHI
;; APPLICANT: IKEDA, HARUO
;; APPLICANT: ISHIKAWA, JUN
;; APPLICANT: HORIKAWA, HIROSHI
;; APPLICANT: SHIBA, TADAYOSHI
;; APPLICANT: SAKAKI, YOSHIYUKI
;; APPLICANT: HATTORI, MASAHIRA
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-262
;; CURRENT APPLICATION NUMBER: US/10/156,761
;; CURRENT FILING DATE: 2002-05-29
;; PRIOR APPLICATION NUMBER: JP 2001-204089
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO 14284
;; LENGTH: 710
;; TYPE: PRT
;; ORGANISM: Streptomyces avermitilis
US-10-156-761-14284

Query Match 53.9%; Score 41; DB 6; Length 710;
Best Local Similarity 63.6%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 11
|||||
Db 600 HTGGGSNSVED 610

RESULT 11
US-10-203-138A-13646
;; Sequence 13646, Application US/10203138A
;; GENERAL INFORMATION:
;; APPLICANT: Molecular Dynamics, Inc.
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

;; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
;; FILE REFERENCE: PB 0004 WO 8
;; CURRENT APPLICATION NUMBER: US/10/203,138A
;; CURRENT FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 04 February 2000 (04.02.00)
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 26 May 2000 (26.05.00)
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)
;; PRIOR APPLICATION NUMBER: GB 24263,6
;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 13438
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 13646
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC007247.2
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.2
US-10-203-138A-13646

Query Match 52.6%; Score 40; DB 6; Length 34;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGVWDPI 10
|||||
Db 5 GGVWDPI 11

RESULT 12
PCT-US02-32727-9150
;; Sequence 9150, Application PC/TUS0232727
;; GENERAL INFORMATION:
;; APPLICANT: Mitcham, Jennifer
;; APPLICANT: Skeiky, Yasir
;; APPLICANT: Persing, David
;; APPLICANT: Bhatia, Ajay
;; APPLICANT: Maisonneuve, Jean Francois
;; APPLICANT: Zhang, Yanni
;; APPLICANT: Wang, Siqing
;; APPLICANT: Jen, Shyian
;; APPLICANT: Lodes, Michael
;; APPLICANT: Benson, Darin
;; APPLICANT: Jones, Robert
;; APPLICANT: Carter, Darrick
;; APPLICANT: Barth, Brenda
;; APPLICANT: Douglass, John
;; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
;; FILE REFERENCE: 210121.514C1
;; CURRENT APPLICATION NUMBER: PCT/US02/32727
;; CURRENT FILING DATE: 2002-10-11
;; NUMBER OF SEQ ID NOS: 30992
;; SEQ ID NO 9150
;; LENGTH: 93
;; TYPE: PRT
;; ORGANISM: Propionibacterium acnes
PCT-US02-32727-9150

Query Match 52.6%; Score 40; DB 1; Length 93;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGVWDPI 10

Db 10 GGGWDSL 17
|||||:

RESULT 13

US-09-978-825-9150
; Sequence 9150, Application US/09978825
; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shylian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: US/09/978,825

; CURRENT FILING DATE: 2003-01-29

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 9150

; LENGTH: 93

; TYPE: PRT

; ORGANISM: Propioni acnes

US-09-978-825-9150

Query Match 52.6%; Score 40; DB 5; Length 93;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGWDP1 10

Db 10 GGGWDSL 17

|||||:

RESULT 14

US-10-057-498-9150

; Sequence 9150, Application US/10057498

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; FILE REFERENCE: 210121.514

; CURRENT APPLICATION NUMBER: US/10/057,498

; CURRENT FILING DATE: 2001-04-20

; NUMBER OF SEQ ID NOS: 29212

; SEQ ID NO 9150

; LENGTH: 93

; TYPE: PRT

; ORGANISM: Propioni acnes

US-10-057-498-9150

Query Match 52.6%; Score 40; DB 6; Length 93;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGWDP1 10

Db 10 GGGWDSL 17

|||||:

RESULT 15

US-10-156-761-10926

; Sequence 10926, Application US/10156761

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10926
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10926

Query Match 52.6%; Score 40; DB 6; Length 152;
Best Local Similarity 33.3%; Pred. No. 2e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 16; Gaps 1;

QY 1 HTG-----GGWDPID 11

Db 105 HTGGEWTTGGDHWVTPDGLWDPID 131

Search completed: March 13, 2003, 15:29:47
Job time : 5.38462 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:12:09 ; Search time 2.07692 Seconds
(without alignments)
555.443 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_l10

Perfect score: 76

Sequence: 1 HTGGVWDPIDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	61.8	573	2 A41319	3-oxosteroid 1-deh
2	45	59.2	381	2 B97182	acyl-protein synth
3	43	56.6	71	2 A34768	ORF1 protein - Orf
4	43	56.6	304	2 H82984	hypothetical prote
5	43	56.6	435	2 B87412	conserved hypothet
6	43	56.6	536	2 T08241	gas-vesicle operon
7	43	56.6	536	2 S15183	hypothetical prote
8	42.5	55.9	597	2 G75070	hypothetical prote
9	42.5	55.9	598	2 B71095	hypothetical prote
10	42	55.3	255	2 S26020	cytochrome-c oxida
11	41	53.9	42	2 E95061	peptide pheromone
12	41	53.9	182	2 S17005	ATP1 protein - yea
13	40	52.6	114	2 T08411	hypothetical prote
14	40	52.6	158	2 B8498	pts iia protein [i
15	40	52.6	158	2 E72124	pts iia protein -
16	40	52.6	193	2 C82683	disulfide oxidore
17	40	52.6	291	2 E71491	probable geranyl t
18	40	52.6	300	2 F69997	hypothetical prote
19	40	52.6	338	2 H84173	acetoin utilizatio
20	40	52.6	345	2 E90817	hypothetical prote
21	40	52.6	345	2 C90974	hypothetical prote
22	40	52.6	345	2 A85677	unknown protein en
23	40	52.6	345	2 E95821	unknown protein en
24	40	52.6	347	2 F90904	hypothetical prote
25	40	52.6	347	2 G85712	unknown protein en
26	40	52.6	478	1 I47154	transcription fact
27	39	51.3	125	1 B43825	angiogenin - rabbi
28	39	51.3	237	2 A82607	hypothetical prote
29	39	51.3	260	2 C75454	hypothetical prote

30	39	51.3	312	2 T36986	probable ribosylgl
31	39	51.3	370	2 F86338	protein F2D10.2 [i
32	39	51.3	386	2 S74778	hypothetical prote
33	39	51.3	418	2 S42031	LDJ2 protein - lee
34	39	51.3	518	2 S42387	MIPP protein homol
35	39	51.3	524	2 S30575	glycoprotein precu
36	39	51.3	579	2 H88478	protein F47D12.7 [
37	39	51.3	807	2 A32582	protein kinase YAK
38	39	51.3	886	2 T10890	cysteine proteinas
39	39	51.3	1276	2 T02711	probable calmoduli
40	38.5	50.7	265	2 B90506	oxidoreductase, al
41	38.5	50.7	327	2 B75341	probable oxidoredu
42	38.5	50.7	610	2 T24352	hypothetical prote
43	38.5	50.7	1077	2 T01474	hypothetical prote
44	38	50.0	97	2 E83584	hypothetical prote
45	38	50.0	131	2 E75550	probable transposa

ALIGNMENTS

RESULT 1

A41319
3-oxosteroid 1-dehydrogenase (EC 1.3.99.4) - Comamonas testosteroni
C:Species: Comamonas testosteroni
C:Date: 05-Jun-1992 #sequence_revision 28-Apr-1993 #text_change 29-Sep-1999
C:Accession: A41319
R:Plesiat, P.; Grandguillot, M.; Harayama, S.; Vragar, S.; Michel-Briand, Y.
J. Bacteriol. 173, 7219-7227, 1991
A:Title: Cloning, sequencing, and expression of the Pseudomonas testosteroni gene enc
A:Reference number: A41319; MUID:92041619; PMID:1657885
A:Accession: A41319
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <PLE>
A:Cross-references: GB:M68488; NID:G485378; PID:AAA25679.1; PID:G485379
A:Note: the authors translated the codon ACC for residue 497 as Tyr
... C:Superfamily: 3-oxosteroid 1-dehydrogenase; 3-oxosteroid 1-dehydrogenase homology
C:Keywords: oxidoreductase
F:450-548/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>

Query Match 61.8%; Score 47; DB 2; Length 573;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGGVWDPIDY 12
Db :|||:|:|:
47 SGGGIWIPLY 57

RESULT 2

B97182
acyl-protein synthetase, luxE [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: B97182
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; J
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97182
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-381 <KUR>
A:Cross-references: GB:AE001437; PID:AAK80245.1; PID:g15025293; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2288

Query Match 59.2%; Score 45; DB 2; Length 381;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 HTGGGVWD 8
    |||||
Db 223 HTGGGGWD 230

RESULT 3
A34768
ORF1 protein - Orf virus (strain N22)
C:Species: Orf virus
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Oct-1999
C:Accession: A34768
R:Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.
Virology 176, 379-389, 1990
A:Title: Sequence analysis of the inverted terminal repetition in the genome of the para
A:Reference number: A34768; MUID:90266454; PMID:2129563
A:Accession: A34768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <FRA>
A:Cross-references: GB:M30023; EMBL:M37623; NID:g332561; PIDN:AAA46787.1; PID:g332563

Query Match 56.6%; Score 43; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 5.3;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGGVWDPID 11
    :|||:|:
Db .32 SGGIWGPLE 41

RESULT 4
H82984
hypothetical protein PA5284 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H82984
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H82984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <STO>
A:Cross-references: GB:AE004941; GB:AE004091; NID:g9951596; PIDN:RAG08669.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5284

Query Match 56.6%; Score 43; DB 2; Length 304;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGVWDPID 11
    | ||||
Db 75 GSVWDPEVD 82

RESULT 5
B87412
conserved hypothetical protein CCI313 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: B87412
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
```

```
A:Accession: B87412
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <STO>
A:Cross-references: GB:AE005673; NID:g13422654; PIDN:AAK23294.1; GSPDB:GN00148
C:Genetics:
A:Gene: CCI313
```

```
Query Match 56.6%; Score 43; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 HTGGGVWDPI 10
    | || |||
Db 372 HNPGGFWDPL 381
```

```
RESULT 6
T08241
gas-vesicle operon protein gvpD - Halobacterium sp. (strain NRC-1) plasmid pNRC100
N:Alternate names: hypothetical protein H0263
C:Species: Halobacterium sp.
A:Variety: strain NRC-1
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000
R:Ng, W.V.; Ciufu, S.A.; Smith, T.M.; Bungarner, R.E.; Baskin, D.; Faust, J.; Hall, B
Genome Res. 8, 1131-1141, 1998
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid o
A:Reference number: Z16408; MUID:99063795; PMID:9847077
A:Accession: T08241
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-536 <NGW>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822302; HALOSP:H0263
A:Experimental source: strain NRC-1
C:Genetics:
A:Gene: gvpD; HALOSP:H0263
A:Genome: plasmid pNRC100
```

```
Query Match 56.6%; Score 43; DB 2; Length 536;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 TGGGVWDPI 10
    || | |||
Db 247 TGNGTWDPL 255
```

```
RESULT 7
S15183
gas-vesicle operon protein gvpD - Halobacterium salinarum plasmids pHH1 and pNRC100
C:Species: Halobacterium salinarum
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Jan-2000
C:Accession: S15183; S06185
R:Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.
Mol. Microbiol. 5, 1159-1174, 1991
A:Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis
A:Reference number: S15183; MUID:92065812; PMID:1956294
A:Accession: S15183
A:Molecule type: DNA
A:Residues: 1-536 <HOR>
A:Cross-references: EMBL:X55648; NID:g43516; PID:g43517
A:Experimental source: plasmid pHH1
A:Genetics: pHH
A:Note: the authors translated the codon ACG for residue 531 as Ile
R:Jones, J.G.; Hackett, N.R.; Halladay, J.T.; Scothorn, D.J.; Yang, C.F.; Ng, W.L.; D
Nucleic Acids Res. 17, 7785-7793, 1989
A:Title: Analysis of insertion mutants reveals two new genes in the pNRC100 gas vesic
A:Reference number: S06184; MUID:90016863; PMID:2552415
A:Accession: S06185
A:Molecule type: DNA
A:Residues: 1-536 <JON>
```

A;Gene: gvpD
A;Gene: plasmid pNFC100
C;Genetics: <PHH>
A;Gene: gvpD
A;Gene: plasmid pHH1

```
Query Match          56.6%; Score 43; DB 2; Length 536;
Best Local Similarity 66.7%; Pred. NO. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

Qy	2	TGGGVWDPI	10
		:	
Db	247	TGNGTWDPL	255

RESULT 8

G75070

hypothetical protein PAB0644 - *Pyrococcus abyssi* (strain Orsay)

C; Species: *Pyrococcus abyssi*
C.Date: 20-Aug-1999 #Accession

C:\Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:\Accession: G75070

R;anonym, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure. *Reference number:* 375001

A:Reference number: A/3001
A:Accession: G75070

A;Status: preliminary

A;Molecule type: DNA

A; Residues: 1-597 <KAW>

A: Experimental source: strain Oregon
A/Cross-References: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB49868.1; PID:g545838

Experimental source: strain vlsd
C;Genetics:

A;Gene: PAB0644

Query Match

Best Local Similarity 66.7%; Pred. No. 54;

```
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
```

0v 1 HTGGGWNRPDV 12

[illegible]

RESULT 9

B71095

hypothetical protein PH1023 - Pyrococcus horikoshii

C; Species: *pyrococcus horikoshii*
C; Date: 14-Aug-1988 #sequences: 14 #...

C, Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C: Accession: B71095

R; Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekita

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,

DNA Res. 5, 55-76, 1998

A:Reference number: A71000; MIMD:98344137; PMID:9670184

A;Accession: B71095
Reference numbers: AF10000, NCID:30344137, FMD:90/9194

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A;RESIDUES: I-598 <KAW>
A:Cross-references: GR:AP000004. NID:G3226121. DIND:DA030120 1. DTG -0057425

A; Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A; Gene: PHT023

Query Match

Best Local Similarity 66.78; Pred. No. 55;
Score 42.5; DB 2; Length 398;

Matches	8; Conservative	0; Mismatches	3; Indels	1; Gaps
Matches	8; Conservative	0; Mismatches	3; Indels	1; Gaps

Db 22 TGGGLWEDLLY 32
||||:|:|

RESULT 12

S17005

A:HT1 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: activator of hexose transport; protein H9332.3; protein YHR093w

C:Species: Saccharomyces cerevisiae

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 29-Oct-1999

C:Accession: S17005; S46717

R:Oezcan, S.; Cirliacy, M.

submitted to the EMBL Data Library, May 1991

A:Reference number: S17005

A:Accession: S17005

A:Molecule type: DNA

A:Residues: 1-182 <OEZ>

A:Cross-references: EMBL:X59464; NID:g3354; PIDN:CAA42071.1; PID:g663230

A:Experimental source: strain MC 971 B

R:Vaudin, M.

submitted to The EMBL Data Library, May 1994

A:Description: The sequence of S. cerevisiae cosmid 9332.

A:Reference number: S46715

A:Accession: S46717

A:Molecule type: DNA

A:Residues: 1-182 <VAU>

A:Cross-references: EMBL:U00060; NID:g487928; PIDN:AAB68925.1; PID:g487931; MIPS:YHR093w

C:Genetics:

A:Gene: SGD:AHT1

A:Cross-references: SGD:S0001135; MIPS:YHR093w

A:Map position: 8R

C:Superfamily: Saccharomyces AHT1 protein

Query Match 53.9%; Score 41; DB 2; Length 182;

Best Local Similarity 55.6%; Pred. No. 28;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPID 11

|||||:

Db 44 GGGIWGPM 52

RESULT 13

T08411

hypothetical protein F18B3.180 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999

C:Accession: T08411

R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub

submitted to The Protein Sequence Database, May 1999

A:Reference number: Z16409

A:Accession: T08411

A:Molecule type: DNA

A:Residues: 1-114 <QUE>

A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.180

A:Experimental source: cultivar Columbia; BAC clone F18B3

C:Genetics:

A:Gene: ATSP:F18B3.180

A:Map position: 3

C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match

Best Local Similarity 100.0%; Pred. No. 25;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGVWDP 9

|||||

Db 99 GGVWDP 104

RESULT 14

E86498

Pts IIA Protein [imported] - Chlamydomophila pneumoniae (strain J138)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E86498
R:Shiral, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86498
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <STO>
A:Cross-references: GB:BA000008; NID:g8978434; PIDN:BA098271.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: ptsN_1
C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannito

Query Match 52.6%; Score 40; DB 2; Length 158;

Best Local Similarity 63.6%; Pred. No. 35;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11

|||:|:|

Db 92 HTQGILWDAID 102

RESULT 15

E72124

pts iia protein - Chlamydomophila pneumoniae (strain CWL029)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000

C:Accession: E72124

R:Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: E72124

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-158 <ARN>

A:Cross-references: GB:AE001591; GB:AE001363; NID:g4376311; PIDN:AAD18213.1; PID:g437

A:Experimental source: strain CWL029

C:Genetics:

A:Gene: ptsN_1

C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannito

F:28-156/Domain: phosphotransferase system mannitol-specific enzyme II factor III hom

Query Match

Best Local Similarity 63.6%; Pred. No. 35;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTGGGVWDPID 11

|||:|:|

Db 92 HTQGILWDAID 102

Search completed: March 13, 2003, 15:17:53

Job time : 3.07692 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:06:24 ; Search time 1.2 Seconds
(without alignments)
414.763 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_110
Perfect score: 76
Sequence: 1 HTGGGVWDPIDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	47	61.8	573	1	301D_COMTE	Q06401	comonomas t
2	43	56.6	536	1	GVDL_HALN1	P13043	halobacteri
3	43	56.6	1371	1	PUR2_CHITE	Q26255	c trifuncti
4	42	55.3	255	1	COX3_ASCSU	P24879	ascaris suu
5	41	53.9	182	1	AHT1_YEAST	P29589	saccharomyc
6	40	52.6	478	1	OCT2_PIG	Q29013	sus scrofa
7	39	51.3	125	1	ANG1_RABIT	P13147	oryctolagus
8	39	51.3	418	1	DNJ2_ALLPO	P42824	allium porr
9	39	51.3	518	1	YNV6_CAEEL	P34569	caenorhabdi
10	39	51.3	579	1	YR47_CAEEL	Q09563	caenorhabdi
11	39	51.3	807	1	YAK1_YEAST	P14680	saccharomyc
12	39	51.3	868	1	PRTT_PORGI	P43158	porphyromon
13	38	50.0	185	1	EPF_DEIRA	Q9ry32	deinococcus
14	38	50.0	256	1	YM56_YEAST	Q30369	saccharomyc
15	38	50.0	272	1	COX3_PYLII	Q37600	pylaiella l
16	38	50.0	387	1	YR96_YEAST	P38332	saccharomyc
17	38	50.0	420	1	TABA_PSESZ	P31851	pseudomonas
18	38	50.0	447	1	DHE4_CORGL	P31026	corynebacte
19	38	50.0	521	1	GLGA_METJA	Q59001	methanococc
20	38	50.0	643	1	YK09_CAEEL	P34304	caenorhabdi
21	38	50.0	738	1	DHET_ACEPU	P28036	acetobacter
22	38	50.0	739	1	DHET_ACEPU	Q44002	acetobacter
23	38	50.0	943	1	LRPA_NEIMB	Q06379	neisseria m
24	38	50.0	944	1	LRPA_NEIMA	Q9jtk4	neisseria m
25	37.5	49.3	637	1	TRG5_ECOLI	Q00184	escherichia
26	37	48.7	32	1	GHR4_RAT	P33581	rattus norv
27	37	48.7	238	1	PRRC_RAT	P33579	rattus norv
28	37	48.7	242	1	Y252_MVCGE	P47494	mycoplasma
29	37	48.7	344	1	PUR5_ECOLI	P08178	escherichia
30	37	48.7	344	1	PUR5_HAEN	P43848	haemophilus
31	37	48.7	357	1	YFQ8_SCHFO	Q10170	schizosacch
32	37	48.7	382	1	SUCL_ARCFU	Q28732	archaeoglob
33	37	48.7	497	1	ACCD_CUSRE	P31562	cuscuta ref

34	37	48.7	512	1	ACCD_TOBAC	P12219	nicotiana t
35	37	48.7	628	1	BGAL_LACAC	Q07684	lactobacill
36	37	48.7	1014	1	BGAL_BACHD	Q9K9C6	bacillus ha
37	37	48.7	1101	1	GUNC_CELFI	P14090	cellulomona
38	37	48.7	1403	1	VG22_HSVII	Q00105	ictaluriid h
39	36.5	48.0	1025	1	HIRA_FUGRU	Q02611	fugu rubrip
40	36	47.4	87	1	SODC_ACTAC	Q59081	actinobacil
41	36	47.4	115	1	YIDD_MYCPA	Q917M0	mycobacteri
42	36	47.4	120	1	Y3C2_MYCTU	O53600	mycobacteri
43	36	47.4	152	1	ANF_RAT	P01161	rattus norv
44	36	47.4	211	1	NADD_MYCTU	O86328	mycobacteri
45	36	47.4	214	1	NADD_MYCLE	Q9CBZ8	mycobacteri

ALIGNMENTS

RESULT 1
301D_COMTE
ID 301D_COMTE STANDARD; PRT; 573 AA.
AC Q06401;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-oxosteroid 1-dehydrogenase (EC 1.3.99.4).
OS Comonomas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 17410;
RC MEDLINE=92041619; PubMed=1657885;
RA Plesiat P., Grandguillot M., Harayama S., Vragar S., Michel-Briand Y.;
RT "Cloning, sequencing, and expression of the pseudomonas testosteroni
gene encoding 3-oxosteroid delta 1-dehydrogenase.";
RL J. Bacteriol. 173:7219-7227(1991).
CC -!- FUNCTION: DEHYDROGENATES STEROIDS BY INTRODUCING A DOUBLE
BOND IN STEROID RING A.
CC -!- CATALYTIC ACTIVITY: A 3-oxosteroid + acceptor = a 3-oxo-delta(1)-
steroid + reduced acceptor.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: FIRST STEP IN STEROID CATABOLISM.
CC -!- SUBCELLULAR LOCATION: Inner membrane.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC -----
CC EMBL; M68488; AAA25679.1; -;
CC EMBL; A22347; CAA01596.1; -;
CC PIR; A41319; A41319.
KW Oxidoreductase; Flavoprotein; Inner membrane; Steroid metabolism;
KW FAD.
FT NP_BIND 7 36 FAD (BY SIMILARITY).
SQ SEQUENCE 573 AA; 62672 MW; 8E941AF569897734 CRC64;
Query Match 61.8%; Score 47; DB 1; Length 573;
Best Local Similarity 54.5%; Pred. No. 4.4;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGGVWDPIDY 12
Db 47 SGGGIWIPLYN 57
:|||||:|

RESULT 2
GVDL_HALN1 STANDARD; PRT; 536 AA.
ID GVDL_HALN1
AC P13043; Q9H119;

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GvpD protein 1.
 GN (GVPD11 OR GVPD OR VNG5029G) AND (GVPD12 OR VNG6028G).
 OS Halobacterium sp. (strain NRC-1), and
 OS Halobacterium sp. (strain NRC-817).
 OG Plasmid pNRC100, Plasmid pNRC200, and Plasmid pHHL.
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091, 148370;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NRC-1; PLASMID=pNRC100;
 RX MEDLINE=90016863; PubMed=2352415;
 RA Jones J.G., Hackett N.R., Halladay J.T., Scothorn D.J.,
 RA Yang C.-F., Ng W.-L., Dassarma S.;
 RT "Analysis of insertion mutants reveals two new genes in the pNRC100
 RT gas vesicle gene cluster of Halobacterium halobium.";
 RL Nucleic Acids Res. 17:7785-7794(1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NRC-1; PLASMID=pNRC100;
 RX MEDLINE=91323716; PubMed=1864501;
 RA Jones J.G., Young D.C., Dassarma S.;
 RT "Structure and organization of the gas vesicle gene cluster on the
 RT Halobacterium halobium plasmid pNRC100.";
 RL Gene 102:117-122(1991).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NRC-1; PLASMID=pNRC100;
 RX MEDLINE=99063795; PubMed=9847077;
 RA Ng W.V., Clufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faust J.,
 RA Hall B., Loretz C., Seto J., Slagel J., Hood L., Dassarma S.;
 RT "Snapshot of a large dynamic replicon in a halophilic archaeon:
 RT megaplasmid or minichromosome?";
 RL Genome Res. 8:1131-1141(1998).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NRC-1; PLASMID=pNRC200;
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D.A., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlshroder M., Spudis J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
 RT "Genome sequence of Halobacterium species NRC-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NRC-817; PLASMID=pHHL;
 RX MEDLINE=92065812; PubMed=1956294;
 RA Horne M., Englert C., Wimmer C., Pfeifer F.;
 RT "A DNA region of 9 kbp contains all genes necessary for gas vesicle
 RT synthesis in halophilic archaeobacteria.";
 RL Mol. Microbiol. 5:1159-1174(1991).
 CC -1- FUNCTION: MAY PLAY A ROLE IN AN ENERGY REQUIRING PROCESS SUCH AS
 CC ASSEMBLY OF GAS VESICLES IN ADDITION TO A POSSIBLE STRUCTURAL OR
 CC REGULATORY FUNCTION.
 CC -----
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 CC EMBL; X15374; CAA33435.1; -;
 CC EMBL; M58557; AAA98195.1; -;
 DR

DR EMBL; AF016485; AAC82808.1; -;
 DR EMBL; AE005141; AAG20725.1; -;
 DR EMBL; X55648; CAA39171.1; -;
 DR PIR; S06185; S06185.
 DR PIR; S15183; S15183.
 DR KW Gas vesicle; Plasmid; ATP-binding; Complete proteome.
 FT NP_BIND 39 46 ATP (POTENTIAL).
 SQ SEQUENCE 536 AA; 59342 MW; 3FC4E4F8F129F9CD CRC64;
 Query Match 56.6%; Score 43; DB 1; Length 536;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGGGWDPI 10
 Db 247 TGGGTWDP 255
 PUR2_CHITE
 RESULT 3
 ID PUR2_CHITE STANDARD; PRT; 1371 AA.
 AC Q26255;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Trifunctional purine biosynthetic protein adenosine-3 [Includes:
 DE Phosphoribosylamine-glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide
 DE ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase);
 DE Phosphoribosylglycinamide cyclase (EC 6.3.3.1) (AIRS)
 DE (Phosphoribosylglycinamide synthetase) (AIR synthase);
 DE (Phosphoribosyl-aminimidazole synthetase) (AIR synthase);
 DE Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (GART) (GAR
 DE transformylase) (5'-phosphoribosylglycinamide transformylase)].
 GN GART.
 OS Chironomus tentans (Midge).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=7153;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92389368; PubMed=1518084;
 RA Clark D.V., Henikoff S.;
 RT "Unusual organizational features of the Drosophila Gart locus are not
 RT conserved within Diptera.";
 RL J. Mol. Evol. 35:51-59(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + 5-phospho-D-ribosylamine + glycine = ADP
 CC + phosphate + N(1)-(5-phospho-D-ribosyl)glycinamide.
 CC -1- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1)-(5-phospho-D-
 CC ribosyl)glycinamide = tetrahydrofolate + N(2)-formyl-N(1)-(5-
 CC phospho-D-ribosyl)glycinamide.
 CC -1- CATALYTIC ACTIVITY: ATP + 2-(formamido)-N(1)-(5-phospho-D-
 CC ribosyl)acetamide = ADP + phosphate + 5-amino-1-(5-phospho-D-
 CC ribosyl)imidazole.
 CC -1- PATHWAY: SECOND, THIRD AND FIFTH STEPS IN DE NOVO PURINE
 CC BIOSYNTHESIS.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GARS FAMILY.
 CC -1- SIMILARITY: TO OTHER AIRS AND GART FROM BACTERIA AND EUKARYOTES.
 CC -----
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 CC -----
 CC EMBL; S43653; AAB23115.1; -;
 CC HSSP; P08178; ICL1.
 DR InterPro; IPR000728; AIRS_related.
 DR InterPro; IPR001555; GART.
 DR InterPro; IPR000115; Gars.
 DR InterPro; IPR004733; PurM_c1igase.
 DR InterPro; IPR004607; PurN.
 DR

DR InterPro: IPR002376; formyl_transf.
DR Pfam: PF00551; formyl_transf; 1.
DR Pfam: PF00586; AIRS; 2.
DR Pfam: PF01071; GARS; 1.
DR Pfam: PF02769; AIRS_C; 2.
DR Pfam: PF02842; GARS_B; 1.
DR Pfam: PF02843; GARS_C; 1.
DR Pfam: PF02844; GARS_N; 1.
DR TIGRFAMs: TIGR00639; PurN; 1.
DR TIGRFAMs: TIGR00877; purD; 1.
DR TIGRFAMs: TIGR00878; purM; 2.
DR TIGRFAMs: TIGR00879; purM; 2.
DR PROSITE: PS00184; GARS; 1.
DR PROSITE: PS00373; GART; 1.

KW Multifunctional enzyme; Purine biosynthesis; Ligase; Transferase.
FT DOMAIN 1 433 GARS.
FT DOMAIN 434 1171 AIRS.
FT DOMAIN 1172 1371 GART.
FT ACT_SITE 1315 1315 BY SIMILARITY.
SQ SEQUENCE 1371 AA; 149103 MW; 7BF4664DB1538946 CRC64;

Query Match 56.6%; Score 43; DB 1; Length 1371;
Best Local Similarity 77.8%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGGVWDPI 10
||||:|
DB 1057 TGGGLWDNI 1065

RESULT 4

ID COX3_ASCSU STANDARD; PRT; 255 AA.
AC P24879;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide III (EC 1.9.3.1).
GN COIII.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OG Mitochondrion.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body wall muscle, and Egg;
RX MEDLINE=92201635; PubMed=1551572;
RA Okimoto R., Macfarlane J.L., Clary D.O., Wolstenholme D.R.;
RT "The mitochondrial genomes of two nematodes, *Caenorhabditis elegans*
and *Ascaris suum*.";
RL Genetics 130:471-498(1992).
CC -!- FUNCTION: Subunits I, II and III form the functional core of
the enzyme complex.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferrocycytochrome
c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
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CC EMBL; X54253; CAA38169.1; -
DR PIR; S26020; S26020.
DR InterPro: IPR000298; Cytc_oxdse_III.
DR Pfam: PF00510; COX3; 1.
DR ProDom: PD000382; Cytc_oxdse_III; 1.
DR PROSITE: PS50253; COX3; 1.
KW Oxidoreductase; Mitochondrion; Transmembrane.
SQ SEQUENCE 255 AA; 29094 MW; 05A992684AC92755 CRC64;

Query Match 55.3%; Score 42; DB 1; Length 255;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTGGGVWDPI 10
||||:|
DB 106 HDVGGVWSPi 115

RESULT 5

AHT1_YEAST
ID AHT1_YEAST STANDARD; PRT; 182 AA.
AC P29589; P38807;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hexose transport activator protein.
GN AHT1 OR YHR093W
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC 971 B;
RA Oezcan S., Ciriacy M.;
RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
Vaudin M.;
RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome
VIII.";
RL Science 265:2077-2082(1994).
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CC EMBL; X59464; CAA42071.1; -
DR EMBL; U00060; AAB68925.1; -
DR PIR; S17005; S17005.
DR PIR; S46717; S46717.
DR SGD: S0001135; AHT1.
SQ SEQUENCE 182 AA; 19776 MW; 7B0723BAA1066713 CRC64;

Query Match 53.9%; Score 41; DB 1; Length 182;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPI 11
||||:|
DB 44 GGGVWPM 52

RESULT 6

OCY2_PIG
ID OCY2_PIG STANDARD; PRT; 478 AA.
AC Q29013; Q29089;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
Octamer-binding transcription factor 2 (OTF-2) (Lymphoid-restricted
Immunoglobulin octamer binding protein NF-A2) (OTF-2 factor).
POU2F2 OR OTF2 OR OCT2.
OS Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Splice;
RC MEDLINE=95030552; PubMed=7943947;
RA Tuggle C.K., Helm J., Rothschild M.F.;
RT "Cloning, sequencing and restriction fragment length polymorphism
analysis of a porcine cDNA for OCT2.";
RL Anim. Genet. 25:141-145(1994).
[2]
SEQUENCE OF 210-350 FROM N.A.
RP STRAIN=Duroc;
RC MEDLINE=94095558; PubMed=8270542;
RA Tuggle C.K.;
RT "Cloning and sequence analysis of the swine Oct-2 POU-domain genomic
region.";
RL J. Anim. Sci. 71:3172-3172(1993).
CC -1- FUNCTION: THIS PROTEIN IS A TRANSCRIPTION FACTOR THAT SPECIFICALLY
BINDS TO THE OCTAMER MOTIF ('ATTTCAT') AND PLAYS AN IMPORTANT
ROLE IN REGULATING TRANSCRIPTION IN A NUMBER OF TISSUES IN
ADDITION TO ACTIVATING IMMUNOGLOBULIN GENE EXPRESSION (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN B-CELLS (BY
SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
CC CLASS-2 SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.

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CC EMBL; U00794; AAA80148.1; -;
CC EMBL; L03842; AAA74657.1; -;
CC HSP; P09086; 1HDP.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR000972; Octamer-bind_TF.
CC InterPro; IPR000327; POU_domain.
CC Pfam; PF00046; homeobox; 1.
CC Pfam; PF00157; pou; 1.
CC PRINTS; PR00029; OCTAMER.
CC PRINTS; PR00028; POU_DOMAIN.
CC ProDom; PD000010; Homeobox; 1.
CC ProDom; PD000583; POU_domain; 1.
CC SMART; SM00389; HOX; 1.
CC SMART; SM00352; POU; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC PROSITE; PS00035; POU_1; 1.
CC PROSITE; PS00465; POU_2; 1.
CC Homeobox; DNA-binding; Transcription regulation; Activator;
Nuclear protein.
CC DOMAIN 199 269 POU.
CC DNA_BIND 297 356 HOMEBOX.
CC DOMAIN 389 410 LEUCINE-ZIPPER.
CC DOMAIN 77 80 POLY-PRO.
CC DOMAIN 417 424 GLY-RICH.
CC DOMAIN 437 440 POLY-PRO.
CC CONFLICT 212 212 Q -> V (IN REF. 2).
CC CONFLICT 215 215 I -> M (IN REF. 2).
CC CONFLICT 222 222 G -> V (IN REF. 2).

FT CONFLICT 233 233 G -> A (IN REF. 2).
FT CONFLICT 238 238 Q -> K (IN REF. 2).
FT CONFLICT 285 285 R -> S (IN REF. 2).
SQ SEQUENCE 478 AA; 51098 MW; FD196758B603B718 CRC64;
Query Match 52.6%; Score 40; DB 1; Length 478;
Best Local Similarity 54.5%; Pred. No. 47; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 3;
QY 2 TGGGVWDPIDY 12
| | | | | | | | | |
Db 466 TGPGLWNPAPY 476
| | | | | | | | | |
RESULT 7
ANGI_RABIT STANDARD; PRT; 125 AA.
ID ANGI_RABIT
AC P31347; 1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 41, Last annotation update)
DE Angiogenin (EC 3.1.1.27.-).
GN ANG
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
angiotensins: discernment of functionally important residues and
regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
HYDROLYZING CELLULAR TRNAs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC PIR; B43825; B43825.
CC PIR; S29833; S29833.
CC HSP; P03950; 1A4Y.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA_PC; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 13 13 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 114 114 BY SIMILARITY.
FT DISULFID 26 81 BY SIMILARITY.
FT DISULFID 39 92 BY SIMILARITY.
FT DISULFID 57 107 BY SIMILARITY.
SQ SEQUENCE 125 AA; 14361 MW; 3A737E595D767B04 CRC64;
Query Match 51.3%; Score 39; DB 1; Length 125;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 HTGGGVWDPIDY 12
| | | | | | | | | |
Db 83 HVGGSPPPCRY 94
| | | | | | | | | |

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RESULT 8
DNJ2_ALLPO          STANDARD;          PRT;          418 AA.
ID  DNJ2_ALLPO
AC  P42824;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DE  16-OCT-2001 (Rel. 40, Last annotation update)
DE  DnaJ protein homolog 2.
GN  LDJ2.
OS  Allium porrum (Leek).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC  Allium.
OX  NCBI_TaxID=4681;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Bessoule J.J., Testet E., Cassagne C.;
RT  "Cloning of a new isoform of a DnaJ protein from Allium porrum
RL  epidermal cells.";
RL  Plant Physiol. Biochem. 32:723-727(1994).
CC  -!- FUNCTION: HAVE A CONTINUOUS ROLE IN PLANT DEVELOPMENT PROBABLY
CC  IN THE STRUCTURAL ORGANIZATION OF COMPARTMENTS (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC  -!- SIMILARITY: CONTAINS 1 J DOMAIN.
CC  -!- SIMILARITY: CONTAINS 1 CR DOMAIN.
CC  -----
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CC  -----
EMBL: X77632; CAA54720.1; -.
DR  HSSP; P25685; 1HDJ.
DR  InterPro; IPR002939; DnaJ_C.
DR  InterPro; IPR001305; DnaJ_CXXCXGKG.
DR  InterPro; IPR001623; DnaJ_N.
DR  InterPro; IPR003095; Hsp_DnaJ.
DR  Pfam; PF00226; DnaJ; 1.
DR  Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR  Pfam; PF01556; DnaJ_C; 1.
DR  PRINTS; PR00625; DNAJPROTEIN.
DR  SMART; SM00271; DnaJ; 1.
DR  PROSITE; PS00636; DNAJ_1; 1.
DR  PROSITE; PS00637; DNAJ_CXXCXGKG; 1.
DR  PROSITE; PS50076; DNAJ_2; 1.
KW  Chapterone, Repeat; Prenylation; Lipoprotein; Multigene family.
FT  DOMAIN 11 76
FT  J-DOMAIN.
FT  DOMAIN 83 88
FT  POLY-GLY.
FT  DOMAIN 81 108
FT  GLY-RICH.
FT  REPEAT 148 155
FT  CXXCXGKG MOTIF.
FT  REPEAT 164 171
FT  CXXCXGKG MOTIF.
FT  REPEAT 191 198
FT  CXXCXGKG MOTIF.
FT  REPEAT 207 214
FT  CXXCXGKG MOTIF.
FT  Lipid 415 415
FT  FARNESYL (BY SIMILARITY).
SQ  SEQUENCE 418 AA; 46584 MW; DCE2A4DF192329E6 CRC64;

Query Match          51.3%; Score 39; DB 1; Length 418;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3 GGGVWDPID 11
DB  ||||| |||
    85 GGGVHDPFD 93

RESULT 9
YINV6_CAEL
ID  YINV6_CAEL          STANDARD;          PRT;          518 AA.
AC  P34569; P34570;

01-FEB-1994 (Rel. 28, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 59.0 kDa protein F16H12.6 in chromosome III.
F16H12.6
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Smith A.;
RT  Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RL  Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC  -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC  -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC  -----
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CC  -----
EMBL: Z30662; CAA83141.1; -.
DR  PIR; S42387; S42387.
DR  Wormpep; T16H12.6; CE00627.
DR  InterPro; IPR000210; BTB_POZ.
DR  InterPro; IPR001798; Kelch.
DR  Pfam; PF00651; BTB; 1.
DR  Pfam; PF01344; Kelch; 6.
DR  PRINTS; PR00501; KELCHREPEAT.
DR  PROSITE; PS50097; BTB; FALSE_NEG.
KW  Hypothetical protein; Repeat.
FT  DOMAIN 1 98
FT  REPEAT 205 255
FT  BTB.
FT  REPEAT 256 302
FT  KELCH 2.
FT  REPEAT 308 354
FT  KELCH 3.
FT  REPEAT 356 402
FT  KELCH 4.
FT  REPEAT 404 450
FT  KELCH 5.
FT  REPEAT 452 498
FT  KELCH 6.
SQ  SEQUENCE 518 AA; 59036 MW; 117A355F4EAD6A9F CRC64;

Query Match          51.3%; Score 39; DB 1; Length 518;
Best Local Similarity 60.0%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  1 HTGGGVWDPI 10
DB  ||||| |||
    368 HGGGEVYDPV 377

RESULT 10
YR47_CAEL
ID  YR47_CAEL          STANDARD;          PRT;          579 AA.
AC  Q09563;
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Hypothetical 66.0 kDa protein F47D12.7 in chromosome III.
DE  F47D12.7.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  STRAIN-Bristol N2;
RT  Taich A.;
RL  Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC  -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC  -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.

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DR EMBL; U22831; AAK20068.1; -
DR WormPep; F47D12.7; CE01951.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR001798; Kelch.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PSS0097; BTB; 1.
KW Hypothetical protein; Repeat.
FT DOMAIN 51 119
FT REPEAT 266 316
FT REPEAT 317 363
FT REPEAT 369 415
FT REPEAT 417 463
FT REPEAT 465 511
FT REPEAT 513 559
SQ SEQUENCE 579 AA; 66042 MW; 3FE770B5E4C2D32F CRC64;

Query Match 51.3%; Score 39; DB 1; Length 579;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 HTGGGVWDPI 10
I I I I I
Db 429 HQGGEVYDPV 438

RESULT 11
YAKI_YEAST
ID YAKI_YEAST STANDARD; PRT; 807 AA.
AC P14680;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase YAKI (EC 2.7.1.-).
GN YAKI OR YJL141C OR J0652.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90108683; PubMed=2558053;
RA Garrett S., Broach J.;
RT "Loss of Ras activity in Saccharomyces cerevisiae is suppressed by
RT disruptions of a new kinase gene, YAKI, whose product may act
RT downstream of the cAMP-dependent protein kinase.";
RL Genes Dev. 3:1336-1348(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / FY1679;
RX MEDLINE=96408771; PubMed=8813765;
RA Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.;
RT "Sequence analysis of a 40.7 kb segment from the left arm of yeast
RT chromosome X reveals 14 known genes and 13 new open reading frames
RT including homologues of genes clustered on the right arm of
RT chromosome XI".
RL Yeast 12:787-797(1996).
CC -1- FUNCTION: THIS PROTEIN OCCURS IN REVERTANT RAS/CAMP MUTANTS
CC AND MAY BE INVOLVED IN CELL-CYCLE REGULATION.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MNB/DYRK SUBFAMILY.

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DR EMBL; X16056; CAA34192.1; -
DR EMBL; X87371; CAA60814.1; -
DR EMBL; Z49417; CAA89437.1; -
DR PIR; A32582; A32582.
DR HSP; P24941; 1A01.
DR SGD; S0003677; YAK1.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 56 85
FT DOMAIN 369 704
FT NP_BIND 375 383
FT BINDING 398 398
FT ACT_SITE 496 496
FT ACT_SITE 127 127
FT MOD_RES 206 206
FT MOD_RES 240 240
FT MOD_RES 295 295
SQ SEQUENCE 807 AA; 91245 MW; E0B7C56FAA35E056 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 807;
Best Local Similarity 55.6%; Pred. No. 11e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HTGGGVWDPI 9
I I I I I
Db 43 HMGGRGNWP 51

RESULT 12
PRTT_PORGI
ID PRTT_PORGI STANDARD; PRT; 868 AA.
AC P43158;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Thiol protease/hemagglutinin prtT precursor (EC 3.4.22.-).
GN PRTT.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 53977;
RX MEDLINE=93114862; PubMed=8093357;
RA Ologoto J.-I., Kuramitsu H.K.;
RT "Isolation and characterization of the Porphyromonas gingivalis prtT
RT gene, coding for protease activity.";
RL Infect. Immun. 61:117-123(1993).
RN [2]
RP REVISIONS, SEQUENCE FROM N.A.
RC STRAIN=ATCC 53977;
RX MEDLINE=95105001; PubMed=7806362;
RA Madden T.E., Clark V.I., Kuramitsu H.K.;
RT "Revised sequence of the Porphyromonas gingivalis prtT cysteine
RT protease/hemagglutinin gene: homology with streptococcal pyrogenic
RT exotoxin B/streptococcal proteinase.";

```

RL Infect. Immun. 63:238-247(1995).
CC -!- FUNCTION: APPEARS TO BE SPECIFIC FOR ARGinine-CONTAINING PEPTIDE
CC BONDS. POSSESSES HEMAGGLUTININ ACTIVITY. C10.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
CC -----
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CC -----
DR EMBL; M83096; ; NOT_ANNOTATED_CDS.
DR MEROPS; C10.002;
DR InterPro; IPR000200; Peptidase_C10.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01640; Peptidase_C10; 1.
DR PRINTS; PR00797; STREPTOPAIN.
KW Hydrolase; Thiol protease; Signal; Hemagglutinin.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 ? POTENTIAL.
FT CHAIN ? 868 THIOLE PROTEASE/HEMAGGLUTININ PRPT.
FT ACT_SITE 184 184 BY SIMILARITY.
FT ACT_SITE 327 327 BY SIMILARITY.
SQ SEQUENCE 868 AA; 96444 MW; 45436ERE32779323 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 868;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GVVDPID 11
DB 736 GFWDPID 742

RESULT 13
EFP_DEIRA
ID EFP_DEIRA STANDARD; PRT; 185 AA.
AC Q9RY32;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Elongation factor P (EF-P).
GN EFP OR DR0119.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
CX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL;
RA MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RA "Genome sequence of the radioresistant bacterium Deinococcus
RA radiodurans R1."
RL Science 286:1571-1577(1999).
CC -!- FUNCTION: Involved in peptide bond synthesis. Stimulates efficient
CC translation and peptide-bond synthesis on native or reconstituted
CC 70S ribosomes in vitro. Probably functions indirectly by altering
CC the affinity of the ribosome for aminoacyl-tRNA, thus increasing
CC their reactivity as acceptors for peptidyl transferase (By
CC similarity).
CC -!- PATHWAY: Protein biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ELONGATION FACTOR P FAMILY.

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CC -----
DR EMBL; AE001874; AAF09709.1;
DR TIGR; DR01119;
DR InterPro; IPR001059; EF-P.
DR Pfam; PF01132; EFP; 1.
DR TIGRFAMs; TIGR00038; efp; 1.
DR PROSITE; PS01275; EFP; 1.
KW Protein biosynthesis; Elongation factor; Complete proteome.
SQ SEQUENCE 185 AA; 20475 MW; 893FD0850AC102D3 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 185;
Best Local Similarity 55.6%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGVWDPID 12
DB 17 GGLWECLDY 25

RESULT 14
YM56_YEAST
ID YM56_YEAST STANDARD; PRT; 256 AA.
AC Q03691;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Hypothetical 28.9 kDa protein in CLN1-RAD14 intergenic region.
GN YMR200W OR YMR325.01.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 39-256 FROM N.A.
RC STRAIN=S288c / AB972;
RA Odell C., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Z48755; CAA88641.1;
DR SGD; S0004813; YMR200W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 236 256 POTENTIAL.
SQ SEQUENCE 256 AA; 28908 MW; 58C71DF16296B23C CRC64;

Query Match 50.0%; Score 38; DB 1; Length 256;
Best Local Similarity 60.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGGVWDPID 11
DB 44 TGGGFYDPVD 53

RESULT 15
COX3_PYLII
ID COX3_PYLII STANDARD; PRT; 272 AA.
AC Q37600;

```

DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide III (EC 1.9.3.1).
GN COX3.
OS Pylaiella littoralis.
OG Mitochondrion.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pylaiella.
OX NCBI_TaxID=2885;
RN [1]
RP SEQUENCE FROM N.A.
RA Fontaine J.-M., Rousvoal S., Delaroque N., Loiseaux-De Goer S.;
RT "Characterisation of the cox3, nad7 and atp6 genes from the
RT mitochondrial genome of the brown alga Pylaiella littoralis.";
RL Plant Physiol. Biochem. 33:605-609(1995).
CC -!- FUNCTION: Subunits I, II and III form the functional core of
CC the enzyme complex.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
CC
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CC
CC -----
DR EMBL; Z37967; CAA86022.1; -.
DR InterPro; IPR000298; CytC_oxdse_III.
DR Pfam; PF0510; COX3; 1.
DR ProDom; PD000382; CytC_oxdse_III; 1.
DR PROSITE; PS0253; COX3; 1.
KW Oxidoreductase; Mitochondrion; Transmembrane.
SQ SEQUENCE 272 AA; 30628 MW; B9EFF7803A08E8DD CRC64;

Query Match 50.0%; Score 38; DB 1; Length 272;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGWVDPID 11
Db 120 GGWVPPPTD 127
| | | | |
| | | | |

Search completed: March 13, 2003, 15:15:16
Job time : 2.2 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 15:11:14 ; Search time 4.33846 Seconds
(without alignments)
569.918 Million cell updates/sec

Title: US-09-822-698A-3_COPY_99_l10
Perfect score: 76
Sequence: 1 HTGGVWDPIDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	46	60.5	171	13 Q98U44	Q98u44 mantidactyl
2	46	60.5	177	13 Q98U43	Q98u43 aglyptodact
3	46	60.5	177	13 Q98U41	Q98u41 boophis tep
4	46	60.5	177	13 Q98U33	Q98u33 nyctibatrac
5	46	60.5	177	13 Q98U32	Q98u32 nyctibatrac
6	46	60.5	177	13 Q98U26	Q98u26 micrixalus
7	46	60.5	177	13 Q98U25	Q98u25 micrixalus
8	46	60.5	177	13 Q98U24	Q98u24 indirana sp
9	46	60.5	177	13 Q98U20	Q98u20 philautus m
10	46	60.5	177	13 Q98U19	Q98u19 philautus w
11	45	59.2	131	4 Q8WXY0	Q8wxy0 homo sapien
12	45	59.2	177	13 Q98U42	Q98u42 boophis xer
13	45	59.2	177	13 Q98U21	Q98u21 rhacophorus
14	45	59.2	381	16 Q97GS7	Q97gs7 clostridium
15	44	57.9	489	2 P72455	P72455 streptomyce
16	43.5	57.2	762	2 Q9RM63	Q9rm63 myroides od

17	43	56.6	51	2	Q9F2F8	Q9f2f8 streptococ
18	43	56.6	71	12	Q85298	Q85298 orf virus.
19	43	56.6	102	2	Q9LCA9	Q9lca9 rhodocyclus
20	43	56.6	304	16	Q9HTS0	Q9hts0 pseudomonas
21	43	56.6	435	16	Q9A8P0	Q9a8p0 caulobacter
22	43	56.6	762	2	Q9RQ15	Q9rq15 neisseria d
23	42.5	55.9	597	17	Q9V038	Q9v038 pyrococcus
24	42.5	55.9	597	17	Q8U2G5	Q8u2g5 pyrococcus
25	42.5	55.9	598	17	O58774	O58774 pyrococcus
26	42	55.3	174	13	Q98U45	Q98u45 mantella ma
27	42	55.3	458	10	Q8RU64	Q8ru64 oryza sativ
28	42	55.3	502	16	Q8Y012	Q8y012 raistonia s
29	41	53.9	42	16	Q9ETQ9	Q9etq9 streptococ
30	41	53.9	324	10	Q9LVW5	Q9lvw5 arabidopsis
31	41	53.9	801	16	Q8XV55	Q8xv55 ralstonia s
32	41	53.9	1456	2	Q9F636	Q9f636 stigmatella
33	40.5	53.3	181	10	Q9C5D5	Q9c5d5 arabidopsis
34	40.5	53.3	388	10	Q9M8R4	Q9m8r4 arabidopsis
35	40	52.6	114	10	Q9SVK9	Q9svk9 arabidopsis
36	40	52.6	158	16	Q9Z9C1	Q9z9c1 chlamydia p
37	40	52.6	176	13	Q98U40	Q98u40 laliostoma
38	40	52.6	177	13	Q98U31	Q98u31 limonectes
39	40	52.6	177	13	Q98U23	Q98u23 indirana sp
40	40	52.6	177	13	Q98U18	Q98u18 philautus c
41	40	52.6	193	16	Q9PDE3	Q9pde3 xylella fas
42	40	52.6	197	2	Q8VNU8	Q8vnu8 chromatium m
43	40	52.6	259	16	Q9ZQ67	Q9zq67 rhizobium m
44	40	52.6	291	16	O84633	O84633 chlamydia t
45	40	52.6	300	16	O34430	O34430 bacillus su

ALIGNMENTS

RESULT 1

Q98U44	ID	Q98U44	PRELIMINARY;	PRT;	171 AA.
AC	Q98U44:				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE	Tyrosinase (Fragment).				
OS	Mantidactylus cf. ulcerosus.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rhacophoridae;				
OC	Mantidactylus.				
OX	NCBI_TaxID=129014;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Bossuyt F.; Milinkovitch M.C.;				
RT	"Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs				
RT	Reveal Co-variation between Larval and Adult Traits.";				
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL:	AF249165;	AAG49808.1;	-	
DR	InterPro:	IPR000561;	EGF-like.		
DR	InterPro:	IPR002049;	Laminin_EGF.		
DR	InterPro:	IPR002227;	Tyrosinase.		
DR	PFam:	PF00264;	tyrosinase;	1.	
DR	PROSITE:	PS00022;	EGF_1;	UNKNOWN_1.	
DR	PROSITE:	PS01248;	LAMININ_TYPE_EGF;	UNKNOWN_1.	
DR	PROSITE:	PS00497;	TYROSINASE_1;	1.	
FT	NON_TER	1			
FT	NON_TER	171			
SQ	SEQUENCE	171 AA;	19816 MW;	50CEFA8130D2A7B CRC64;	

Query Match 60.5%; Score 46; DB 13; Length 171;

Best Local Similarity 70.0%; Pred. No. 9.4;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12

|||||

Db 133 GGGVWENIDF 142

```
RESULT 2
Q98043 ID Q98043 PRELIMINARY; PRT; 177 AA.
AC Q98043;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tyrosinase (Fragment).
OS Aglyptodactylus madagascariensis (Madagascar jumping frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Aglyptodactylus
OX NCBI_TaxID=68424;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249166; AAG49809.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20410 MW; A4E5A34F90563FF1 CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
DB 133 GGGVWENIDF 142

RESULT 3
Q98041 ID Q98041 PRELIMINARY; PRT; 177 AA.
AC Q98041;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Boophis tephraeomystax.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Boophis.
OX NCBI_TaxID=68440;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249168; AAG49811.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20542 MW; 22C28DBB1217467B CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
```

```
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
DB 133 GGGVWENIDF 142

RESULT 4
Q98033 ID Q98033 PRELIMINARY; PRT; 177 AA.
AC Q98033;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Nyctibatrachus major.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Nyctibatrachus.
OX NCBI_TaxID=129023;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249176; AAG49819.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20589 MW; 1B647613316D7C42 CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
DB 133 GGGVWENIDF 142

RESULT 5
Q98032 ID Q98032 PRELIMINARY; PRT; 177 AA.
AC Q98032;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Nyctibatrachus alliciae.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Nyctibatrachus.
OX NCBI_TaxID=129021;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249177; AAG49820.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
```


DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS00497; TYROSINASE_1; UNKNOWN_1.
 FT NON_TER 1 177
 FT NON_TER 177 177
 SQ SEQUENCE 177 AA; 20556 MW; 2C67161CDF6FB392 CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 9.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
 Db 133 GGGVWENIDF 142

RESULT 6
 ID Q98U26 PRELIMINARY; PRT; 177 AA.

AC Q98U26;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Micrixalus fuscus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Micrixalus.
 OC NCBI_TaxID=129016;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249183; AAG49826.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 FT NON_TER 1 177
 FT NON_TER 177 177
 SQ SEQUENCE 177 AA; 20560 MW; A76738DA4102C9CE CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 9.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
 Db 133 GGGVWENIDF 142

RESULT 7
 ID Q98U25 PRELIMINARY; PRT; 177 AA.

AC Q98U25;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Micrixalus kottigeharensis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Micrixalus.
 OC NCBI_TaxID=130786;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs

RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF249184; AAG49827.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 FT NON_TER 1 177
 FT NON_TER 177 177
 SQ SEQUENCE 177 AA; 20574 MW; 05A658678D3BF9D4 CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 9.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
 Db 133 GGGVWENIDF 142

RESULT 8
 ID Q98U24 PRELIMINARY; PRT; 177 AA.

AC Q98U24;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Indirana sp. 1.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Indirana.
 OC NCBI_TaxID=147865;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bossuyt F., Milinkovitch M.C.;
 RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
 RT Reveal Co-variation between Larval and Adult Traits.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249185; AAG49828.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR002227; Tyrosinase.
 DR Pfam; PF00264; tyrosinase; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 FT NON_TER 1 177
 FT NON_TER 177 177
 SQ SEQUENCE 177 AA; 20434 MW; 29EB35222BA6D60B CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
 Best Local Similarity 70.0%; Pred. No. 9.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
 Db 133 GGGVWENIDF 142

RESULT 9
 ID Q98U20 PRELIMINARY; PRT; 177 AA.

AC Q98U20;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tyrosinase (Fragment).
 OS Philautus microtypanum.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Philautus.
OX NCBI_TaxID=129024;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249189; AAG49832.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR SMART; SM00001; EGF-like; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20464 MW; 4E2C1654EA212ADE CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12
Db 133 GGGWENIDF 142
|||||: ||:

RESULT 10
Q98U19 PRELIMINARY; PRT; 177 AA.
AC Q98U19;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Philautus wynaadensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Philautus.
OX NCBI_TaxID=130794;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249190; AAG49833.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20516 MW; 51214062A983B9DE CRC64;

Query Match 60.5%; Score 46; DB 13; Length 177;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12
Db 133 GGGWENIDF 142
|||||: ||:

RESULT 11
Q8WYU PRELIMINARY; PRT; 177 AA.
```

```
ID Q8WYU PRELIMINARY; PRT; 131 AA.
AC Q8WYU;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 13.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289615; AAL55799.1; -.
DR Hypothetical protein.
KW SEQUENCE 131 AA; 13879 MW; B1D6A5917F3608ED CRC64;

Query Match 59.2%; Score 45; DB 4; Length 131;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGVWDP 9
Db 40 TGGGVWQP 47
|||||: |

RESULT 12
Q98U42 PRELIMINARY; PRT; 177 AA.
AC Q98U42;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Boophis xerophilus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Boophis.
OX NCBI_TaxID=128996;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249167; AAG49810.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20587 MW; DB6493AF16D0F020 CRC64;

Query Match 59.2%; Score 45; DB 13; Length 177;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGVWDPIDY 12
Db 133 GGGWENIDF 142
|||||: ||:

RESULT 13
Q98U21 PRELIMINARY; PRT; 177 AA.
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AC Q98U21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Rhacophorus malabaricus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
OC Rhacophorus.
OX NCBI_TaxID=129031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bossuyt F., Milinkovitch M.C.;
RT "Convergent Adaptive Radiations in Madagascar and Asian Ranid Frogs
RT Reveal Co-variation between Larval and Adult Traits.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF249188; AAG49831.1; -.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR002227; Tyrosinase.
DR Pfam: PF00264; tyrosinase; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE: PS00497; TYROSINASE_1; 1.
FT NON_TER 1
FT NON_TER 177
SQ SEQUENCE 177 AA; 20426 MW; 16A9E9F4F1BE2035 CRC64;

Query Match 59.2%; Score 45; DB 13; Length 177;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGVWDPIDY 12
   |||||:|:
Db 133 GGGVWVDF 142

RESULT 14
Q97GS7
ID Q97GS7 PRELIMINARY; PRT; 381 AA.
AC Q97GS7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Acyl-protein synthetase, luxE.
GN CAC2288.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007729; AAK80245.1; -.
KW Complete proteome.
SQ SEQUENCE 381 AA; 43104 MW; 68D0790AC06AA70 CRC64;

Query Match 59.2%; Score 45; DB 16; Length 381;
Best Local Similarity 87.5%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTGGGVWD 8
   |||||
Db 223 HTGGGVWD 230
```

```
RESULT 15
P72455
ID P72455 PRELIMINARY; PRT; 489 AA.
AC P72455;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NADH:N-amidino-scylo-inosamine oxidoreductase.
GN STSB.
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=97385085; PubMed=9238101;
RA Ahlert J., Distler J., Mansouri K., Piepersberg W.;
RT "Identification of stsc, the gene encoding the L-glutamine:scyllo-
RT inosose aminotransferase from streptomycin-producing Streptomyces.";
RL Arch. Microbiol. 168:102-113(1997).
DR EMBL: Y08763; CAA70011.1; -.
DR InterPro: IPR000205; NAD_binding.
SQ SEQUENCE 489 AA; 51576 MW; 73B6863C3FAA3C93 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 489;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGGVWDP 9
   :|||:|
Db 166 SGGGLWDP 173

Search completed: March 13, 2003, 15:17:01
Job time : 5.33846 secs
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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:04 ; Search time 20.076 Seconds
(without alignments)
1460.205 Million cell updates/sec

Title: US-09-822-698A-24
Perfect score: 1146
Sequence: 1 EIVLQSPSLPVTGPEPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
A_Geneseq_101002.*			
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1146	100.0	220	AAE12714	Human recombinant
2	1073.5	93.7	239	AA82615	Human PTHrP monocl
3	1069.5	93.0	239	AA82616	Human PTHrP monocl
4	1065.5	93.0	239	AA82617	Human PTHrP monocl
5	1058.5	92.4	239	AA82611	Human PTHrP monocl
6	1053.5	91.9	239	AA82610	Human PTHrP monocl
7	1048.5	91.5	239	AA82614	Human PTHrP monocl
8	1034.5	90.3	239	AA82612	Human PTHrP monocl
9	1034.5	90.3	239	AA82613	Human PTHrP monocl
10	1031.5	90.0	239	AA82619	Human PTHrP monocl

11	1021.5	89.1	239	21	AA82618	Human PTHrP monocl
12	1015.5	88.6	238	22	AA82617	Humanised 323/A3 (
13	1015.5	88.6	238	22	AA82616	Humanised 323/A3 (
14	1015.5	88.6	238	22	AA82615	Humanised 323/A3 (
15	1015.5	88.6	238	22	AA82614	Humanised 323/A3 (
16	992.5	86.6	239	18	AAW01819	Primate anti-hu
17	992.5	86.6	239	19	AAW01876	Anti-human Fas hu
18	992.5	86.6	239	19	AAW01878	Anti-human Fas hu
19	992.5	86.6	239	19	AAW01878	Macaque primatized
20	992.5	86.6	239	21	AA812913	Anti-human Fas imm
21	992.5	86.6	239	21	AA812915	Anti-human Fas imm
22	992.5	86.6	239	23	AAU11540	Protein sequence o
23	988.5	86.3	239	19	AAW01877	Anti-human Fas hu
24	988.5	86.3	239	19	AAW01879	Anti-human Fas hu
25	988.5	86.3	239	21	AA812914	Anti-human Fas imm
26	988.5	86.3	239	21	AA812916	Anti-human Fas imm
27	987.5	86.2	238	22	AAU07744	Humanised monoclon
28	987	86.1	238	17	AA82615	Monoclonal antibod
29	986.5	86.1	238	18	AAW14942	3P4 Human IgG4 exp
30	986.5	86.1	238	18	AAW14937	Murine anti-porcine
31	978.5	85.4	238	22	AAE03754	Chimeric 2403 IgG
32	974.5	85.0	239	21	AAU07288	Protein #1 in inve
33	971	84.7	228	23	AAE20274	Human lung specifi
34	963.5	84.1	241	21	AA82615	Human IGFAM-15 imm
35	952.5	83.1	242	16	AA82615	Chimeric 6G4.2.5.1
36	952.5	83.1	242	18	AAW42323	Murine variable re
37	952.5	83.1	242	18	AAW42323	Chimeric anti IL-8
38	952.5	83.1	242	18	AAW23790	Chimeric monoclon
39	952.5	83.1	242	19	AAW69311	Anti-IL-8 mouse-hu
40	952.5	83.1	242	19	AAW40126	Chimeric Mab 6G4.2
41	952.5	83.1	242	19	AAW3745	Chimeric anti IL-8
42	952.5	83.1	242	20	AAW29442	Chimeric 6G4.2.5.1
43	952.5	83.1	242	21	AA82615	Murine 6G4-2.5 ant
44	952.5	83.1	242	21	AAW77748	Chimeric 6G4.2.5 a
45	929	81.1	218	22	AAE03756	Chimeric antibody

ALIGNMENTS

RESULT 1	
AAE12714	AAE12714 standard; Protein; 220 AA.
ID	AAE12714 standard; Protein; 220 AA.
XX	AAE12714;
AC	AC
XX	04-JAN-2002 (first entry)
DT	04-JAN-2002 (first entry)
XX	Human recombinant immunoglobulin (Ig) light chain region.
DE	Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX	light chain region; cancer; breast; ovary; lung; bladder;
KW	cytostatic; therapy; immunoglobulin; Ig.
KW	cytostatic; therapy; immunoglobulin; Ig.
XX	XX
OS	Homo sapiens.
XX	XX
FN	WO200175110-A2.
XX	XX
PD	11-OCT-2001.
XX	XX
PF	30-MAR-2001; 2001WO-US10589.
XX	XX
PR	30-MAR-2000; 2000US-0538913.
XX	XX
FA	(DYAX-) DYAX CORP.
XX	XX
PI	Hoogenboom HRJM, Henderikx MPG;
XX	XX
DR	WPI: 2001-626437/72.
DR	N-PSDB; AAD20744.
XX	XX
PT	Novel isolated tumor-associated antigen mucin-1-specific binding member
PT	for diagnosing and treating cancer, comprises mucin-1 binding domain or

its portion for binding to an epitope of the protein core of mucin-1 -
Claim 12; Page 103; 126pp; English.

The invention relates to an isolated tumour-associated antigen mucin-1 (MUC-1)-specific binding member comprising an antigen binding domain region having an antibody variable light (VL) or heavy (VH) region, or a complementarity determining region (CDR) of VL or VH. MUC1-specific binding member is useful for diagnosing cancer, preferably adenocarcinoma. The binding of MUC1-specific binding member to MUC1 is detected by a detection method selected from enzyme-linked immunosorbent assay, magnetic resonance imaging, scintillation counting, and x-ray film.

MUC1-specific binding member is useful for treating cancer, preferably adenocarcinoma, in an individual, where the cancer is present in tissue of the breast, ovary, lung, or bladder of the individual. MUC1-specific binding member is useful for diagnosing and imaging MUC1-expressing cancer cells and tissues, for purifying or isolating non-glycosylated, underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-containing molecules, and for therapeutically or prophylactically treating cancer. The present sequence is human recombinant immunoglobulin (IgA) light chain region (variable VL and CL constant kappa light chain).

xx	Sequence	220	AA;	Query Match	100.0%;	Score	1146;	DB	22;	Length	220;
SQ				Best Local Similarity	100.0%;	Pred. NO.	3e-70;				
				Matches	220;	Conservative					
						Mismatches	0;			Indels	0;
						Gaps	0;				

[illegible]

RESULT 2	AA	PROTEIN	SEQUENCE
XX	AY82615	standard; Protein; 239 AA.	
XX	XX		
XX	AC		
XX	AY82615;		
DT	02-AUG-2000	(first entry)	
DE	XX	Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.	
XX	XX		
KW	Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;		
KW	hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;		
KW	fracture; cachexia; tooth disease; periodontal disease; gingiva;		
KW	sepsis; systemic inflammatory response syndrome; SIRS;		
KW	hypercholesterolaemia; antiarthritis; cytostatic; antiinflammatory.		

XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Misc-difference
FT	Location/Qualifiers 155
XX	/note= "possible Ala"
PN	JP2000080100-A.
XX	
PD	21-MAR-2000.
XX	
PF	12-OCT-1998;
XX	98JP-0304793.

PR	17-JUN-1998;	98JP-0188196.
PR	26-JUN-1998;	98JP-0196729.
XX		
XX	(NISB) JAPAN TOBACCO INC.	
XX		
DR	WPI: 2000-286723/25.	
DR	N-PSDB; AAL13925.	
XX		
PT	A human monoclonal antibody to parathyroid hormone related protein. -	
PT	useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone	
PT	including metastasis, and pain	
XX		
PS	Claim 31; Page 45-46; 88pp; Japanese.	
XX		
CC	The present invention describes a human monoclonal antibody to	
CC	parathyroid hormone related protein (PTHrP). The monoclonal antibody or	
CC	its fragments, following the stimulation of PTHrP has the following	
CC	properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits	
CC	the release of calcium from bone; or (c) inhibits elevation of blood	
CC	calcium content. The monoclonal antibody can be used in the treatment	
CC	of hypercalcemia, rheumatoid arthritis, cancer of bone including	
CC	metastasis, pain, fracture, cachexia, diseases of teeth, periodontal	
CC	diseases and gingivitis, sepsis, systemic inflammatory response syndrome	
CC	(SIRS) and hypophosphatemia. It has antiarthritic, cytostatic and	
CC	antiinflammatory activities. The present sequence represents a	
CC	human PTHrP monoclonal antibody clone protein sequence from the	
CC	present invention.	
XX		
XX	Sequence 239 AA;	
SO		

Query Match	93.78%	Score 1073.5;	DB 21;	Length 239;
Best Local Similarity	94.1%;	Prod. No. 2.7e-65;		
Matches 207;	Conservative	6;	Mismatches	6;
			Indels	1;
			Gaps	1;
Qy	1	EVIVTQSPLSLVPTGPEPASISCRSSQSLLSNGVYTLDWLQKPGSQPOLLIYSGSHRA	60	
	:			
Db	21	DIVMTQSPLSLVPTGPEPASISCRSSQSLLSNGVYTLDWLQKPGSQPOLLIYSGSHRA	80	
	:			
Qy	61	SGVPDRFSGSYSGDTFTLIRISRVEAEDGVYVYCMQGLQSPTEFGPTKVDIKRGTVAAAPS	120	
	:			
Db	81	SGVPDRFSGSYSGDTFTLIRISRVEAEDGVYVYCMQGLQSPTEFGPTKVDIKR-TVAAAPS	139	
	:			
Qy	121	VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS	180	
	:			
Db	140	VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS	199	
	:			
Qy	181	LSSTLTLSKADYERHKVYACEVTHQGLSPVTTKSFNRGEC	220	
	:			
Db	200	LSSTLTLSKADYERHKVYACEVTHQGLSPVTTKSFNRGEC	239	
	:			

RESULT 3	
AAV82616	AAV82616 standard; Protein; 239 AA.
XX	ID
XX	AC
XX	AAV82616;
DT	02-AUG-2000 (first entry)
XX	Human PTHrP monoclonal antibody clone 2c4-12-20 protein SEQ ID NO:16.
DE	
XX	Human; parathyroid hormone related protein; PTHrP; monoclonal antibody
KW	hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW	fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW	sepsis; systemic inflammatory response syndrome; SIRS;
KW	hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Misc-difference 5
FT	/label= Val, Ala, Asp, Gly
FT	Misc-difference 13

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FT FT Misc-difference 25 /note= "possibly Leu"
FT FT /label= Ile, Thr, Asn, Ser
FT FT Misc-difference 27 /label= Phe, Thr, Tyr, Cys
FT FT /label= Phe, Ser, Tyr, Cys
FT FT Misc-difference 216 /note= "possible Val"
FT FT
XX PN JP2000080100-A.
XX PD 21-MAR-2000.
XX PF 12-OCT-1998; 98JP-0304793.
XX PR 17-JUN-1998; 98JP-0188196.
XX PR 26-JUN-1998; 98JP-0196729.
XX PA (NISR ) JAPAN TOBACCO INC.
XX XX WPI; 2000-286723/25.
XX DR N-PSDB; AAA13926.
XX
XX A human monoclonal antibody to parathyroid hormone related protein. -
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Claim 31; Page 48-49; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
XX
XX Query Match 93.3%; Score 1069.5; DB 21; Length 239;
XX Best Local Similarity 93.6%; Pred. No. 4.9e-65;
XX Matches 206; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
XX
XX QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
XX DB 21 DIVMXQXPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYLSNRA 80
XX
XX QY 61 SGVPDRFSGSGVTDFTLRISVEAEDGVVYCMQGLQSPFTFGTKVDIKRGTVAAPS 120
XX DB 81 SGVPDRFSGSGVTDFTLRISVEAEDGVVYCMQALQTPFTFGTKVDIKR-TVAAPS 139
XX
XX QY 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180
XX DB 140 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 199
XX
XX QY 181 LSLTSLTKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 220
XX DB 200 LSLTSLTKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 239
XX
XX RESULT 4
XX ID AAY82617
XX AC AAY82617;
XX DT 02-AUG-2000 (first entry)
XX

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DE XX Human PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.
KW KW Hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW KW sepsis; systemic inflammatory response syndrome; SIRS;
KW KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 3 /label= Phe, Leu, Ile, Val
XX FT Misc-difference 4 /label= Leu, Pro, His, Arg
XX FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
XX FT Misc-difference 117 /label= Leu, Ile, Val
XX PN JP2000080100-A.
XX PD 21-MAR-2000.
XX PF 12-OCT-1998; 98JP-0304793.
XX PR 17-JUN-1998; 98JP-0188196.
XX PR 26-JUN-1998; 98JP-0196729.
XX PA (NISR ) JAPAN TOBACCO INC.
XX XX WPI; 2000-286723/25.
XX DR N-PSDB; AAA13927.
XX
XX A human monoclonal antibody to parathyroid hormone related protein. -
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Claim 31; Page 51-52; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
XX
XX Query Match 93.0%; Score 1065.5; DB 21; Length 239;
XX Best Local Similarity 93.6%; Pred. No. 9.2e-65;
XX Matches 206; Conservative 5; Mismatches 8; Indels 1; Gaps 1;
XX
XX QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
XX DB 21 DIVMXQXPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYLSNRA 80
XX
XX QY 61 SGVPDRFSGSGVTDFTLRISVEAEDGVVYCMQGLQSPFTFGTKVDIKRGTVAAPS 120
XX DB 81 SGVPDRFSGSGVTDFTLRISVEAEDGVVYCMQAXQTPTFTFGTKVDIKR-TVAAPS 139
XX
XX QY 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180
XX DB 140 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 199
XX
XX QY 181 LSLTSLTKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 220

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Db	200	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	239
RESULT 5			
AY82611			
ID	AY82611	standard; Protein; 239 AA.	
XX	AY82611;		
AC	AY82611;		
DT	02-AUG-2000	(first entry)	
XX	Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.		
DE	Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;		
XX	hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;		
KW	fracture; cachexia; tooth disease; periodontal disease; gingiva;		
KW	sepsis; systemic inflammatory response syndrome; SIRS;		
KW	hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	JP2000080100-A.		
PN	21-MAR-2000.		
XX	12-OCT-1998; 98JP-0304793.		
XX	17-JUN-1998; 98JP-0188196.		
PR	26-JUN-1998; 98JP-0196729.		
XX	(NISR) JAPAN TOBACCO INC.		
XX	WPI: 2000-286723/25.		
DR	N-PSDB; AAA13921.		
XX	A human monoclonal antibody to parathyroid hormone related protein.		
PT	useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone		
PT	including metastasis, and pain		
XX	Claim 31; Page 34-35; 88pp; Japanese.		
XX	The present invention describes a human monoclonal antibody to		
CC	parathyroid hormone related protein (PTHrP). The monoclonal antibody or		
CC	its fragments, following the stimulation of PTHrP has the following		
CC	properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits		
CC	the release of calcium from bone; or (c) inhibits elevation of blood		
CC	calcium content. The monoclonal antibody can be used in the treatment		
CC	of hypercalcaemia, rheumatoid arthritis, cancer of bone including		
CC	metastasis, pain, fracture, cachexia, diseases of teeth, periodontal		
CC	diseases and gingiva, sepsis, systemic inflammatory response syndrome		
CC	(SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and		
CC	antiinflammatory activities. The present sequence represents a		
CC	human PTHrP monoclonal antibody clone protein sequence from the		
XX	present invention.		
XX	Sequence 239 AA;		
Query Match	92.4%;	Score 1058.5; DB 21; Length 239;	
Best Local Similarity	92.7%;	Pred. No. 2,7e-64;	
Matches	204; Conservative	8; Mismatches 7; Indels 1; Gaps 1;	
Qy	1	EIVLTQSPSLPVTGPEPASTICRSSQSLHNSGYTYLDWYLRKPGSQPOLLYSGSHRA	60
Db	21	DIWMTQSPSLPVTGPEPATISCRSSQSLHNRNNTLDWFLQKPGSQPOLLYLGSNRA	80
Qy	61	SGVPRFSGSVSGDTFTLRISRVRAEDGVYVCMQGLQSPETFGTKVDIKRGTVAAPS	120
Db	81	SGVPRFSGSGSGDFTLKLRSRVAEDVGLYCMQALQIPFTFGTKVDIKR-TVAAPS	139
Qy	121	VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEFQDSKDSYS	180
Db	140	VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEFQDSKDSYS	199

Qy	181	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	220
Db	200	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	239
RESULT 6			
AY82610			
ID	AY82610	standard; Protein; 239 AA.	
XX	AY82610;		
AC	AY82610;		
DT	02-AUG-2000	(first entry)	
XX	Human PTHrP monoclonal antibody clone 15H7-8-3 protein SEQ ID NO:4.		
DE	Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;		
XX	hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;		
KW	fracture; cachexia; tooth disease; periodontal disease; gingiva;		
KW	sepsis; systemic inflammatory response syndrome; SIRS;		
KW	hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	JP2000080100-A.		
PN	21-MAR-2000.		
XX	12-OCT-1998; 98JP-0304793.		
XX	17-JUN-1998; 98JP-0188196.		
PR	26-JUN-1998; 98JP-0196729.		
XX	(NISR) JAPAN TOBACCO INC.		
XX	WPI: 2000-286723/25.		
DR	N-PSDB; AAA13920.		
XX	A human monoclonal antibody to parathyroid hormone related protein.		
PT	useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone		
PT	including metastasis, and pain		
XX	Claim 31; Page 33; 88pp; Japanese.		
XX	The present invention describes a human monoclonal antibody to		
CC	parathyroid hormone related protein (PTHrP). The monoclonal antibody or		
CC	its fragments, following the stimulation of PTHrP has the following		
CC	properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits		
CC	the release of calcium from bone; or (c) inhibits elevation of blood		
CC	calcium content. The monoclonal antibody can be used in the treatment		
CC	of hypercalcaemia, rheumatoid arthritis, cancer of bone including		
CC	metastasis, pain, fracture, cachexia, diseases of teeth, periodontal		
CC	diseases and gingiva, sepsis, systemic inflammatory response syndrome		
CC	(SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and		
CC	antiinflammatory activities. The present sequence represents a		
CC	human PTHrP monoclonal antibody clone protein sequence from the		
XX	present invention.		
XX	Sequence 239 AA;		
Query Match	91.9%;	Score 1053.5; DB 21; Length 239;	
Best Local Similarity	92.7%;	Pred. No. 6e-64;	
Matches	204; Conservative	5; Mismatches 10; Indels 1; Gaps 1;	
Qy	1	EIVLTQSPSLPVTGPEPASICRSSQSLHNSGYTYLDWYLRKPGSQPOLLYSGSHRA	60

Db 21 DIVMTQXPLSLPVTGPEPASISCRFSQSLHSGNNYLDWLQKPGSQPQLIYLGSNRA 80
QY 61 SGVPRDFSGSVSGTDFTLIRISVEAEDGVYVCMQGLQSPFTFGTGVKIDIKRGTVAAPS 120
Db 81 SGVPRDFSGSVSGTDFTLIRISVEAEDGVYVCMQGLQSPFTFGTGVKIDIKR-TVAAPS 139
QY 121 VFIFPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 140 VFIFPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7
AAY82614
ID AAY82614 standard; Protein; 239 AA.
XX AC AAY82614;
XX DT 02-AUG-2000 (first entry)
XX DE Human PTHrP monoclonal antibody clone 2F8-10-3 protein SEQ ID NO:12.
XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Misc-difference 25 /label= Ile, Thr, Asn, Ser
FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 117 /label= Leu, Ile, Val
FT Misc-difference 146 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 216 /note= "possible Val"
XX PN JP2000080100-A.
XX PD 21-MAR-2000.
XX PF 12-OCT-1998; 98JP-0304793.
XX PR 17-JUN-1998; 98JP-0188196.
XX PS 26-JUN-1998; 98JP-0196729.
XX PA (NISR) JAPAN TOBACCO INC.
XX PN WPI; 2000-286723/25.
XX DR N-PSDB; AAA13924.

XX A human monoclonal antibody to parathyroid hormone related protein. -
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX Claim 31; Page 43; 88pp; Japanese.
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including

CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX SQ Sequence 239 AA;
Query Match 91.5%; Score 1048.5; DB 21; Length 239;
Best Local Similarity 92.3%; Pred. No. 1.3e-63;
Matches 203; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
QY 1 EIVLTQSPISLPLVTGPEPASISCRSSQSLHSGNNYLDWLQKPGSQPQLIYLGSNRA 60
Db 21 DIVMTQXPLSLPVTGPEPASISCRSSQSLHSGNNYLDWLQKPGSQPQLIYLGSNRA 80
QY 61 SGVPRDFSGSVSGTDFTLIRISVEAEDGVYVCMQGLQSPFTFGTGVKIDIKRGTVAAPS 120
Db 81 SGVPRDFSGSVSGTDFTLIRISVEAEDGVYVCMQGLQSPFTFGTGVKIDIKR-TVAAPS 139
QY 121 VFIFPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 140 VFIFPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8
AAY82612
ID AAY82612 standard; Protein; 239 AA.
XX AC AAY82612;
XX DT 02-AUG-2000 (first entry)
XX DE Human PTHrP monoclonal antibody clone 1B3-9-16 protein SEQ ID NO:8.
XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 25 /label= Ile, Thr, Asn, Ser
FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 84 /note= "possibly Pro"
XX PN JP2000080100-A.
XX PD 21-MAR-2000.
XX PF 12-OCT-1998; 98JP-0304793.
XX PR 17-JUN-1998; 98JP-0188196.
XX PS 26-JUN-1998; 98JP-0196729.
XX PA (NISR) JAPAN TOBACCO INC.
XX PN WPI; 2000-286723/25.
XX DR N-PSDB; AAA13922.
XX A human monoclonal antibody to parathyroid hormone related protein. -
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain

	Query Match	90.0%;	Score 1031.5;	DB 21;	Length 239;
	Best Local Similarity	90.9%;	Pred. No. 1.8e-62;		
	Matches 200;	Conservative	3;	Mismatches 16;	Indels 1; Gaps 1;
y	1	EIVTQSPSLPVTTPGEPASISCRSSQSLHSHGTYLDWYLPKQSGPOLLIVYSGSHRA	60		
b	21	DIVMXQXPXXLPVTTPGEPASISCRSGORLLHRGNTYLDWYLPKQSGPOLLIVYLSGDR	80		
y	61	SCVDPDRSGSVGCTDTLIRSRVEADGVVYCMGLQSPETFGPGTKVDIKGTVAAPS	120		
b	81	SCVDPDRSGSGGTDFTLIRSRVEADGVVYCMQXQIPETFGPGTKVDIKR-TVAAPS	139		
y	121	VEIFPPSPDEQLKSGTASVVCCLNNFYPREAKYQWKVDNALQSGNSQESFVTEQDSKDSTYS	180		

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CC present invention..
XX
XX
SQ Sequence 239 AA;

Query Match 89.1%; Score 1021.5; DB 21; Length 239;
Best Local Similarity 90.0%; Pred. No. 8.8e-62;
Matches 198; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLSPLVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSHRA 60
   :||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 DIVMXQXPLSLPVTGEPASISCRSSQSLHNSGYFDWYLOKPGQSPOLLIIYSGSHRA 80

QY 61 SGVPDRFSGSVSGTQFTLRISRVEADGVVYCHOGLOSFTFGPGTKVDIKRGTVAAPS 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 SGVPDRFSGSGGTDFTLKISRVEADGVVYCMQTQTGFTFGPGTKVDIKR-TVAAIPS 139

QY 121 VFIFPPSDQLKSGTASVVCLNNFYPREAKVQNKVDNALQSGNSQESVTEQDSKDSYTS 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 VFIFPPSDQLKSGTASVVCLNNFYPREAKVQNKVDNALQSGNSQESVTEQDNKDSYTS 199

QY 181 LSSTLILSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
   ||||| ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 200 LSSTLTVSKAEYEHXVYAXVXHQGLSSPVTKSFNRGEC 239

RESULT 12
AAB72227
ID AAB72227 standard; Protein; 238 AA.
XX
XX AAB72227;
AC
XX
XX
DT 10-MAY-2001 (first entry)
XX
XX
DE Humanised 323/A3 (IgG1) antibody light chain amino acid sequence.
XX
XX Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
KW light chain.
XX
XX OS Mus sp.
XX OS Homo sapiens.
XX
XX PN WO200107082-A1.
XX
XX PD 01-FEB-2001.
XX
XX PF 23-JUL-1999; 99WO-EP05271.
XX
XX PR 23-JUL-1999; 99WO-EP05271.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Knick VC, Stimmel JB, Thurmond LM;
PI
XX WPI: 2001-182729/18.
DR N-PSDB; AAF63373.
XX
XX Combination for treating cancer (e.g. breast, gastric or prostate
PT cancers), or in the manufacture of a medicament for anti-cancer
PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
PT with a chemotherapeutic agent -
XX
XX Disclosure; Fig 15; 103pp; English.
XX
XX This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy,
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
CC co-administered to a patient with an anti-Ep-CAM antibody. The

```

CC	combination is useful for treating cancer, particularly colorectal
CC	cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
CC	lung cancer. The present sequence represents the light chain of
CC	anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be used
CC	in the combination of the invention.
XX	
SQ	Sequence 238 AA;
	Query Match 88.6%; Score 1015.5; DB 22; Length 238;
	Best Local Similarity 90.5%; Pred. No. 2.2e-61;
	Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;
Qy	1 EIVLTQSPLSLVTPGPASISCRSSQSLHSHNGYTYLDWYLOKPGOSPOLLIIYSGSHRA 60 : : : : : : : : : : :
Db	20 DIVMTQSPLSLVTPGPASISCRSKNLLHSNGITYLYWYLOKPGOSPOLLIIYQMSNLA 79 : : : : : : : : : : :
Qy	61 SGVPDRFSGSVSGTDFTLAISRVEAEDCVVYCYMGLSQSPFTFGPTKVDIRKGTVAAPS 120 : : : : : : : : : : :
Db	80 SGVPDRFSSSGTGDTFLAISRVEAEDGVVYCAQNLEIPRTFQGKTKEIKR-TVAAPS 138 : : : : : : : : : : :
Qy	121 VFIFPPSDEQLKSGTASVVCILLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180 : : : : : : : : : : :
Db	139 VFIFPPSDEQLKSGTASVVCILLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 198 : : : : : : : : : : :
Qy	181 LSSTLTSKADYEKKHYACEVTHOGLSPVTKSFNRGEC 220 : : : : : : : : : : :
Db	199 LSSTLTSKADYEKKHYACEVTHOGLSPVTKSFNRGEC 238 : : : : : : : : : : :
RESULT 13	
AAB72231	
ID	AAB72231 standard; Protein; 238 AA.
XX	
AC	AAB72231;
XX	
DT	10-MAY-2001 (first entry)
XX	
DE	Humanised 323/A3 (IgG1) antibody kappa light chain amino acid sequence.
XX	
KW	Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW	chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
KW	light chain.
XX	
OS	Mus sp.
OS	Homo sapiens.
XX	
PN	WO200107082-A1.
XX	
PD	01-FEB-2001.
XX	
PF	23-JUL-1999; 99WO-EP05271.
XX	
PR	23-JUL-1999; 99WO-EP05271.
XX	
PA	(GLAX) GLAXO GROUP LTD.
XX	
PI	Knick VC, Stimmel JB, Thurmond LM;
XX	
DR	WPI; 2001-182729/18.
XX	
PT	Combination for treating cancer (e.g. breast, gastric or prostate
PT	cancers), or in the manufacture of a medicament for anti-cancer
PT	therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
PT	with a chemotherapeutic agent -
XX	
PS	Example 3; Fig 6; 103pp; English.
XX	
CC	This invention relates to a combination of an anti-Ep-CAM (cyclic
CC	adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC	capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC	phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC	replication. The antibody exhibits cytostatic activity and is useful in
CC	the manufacture of a medicament for use in anti-cancer therapy,

CC characterised in that a chemotherapeutic agent, which is capable of
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
 CC co-administered to a patient with an anti-Ep-CAM antibody. The
 CC combination is useful for treating cancer, particularly colorectal
 CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
 CC lung cancer. The present sequence represents the kappa light chain of
 CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be
 CC used in the combination of the invention.

XX Sequence 238 AA;

Query Match 88.6%; Score 1015.5; DB 22; Length 238;
 Best Local Similarity 90.5%; Pred. No. 2.2e-61;
 Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60
 :||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|:|
 Db 20 DIVMTQSLSPVTPGEPASISCRSSKNLLHNSGITYLYWYLOKPGSQPLLIIYQMSNLA 79
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 QY 61 SGVDPDRFSGVSGTDFTLIRSRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 Db 80 SGVDPDRFSSSGSGTDFTLKISRVEAEDVGYVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 QY 121 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 180
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 Db 139 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 198
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 QY 181 LSSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSFNRGEC 220
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 Db 199 LSSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 14
 AAB72233
 ID AAB72233 standard; Protein; 238 AA.
 AC AAB72233;
 DT 10-MAY-2001 (first entry)
 DE Humanised 323/A3 (IgG4cys) antibody kappa light chain amino acid.
 XX Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
 KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
 KW light chain.
 XX Mus sp.
 OS Homo sapiens.
 XX WO200107082-A1.
 XX 01-FEB-2001.
 XX 23-JUL-1999; 99WO-EP05271.
 XX 23-JUL-1999; 99WO-EP05271.
 XX (GLAX) GLAXO GROUP LTD.
 XX Knick VC, Stimmel JB, Thurmond LM;
 XX WPI; 2001-182729/18.
 XX Combination for treating cancer (e.g. breast, gastric or prostate
 PT cancers), or in the manufacture of a medicament for anti-cancer
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
 PT with a chemotherapeutic agent -
 XX Example 7; Fig 11; 103pp; English.
 XX This invention relates to a combination of an anti-Ep-CAM (cyclic
 CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
 CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)

CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
 CC replication. The antibody exhibits cytostatic activity and is useful in
 CC the manufacture of a medicament for use in anti-cancer therapy,
 CC characterised in that a chemotherapeutic agent, which is capable of
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
 CC co-administered to a patient with an anti-Ep-CAM antibody. The
 CC combination is useful for treating cancer, particularly colorectal
 CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
 CC lung cancer. The present sequence represents the kappa light chain of
 CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG4cys) which can be
 CC used in the combination of the invention.

XX Sequence 238 AA;

Query Match 88.6%; Score 1015.5; DB 22; Length 238;
 Best Local Similarity 90.5%; Pred. No. 2.2e-61;
 Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60
 :||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|:|
 Db 20 DIVMTQSLSPVTPGEPASISCRSSKNLLHNSGITYLYWYLOKPGSQPLLIIYQMSNLA 79
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 QY 61 SGVDPDRFSGVSGTDFTLIRSRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 Db 80 SGVDPDRFSSSGSGTDFTLKISRVEAEDVGYVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 QY 121 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 180
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 Db 139 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 198
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 QY 181 LSSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSFNRGEC 220
 |||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
 Db 199 LSSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 15
 AAB72235
 ID AAB72235 standard; Protein; 238 AA.
 AC AAB72235;
 DT 10-MAY-2001 (first entry)
 DE Humanised 323/A3 (IgG2cys) antibody kappa light chain amino acid.
 XX Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
 KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
 KW light chain.
 XX Mus sp.
 OS Homo sapiens.
 XX WO200107082-A1.
 XX 01-FEB-2001.
 XX 23-JUL-1999; 99WO-EP05271.
 XX 23-JUL-1999; 99WO-EP05271.
 XX (GLAX) GLAXO GROUP LTD.
 XX Knick VC, Stimmel JB, Thurmond LM;
 XX WPI; 2001-182729/18.
 XX Combination for treating cancer (e.g. breast, gastric or prostate
 PT cancers), or in the manufacture of a medicament for anti-cancer
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
 PT with a chemotherapeutic agent -
 XX Example 8; Fig 13; 103pp; English.

CC This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy.
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
CC co-administered to a patient with an anti-Ep-CAM antibody. The
CC combination is useful for treating cancer, particularly colorectal
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
CC lung cancer. The present sequence represents the kappa light chain of
CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG2cys) which can be
CC used in the combination of the invention.

XX	Sequence	238 AA;
SQ	Query Match	88.6%; Score 1015.5; DB 22; Length 238;
	Best Local Similarity	90.5%; Pred. No. 2.2e-61;
	Matches 199; Conservative	8; Mismatches 12; Indels 1; Gaps 1;
QY	1	EIVLTQSPVLSPLPTGEPASISCRSSQSLHSHNGITYLDWYLQKPGQSPQLLIYSGSHRA 60
Db	20	DIWMTQSPVLSPLPTGEPASISCRSSKLLHSHNGITYLYWYLQKPGSPQLLIYQMSNLA 79
QY	61	SGVPDRFSGSVSGTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
Db	80	SGVPDRFSSSGSGTDFTLKISRVEAEDGVYYCAQNLEIPRTFGGQTKVEIKR-TVAAAPS 138
QY	121	VFIFPPSDEQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 180
Db	139	VFIFPPSDEQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 198
QY	181	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
Db	199	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Search completed: March 14, 2003, 11:47:38
Job time : 22.076 secs

03-08-491-334A-30

;; APPLICANT: GONZ


```

; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-09-121-952A-42
;
; Query Match 83.1%; Score 952.5; DB 4; Length 242;
; Best Local Similarity 84.1%; Pred. No. 3.5e-77;
; Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps
;
; QY 1 EIVLTQSLSPVLPVTPGPASISCRSSQSLHNSGTYILDWLQKPGOSPOLLITYSGSHRA 60
; :|||||:|||||:|:|||||:|||||:|:|||||:|||||:|||||:|||||:|:|
; Db 24 DIVMTQTPLSPVLSGLQDASISCRSSQSIVHGVTGNTLHWYLDQKPGSPKLLIYKVSNR 83
;
; QY 61 SGVPRFSGSSVGGTDFLTRLSRVEAEDGVVYCMGLOGSPFTFGPTKVDIKRGTVAA 120
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
; Db 84 SGVPRFSGSSVGGTDFLTRLSRVEAEDGLVFCSSQSTHVPLTFGAGTKLELR- 142
;
; QY 121 VFIFPPSEDLKSGTASVWCLLNPNFYPRKAYQWKNALOSGNSQSBSVTEQDSKOSTYS 180
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
; Db 143 VFIFPPSEDLKSGTASVWCLLNPNFYPRKAYQWKNALOSGNSQSBSVTEQDSKOSTYS 202
;
; QY 181 LSTLTSLKADYEHKKVYACVETHQGLSSPVTKSNRGEC 220
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
; Db 203 LSTLTSLKADYEHKKVYACVETHQGLSSPVTKSNRGEC 242
;
; RESULT 10
; US-09-234-340A-42
; Sequence 42, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-234-340A-42

Query Match      83.1%; Score 952.5; DB 4; Length 242;
Best Local Similarity 84.1%; Pred. No. 3.5e-77;
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLWDYLOKPGQSPQLLIYSGSHRA 60
Db 24 DIVMTQTPSLPVSLGQDASISCRSSQSLVHGIGNTLHWYLOKPGQSPKLLIYKVSRRF 83
QY 61 SGVPDRFSGSGVSGTDFTLRISRVEAEDGVYICMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 84 SGVPDRFSGSGVSGTDFTLRISRVEAEDGLYFCQSQSTHVLPTFGAGTKLELKR-AVAAPT 142
QY 121 VFIPTSPDEOLKSGTASVVCLLNNFYPRAKQVQKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 143 VFIPPSSEQLKSGTASVVCLLNNFYPRAKQVQKVDNALQSGNSQESVTEQDSKSDSTYS 202
QY 181 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 203 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 242

RESULT 11
US-09-301-593-36
; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Legier, Olivier
; APPLICANT: Saidanha, Jose W.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; EARLIER FILING DATE: 1999-04-29
; EARLIER FILING DATE: 1998-04-30
; EARLIER FILING DATE: 1998-04-30
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-301-593-36

Query Match      78.4%; Score 899; DB 4; Length 240;
Best Local Similarity 81.9%; Pred. No. 2e-72;
Matches 181; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNS-NGYTYLDWYLOKPGQSPQLLIYSGSHR 59
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSRQKNYLAWYQKPGQPKLLIFWASTR 80
QY 60 ASGVDPDRFSGSGVSGTDFTLRISRVEAEDGVYICMQGLQSPFTFGPGTKVDIKRGTVAAAP 119
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Db 81 ESGVPDRFSGSGVSGTDFTLTSSQLQAEADVAYYCQQYFSYPLTFGGQTKVEIKR-TVAAP 139
QY 120 SVFIPTSPDEOLKSGTASVVCLLNNFYPRAKQVQKVDNALQSGNSQESVTEQDSKSDSTY 179
Db 140 SVFIPTSPDEOLKSGTASVVCLLNNFYPRAKQVQKVDNALQSGNSQESVTEQDSKSDSTY 199
QY 180 SLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 SLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 12
US-09-027-449-72
; Sequence 72, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-027-449-72

Query Match      78.0%; Score 893.5; DB 3; Length 219;
Best Local Similarity 79.5%; Pred. No. 5.4e-72;
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
```

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QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLWDYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIQMTQSPSLSASVGDGVRTITCRSSQSLVHGIGATYLNHWYQKPGKAPKLLIYKVSRRF 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVYICMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGLYFCQSQSTHVLPTFGQTKVEIKR-TVAAPS 119
QY 121 VFIPTSPDEOLKSGTASVVCLLNNFYPRAKQVQKVDNALQSGNSQESVTEQDSKSDSTYS 180
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GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hsei, Vanessa

APPLICANT: Koumenis, Iphigenia

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

APPLICANT: ZAPALA, GERARDO A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998

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1 FILING DATE: 24 JUL 1990
2
3 CLASSIFICATION: 514
4
5 PRIOR APPLICATION DATA:
6   APPLICATION NUMBER: 60/074330
7   FILING DATE: 22-JAN-1998
8
9 PRIOR APPLICATION DATA:
10  APPLICATION NUMBER: 60/075467
11  FILING DATE: 20-FEB-1998
12
13 ATTORNEY/AGENT INFORMATION:
14  NAME: Love, Richard B.
15
16 REGISTRATION NUMBER: 34,659
17 REFERENCE/DOCKET NUMBER: P1085R4
18
19 TELECOMMUNICATION INFORMATION:
20  TELEPHONE: 650/225-5530
21  TELEFAX: 650/952-9881
22
23 INFORMATION FOR SEQ ID NO: 72:
24  SEQUENCE CHARACTERISTICS:
25    LENGTH: 219 amino acids
26    TYPE: Amino Acid
27    TOPOLOGY: Linear
28
29 US-09-121-952A-72

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Best Local Similarity 79.3%; Pred. NO. 3.4E-72;
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
1 EVITOSPISLPVTGCEPASISCRSSOSLIASNGYTYVDWYLOKPGOSPOLLITYSGSHRA 60

1	DIOMTQSPSSLSASGDRVITITCRSSQSLSVHGIGATYLHWYQKPGKAPKLIIYKVS	NRF	60
61	SGVPDRFSGVSGDFTLRISRVAEAGVGVIYCMQGLQSPFTFGPTKVDILKRGTVAA	PS	120
61	SGVPSRFSGSGDFTLTLSLQPEDFATYYCSQSTHVPLTFGQGTKEIKR-TVAA	PS	119
121	VFIFPPSDQLKGTASVWCLLNNFYPRRAKQVWKVDNALQSGNSQESVTEQDSK	STYS	180
120	VFIFPPSDQLKGTASVWCLLNNFYPRRAKQVWKVDNALQSGNSQESVTEQDSK	STYS	179
181	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC		220
180	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC		219

US-09-234-340A-72
; Sequence 72, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hselt, Vanessa

APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokhi, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-72

Query Match 78.0%; Score 893.5; DB 4; Length 219;
Best Local Similarity 79.5%; Pred. No. 5.4e-72;
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
DB 1 DIQMTQSPFSLASVGRVITTCSSQSLVHGIGATYLVHWYQKPGKAPKLLIYKYSNRF 60
QY 61 SGVPDRFSGVSGPDFTLRIISRVEADGVYCYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
DB 61 SGVPSRFSGSGSGDFTLTISLQPEDFATYYCSQSHPHPLTEFCQGTKEIKR-TVAAPS 119
QY 121 VFIPPPDEQLKSGTASVWCLLNFFPREAKVOMKVDNALQSGNSQESVTEQDSKDSSTYS 180
DB 120 VFIPPPDEQLKSGTASVWCLLNFFPREAKVOMKVDNALQSGNSQESVTEQDSKDSSTYS 179
QY 181 LSSTLTSLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220
DB 180 LSSTLTSLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 219

Search completed: March 14, 2003, 11:50:17
Job time : 7.90114 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:47:44 ; Search time 6.69202 seconds
(without alignments)
1515.277 Million cell updates/sec

Title: US-09-822-698A-24
Perfect score: 1146
Sequence: 1 EIVLTQSPSLPLVPTGEPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*

6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*

7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*

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9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*

11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*

12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*

13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	1146	100.0	220 10	US-09-822-698A-24
2	1050.5	91.7	239 9	US-09-924-340-8
3	1050.5	91.7	239 9	US-09-992-600A-8
4	992.5	86.6	239 9	US-10-124-905-6
5	992.5	86.6	239 9	US-09-948-429B-6
6	971	84.7	228 9	US-09-909-567B-50
7	952.5	83.1	242 9	US-09-726-258-42
8	898	78.4	240 10	US-09-799-514-8
9	893.5	78.0	219 9	US-09-726-258-72
10	893.5	78.0	239 9	US-09-249-011A-22
11	893.5	78.0	242 9	US-09-726-258-51
12	893.5	78.0	242 9	US-09-726-258-56
13	893.5	78.0	242 9	US-09-726-258-62
14	889	77.6	220 10	US-09-995-693-1
15	889	77.6	236 10	US-09-859-053-34
16	882	77.0	236 10	US-09-859-053-38
17	879	76.7	218 9	US-09-925-179-67
18	872	76.1	218 9	US-09-925-179-9
19	872	76.1	218 10	US-09-802-077-9

20	872	76.1	218	10	US-09-802-096-9	Sequence 9, Appl
21	872	76.1	218	10	US-09-920-171-13	Sequence 13, Appl
22	869	75.8	239	10	US-09-825-012-9	Sequence 9, Appl
23	865	75.5	218	10	US-09-920-171-15	Sequence 15, Appl
24	865	75.5	218	10	US-09-920-171-17	Sequence 17, Appl
25	865	75.5	218	10	US-09-920-171-19	Sequence 19, Appl
26	865	75.5	218	10	US-09-920-171-24	Sequence 24, Appl
27	865	75.5	220	10	US-09-917-410-5	Sequence 5, Appl
28	863	75.3	218	10	US-09-917-410-2	Sequence 2, Appl
29	854.5	74.6	235	10	US-09-910-059-97	Sequence 97, Appl
30	853	74.6	234	10	US-09-740-002-24	Sequence 24, Appl
31	848.5	74.0	235	10	US-09-910-059-17	Sequence 17, Appl
32	846.5	73.9	235	10	US-09-910-059-52	Sequence 52, Appl
33	846	73.8	212	12	US-10-011-125-5	Sequence 5, Appl
34	843.5	73.6	669	9	US-09-807-721-2	Sequence 2, Appl
35	843	73.6	214	10	US-09-940-166A-2	Sequence 2, Appl
36	843	73.6	214	10	US-09-811-384-11	Sequence 11, Appl
37	843	73.6	237	10	US-09-940-166A-6	Sequence 6, Appl
38	841.5	73.4	213	9	US-09-996-288-231	Sequence 231, App
39	840.5	73.3	235	10	US-09-910-059-99	Sequence 99, Appl
40	839	73.2	237	10	US-09-056-160B-100	Sequence 100, App
41	839	73.2	491	12	US-10-011-125-2	Sequence 2, Appl
42	838	73.1	237	9	US-09-726-258-25	Sequence 25, Appl
43	836.5	73.0	213	9	US-09-996-288-209	Sequence 209, App
44	836.5	73.0	213	9	US-09-996-288-237	Sequence 237, App
45	836.5	73.0	213	9	US-09-996-288-247	Sequence 247, App

ALIGNMENTS

RESULT 1

US-09-822-698A-24

; Sequence 24, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 24

; LENGTH: 220

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1

US-09-822-698A-24

Query Match	100.0%;	Score 1146;	DB 10;	Length 220;
Best Local Similarity	100.0%;	Pred. No. 3.7e-50;		
Matches 220;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EIVLTQSPSLPLVPTGEPASISCSRLHNSGTYLDWYLRKPGSQPLLIIYSGSHRA	60	
Db	1	EIVLTQSPSLPLVPTGEPASISCSRLHNSGTYLDWYLRKPGSQPLLIIYSGSHRA	60	
Qy	61	SGVPDRSGSGVSGDFTLRISRVAEADVGVYCMGLOSPTFTGPGTKVDIKRGTVAAPS	120	
Db	61	SGVPDRSGSGVSGDFTLRISRVAEADVGVYCMGLOSPTFTGPGTKVDIKRGTVAAPS	120	
Qy	121	VFIPPPDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS	180	
Db	121	VFIPPPDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS	180	
Qy	181	LSSTLTLSKADYERHKHYACVETHQGLSSPVTKSFNRGEC	220	
Db	181	LSSTLTLSKADYERHKHYACVETHQGLSSPVTKSFNRGEC	220	

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; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-992-600A-8

Query Match          91.7%; Score 1050.5; DB 9; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.9e-45;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSLPLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGSHRA 60
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Db 21 DIVMTQSPFLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGNRA 80
   :||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1|||||
Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKRGTVAAPS 120
   :||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1|||||
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKR-TVAAPS 139
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Qy 121 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSY 180
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Db 140 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSY 199
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Qy 181 LSSTLTLSKADYEKKHKYACEVTHOGLSPVTKSFNRGEC 220
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Db 200 LSSTLTLSKADYEKKHKYACEVTHOGLSPVTKSFNRGEC 239
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RESULT 4
US-10-124-905-6
; Sequence 6, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620

; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-992-600A-8

Query Match          91.7%; Score 1050.5; DB 9; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.9e-45;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSLPLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGSHRA 60
   :||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1|||||
Db 21 DIVMTQSPFLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGNRA 80
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Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKRGTVAAPS 120
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Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKR-TVAAPS 139
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Qy 121 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSY 180
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Db 140 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSY 199
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Qy 181 LSSTLTLSKADYEKKHKYACEVTHOGLSPVTKSFNRGEC 220
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Db 200 LSSTLTLSKADYEKKHKYACEVTHOGLSPVTKSFNRGEC 239
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RESULT 3
US-09-992-600A-8
; Sequence 8, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992.600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-924-340-8

Query Match          91.7%; Score 1050.5; DB 9; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.9e-45;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSLPLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGSHRA 60
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Db 21 DIVMTQSPFLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGNRA 80
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Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKRGTVAAPS 120
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Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKR-TVAAPS 139
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Qy 121 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSY 180
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Db 140 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSY 199
   :||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1|||||
Qy 181 LSSTLTLSKADYEKKHKYACEVTHOGLSPVTKSFNRGEC 220
   :||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1|||||
Db 200 LSSTLTLSKADYEKKHKYACEVTHOGLSPVTKSFNRGEC 239
   :||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1||||| 1|||||

RESULT 2
US-09-924-340-8
; Sequence 8, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-924-340-8

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; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-992-600A-8

Query Match          91.7%; Score 1050.5; DB 9; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.9e-45;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSLPLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGSHRA 60
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 21 DIVMTQSPFLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGNRA 80
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKRGTVAAPS 120
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKR-TVAAPS 139
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 121 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSYTS 180
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 140 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSYTS 199
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 181 LSSTLTLSKADYEKKHKYVACEVTHQGLSPVTKSFNRGEC 220
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 200 LSSTLTLSKADYEKKHKYVACEVTHQGLSPVTKSFNRGEC 239
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

RESULT 4
US-10-124-905-6
; Sequence 6, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620

; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-992-600A-8

Query Match          91.7%; Score 1050.5; DB 9; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.9e-45;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSLPLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGSHRA 60
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 21 DIVMTQSPFLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGNRA 80
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKRGTVAAPS 120
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKR-TVAAPS 139
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 121 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSYTS 180
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 140 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSYTS 199
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 181 LSSTLTLSKADYEKKHKYVACEVTHQGLSPVTKSFNRGEC 220
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 200 LSSTLTLSKADYEKKHKYVACEVTHQGLSPVTKSFNRGEC 239
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

RESULT 3
US-09-992-600A-8
; Sequence 8, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992.600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-924-340-8

Query Match          91.7%; Score 1050.5; DB 9; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.9e-45;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSLPLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGSHRA 60
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 21 DIVMTQSPFLPVTGPEPASISCRSSQSLHSHNGVYLDWYLQKPGQSPQLLIYSGNRA 80
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKRGTVAAPS 120
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMOGLQSPFTFGTGKVDIKR-TVAAPS 139
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 121 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSYTS 180
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 140 VFIPPPSDEQLKSGTASVVCLLNFPYFREAKYQWKVDNALQSGNSQESVTEQDSKDSYTS 199
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

Qy 181 LSSTLTLSKADYEKKHKYVACEVTHQGLSPVTKSFNRGEC 220
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
Db 200 LSSTLTLSKADYEKKHKYVACEVTHQGLSPVTKSFNRGEC 239
   :|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||

RESULT 3
US-09-992-600A-8
; Sequence 8, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992.600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698

```


TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-124-905-6

Query Match 86.6%; Score 992.5; DB 9; Length 239;
Best Local Similarity 87.7%; Pred. No. 1.3e-42;
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
Db 21 EVVMTQSPSLPITGPEPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLLIYKVSNRD 80
QY 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 81 SGVPDRFSGSVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 139
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199
QY 181 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5
US-09-948-429B-6
Sequence 6, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-429B-6

Query Match 86.6%; Score 992.5; DB 9; Length 239;
Best Local Similarity 87.7%; Pred. No. 1.3e-42;
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
Db 21 EVVMTQSPSLPITGPEPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLLIYKVSNRD 80
QY 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 81 SGVPDRFSGSVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 139
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199
QY 181 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 6
US-09-909-567B-50
Sequence 50, Application US/09909567B
Publication No. US20030022257A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto A.
APPLICANT: Nair, Manoj
APPLICANT: Chen, Seiyu
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: US/09/909,567B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/219,834
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapien
US-09-909-567B-50

Query Match 84.7%; Score 971; DB 9; Length 228;
Best Local Similarity 86.4%; Pred. No. 1.4e-41;
Matches 191; Conservative 14; Mismatches 14; Indels 2; Gaps 2;
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
Db 9 EIVMTQTPUSLTITGPEQASMSCRSSQSLHSDGYTYLWFLQKPGQSPQLLIYEVSNRF 68
QY 61 SGV-PDRFSGSVSGDTFTLRISRVEAEDGVYVYCMQGLQSPFTFGPGTKVDIKRGTVAAP 119
Db 69 SGVSPIRFSGSGGREFTLRISRVEADAGVYVYCMQTQTPTPTFGQGRLEIKR-TVAAP 127
QY 120 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTY 179
Db 128 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTY 187
QY 180 SLSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 188 SLSTLTLSKADYEKKHYKHYACEVTHQGLSSPVTKSFNRGEC 228

RESULT 7
US-09-726-258-42
Sequence 42, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:

```

;
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-09-726-258-42
;
; Query Match      83.1%; Score 952.5; DB 9; Length 242;
; Best Local Similarity 84.1%; Pred. No. 1.2e-40;
; Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;
;
; Qy 1 EIVLTQSPVLPVTPGPASISCRSSQSLH-SNGYTYLDWYLNQKPGQSPOLLIIYSGSHR 60
; Db 24 DIVMTQTPSLPVSGLGQASISCRSSQSLVHGIGNTYLHWYLNQKPGQSPKLLIYKYSNRF 83
;
; Qy 61 SGVPDRFSGVSGTDFTLIRISRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
; Db 84 SGVPDRFSGVSGTDFTLIRISRVEAEADGLYFCQSQSTHVPVLTFCAGTKLELKR-AVAAPT 142
;
; Qy 121 VFIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180
; Db 143 VFIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 202
;
; Qy 181 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 220
; Db 203 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 242
;
; RESULT 8
; US-09-799-514-8
; Sequence 8, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and An
;
; FILE REFERENCE: PT015P1
; CURRENT APPLICATION NUMBER: US/09/799,514
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,248
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
;
; US-09-799-514-8
;
; Query Match      78.4%; Score 898; DB 10; Length 240;
; Best Local Similarity 80.5%; Pred. No. 5.9e-38;
; Matches 178; Conservative 18; Mismatches 23; Indels 2; Gaps 2;
;
; Qy 1 EIVLTQSPVLPVTPGPASISCRSSQSLH-SNGYTYLDWYLNQKPGQSPOLLIIYSGSHR 59
; Db 21 DIVMTQSPDSLAVSLGERATINCKSSQTVLYSSDNKNYLAWYQKPGOPPKLLIYWASTR 80
;
; Qy 60 ASGVDPDRFSGVSGTDFTLIRISRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 119
; Db 81 ESGVPDRFSGVSGTDFTLIRISRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 139
;
; Qy 120 SVFIFFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTY 179
; Db 140 SVFIFFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTY 199
;
; Qy 180 SLSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 220
; Db 200 SLSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 240
;
; RESULT 9
; US-09-726-258-72
; Sequence 72, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-09-726-258-42
;
; Query Match      83.1%; Score 952.5; DB 9; Length 242;
; Best Local Similarity 84.1%; Pred. No. 1.2e-40;
; Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;
;
; Qy 1 EIVLTQSPVLPVTPGPASISCRSSQSLH-SNGYTYLDWYLNQKPGQSPOLLIIYSGSHR 60
; Db 24 DIVMTQTPSLPVSGLGQASISCRSSQSLVHGIGNTYLHWYLNQKPGQSPKLLIYKYSNRF 83
;
; Qy 61 SGVPDRFSGVSGTDFTLIRISRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
; Db 84 SGVPDRFSGVSGTDFTLIRISRVEAEADGLYFCQSQSTHVPVLTFCAGTKLELKR-AVAAPT 142
;
; Qy 121 VFIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180
; Db 143 VFIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 202
;
; Qy 181 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 220
; Db 203 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 242
;
; RESULT 8
; US-09-799-514-8
; Sequence 8, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and An
```


Qy	121	VFI	PPS	DEQLK	SGTASV	CVCLLN	NNF	YP	PRAK	VQV	KVQW	VDNAL	QSGNS	QSGESV	TEQDSK	SDSIYS	180
Db	143	VF	IP	PS	DEQLK	SGTASV	CVCLLN	NNF	YP	PRAK	VQV	KVQW	VDNAL	QSGNS	QSGESV	TEQDSK	SDSIYS
Qy	181	LS	ST	LT	LS	KADY	EKKH	KYAC	EV	THQ	LS	SPVT	KSF	NR	GEC	220	
Db	203	LS	ST	LT	LS	KADY	EKKH	KYAC	EV	THQ	LS	SPVT	KSF	NR	GEC	242	

RESULT 12
US-09-726-258-56
; Sequence 56, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA: 09/234, 182
APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION DATA: 60/094003
APPLICATION NUMBER:
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-726-258-56

	Query Match	78.0%;	Score 893.5;	DB 9;	Length 242;
	Best Local Similarity	79.5%;	Pred. No. 9.3e-36;		
	Matches 175; Conservative	14;	Mismatches 30;	Indels 1;	Gaps 1;
QY	1	EVLVTQSPLSLPVTGEFASISCRSSQLHSNGVITYLDWLQKPGQPQLLIYSGSHRA	60		
	:	: : :	:	: :	:
	:	: : :	:	: :	:
DB	24	DIQMTQSPSSLASASGDRVITICRSSQLVHGIGATYLHWYQQKFGKAPKLLIYKVSNR	83		
	:	: : :	:	: :	:
QY	61	SGVPDRFSGSVSGDTFTLRIRSEAEADVGVGYCMOGLOSPTFFGGCTKVDTKRGTVAAPS	120		
	:	: : :	:	: :	:
	:	: : :	:	: :	:
DB	84	SGVPSRFSGSGLTDTLTITSLQPEDFATYYCSQSTHVPITFFGGTGKVEIKR-TVAAPS	142		
	:	: : :	:	: :	:
QY	121	VFIETPPSDRLKSGTASVVCLLNPNFYPREAKVOWKDVALOSGNQSQESTVEDSKDSTYS	180		

Db	143	VFIFFPSDEQLKSGTASVWCLLNFFYPREAKYQWKVDNALGSGNSQESVTEQDSKSTYS	202
QY	181	LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSNRGEC	220
Dh	203	I SSTLTLSKADYEKKHYACEVTHQGISSPVTKSNRGEC	242

```

RESULT 13
US-09-726-258-62
; Sequence 62, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09726-258

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/234,182
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/094003
 FILING DATE: 24-JUL-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P1085R4-1A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5530
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 242 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

Query Match	78.0%	Score 893.5;	DB 9;	Length 242;
Best Local Similarity	79.5%;	Pred. No. 9.3e-38;		
Matches 175;	Conservative 14;	Mismatches 30;	Indels 1;	Gaps 1;

Qy	1	EIVTQSPSLPVTPGPGASISCRSSQSLHNSNCYTVLDWYLOKPGQSPOLLITYSCSHRA	60
Db	24	DIQMTQSPSSLSASVGRVITICRSSLVHGIGETYLHWYQQKPKAKLLLYKYKYNRF	83
Qy	61	SGVDFRRSGSVSGTHDFTLRISREAEADVYVYCMOGLQSPFTGPGTKVDIKRGTVAAPS	120
Db	84	SGVSRFRSGSGSGHDTLTLSLQGPDAFYICQSTHVELTFGQGTKEIKR-TVAAPS	142
Qy	121	VFIPPPDEQLKSGTASVVCLLNNFYIPREAKVOMKVDNALQSGNSQESVTEQDSKOSTYS	180
Db	143	VFIPPPDEQLKSGTASVVCLLNNFYIPREAKVOMKVDNALQSGNSQESVTEQDSKOSTYS	202

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model
Run on: March 14, 2003, 11:45:54 ; Search time 8.9924 Seconds
(without alignments)
2351.940 Million cell updates/sec

Title: US-09-822-698A-24
Perfect score: 1146
Sequence: 1 EIVLTQSPKSLPVTGPGEAS.....EVTHQGLSSPVTKSFNRGEC 220
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	893.5	78.0	215	2 JE0242	Ig kappa chain NIG
2	877.5	76.6	215	2 JE0244	Ig kappa chain NIG
3	869.5	75.9	215	2 JE0243	Ig kappa chain NIG
4	847.5	74.0	215	2 A23746	Ig kappa chain V-I
5	823	71.8	216	2 JE0241	Ig kappa chain Am3
6	785.5	68.5	219	2 S52028	Ig kappa chain - m
7	782.5	68.3	219	2 PC4203	Ig kappa chain (mc)
8	777.5	67.8	217	2 S42772	Ig kappa chain - m
9	777.5	67.8	219	2 S16112	Ig kappa chain V r
10	769.5	67.1	219	2 S38865	Ig kappa chain - m
11	750.5	65.5	225	2 JL0029	Ig kappa chain pre
12	725	63.3	240	2 S06084	Ig kappa chain pre
13	690	60.2	220	2 A31790	Ig kappa chain V r
14	677	59.1	218	2 S68241	Ig kappa chain V r
15	671	58.6	218	2 JC5810	Ig kappa chain V r
16	662	57.8	214	2 S68212	monoclonal antibod
17	651.5	56.8	197	2 S29593	Ig kappa chain (Ma
18	640	55.8	210	2 A56169	Ig kappa chain (WM
19	640	55.8	234	2 S14237	Ig kappa chain V r
20	636	55.5	234	2 S01320	Ig kappa chain pre
21	634.5	55.4	225	2 S37484	Ig kappa chain pre
22	627	54.7	230	2 S33161	Ig kappa chain - m
23	621.5	54.2	235	2 S25058	Ig kappa chain - s
24	611.5	53.4	178	2 PT0219	Ig kappa chain - m
25	587.5	51.3	135	2 S52059	Ig kappa chain V-C
26	549.5	47.9	121	2 S40371	JC-kappa protein -
27	548	47.8	106	1 K3HU	Ig kappa chain - h
28	546.5	47.7	135	2 S40342	Ig kappa chain C r
29	535.5	46.7	136	2 S40357	Ig kappa chain V-J

30	528.5	46.1	124	2 S03876	Ig kappa chain V-I
31	528	46.1	112	2 S58207	Ig light chain V r
32	527	46.0	117	1 K2HUGM	Ig kappa chain pre
33	524.5	45.8	125	2 S40356	Ig kappa chain - h
34	524	45.7	132	2 S26882	Ig kappa chain V r
35	523.5	45.7	229	2 A20969	Ig kappa chain pre
36	522	45.5	112	2 S58206	Ig light chain V r
37	513	44.8	99	2 A37927	Ig kappa chain C r
38	507.5	44.3	126	2 S40339	Ig kappa chain - h
39	507	44.2	99	2 S26653	Ig kappa chain C r
40	500	43.6	113	1 K2HUTW	Ig kappa chain V-I
41	494	43.1	131	2 S40372	Ig kappa chain V-J
42	489.5	42.7	238	2 A49633	Ig lambda-like cha
43	478.5	41.8	112	1 K2HUML	Ig kappa chain V-I
44	478	41.7	123	2 S40319	Ig kappa chain V r
45	473.5	41.3	130	2 S40321	Ig kappa chain - h

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis:

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 893.5; DB 2; Length 215;

Best Local Similarity 81.4%; Pred. No. 2.4e-56;

Matches 179; Conservative 14; Mismatches 22; Indels 5; Gaps 3;

QY	1	EIVLTQSPKSLPVTGPGEASISCRSSQLLHNSNGTYLDWYLQKPGQSPQLLIYSGSHRA	60
Db	1	EIVLTQSPKSLPVTGPGEATLSCASQSV--SN--NYLAWYQKPGQAPSLIYDASSRA	56
QY	61	SGVPDRFSGSVSGTDFTLIRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS	120
Db	57	TGIPDRFSGSGSGTDFTLTISGLEPEDFAVYCCQYDRPPWTFGGQTKVEIKR--TVAAPS	115
QY	121	VFIFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS	180
Db	116	VFIFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS	175
QY	181	LSSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC	220
Db	176	LSSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC	215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yanaki, S.; Kazi, H.

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 785.5; DB 2; Length 219;
Best Local Similarity 67.7%; Pred. No. 1.1e-48;
Matches 149; Conservative 29; Mismatches 41; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGOSPQLLIYSGSHRA 60
Db 1 DVVMTQTPSLSPVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGOSPQLLIYKVSNR 60
QY 61 SGVPDRFSGSVGDTFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 120
Db 61 SGVPDRFSGSGGDTFTLRISRVEAEDLVGYVFCQSHVPTFTGGGTNLEIKRAD-AA 119
QY 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 180
Db 120 VSIFPPSDEQLTSGGASVVCFLNFFPKDINVKWKIDGSRQNGVLNSWTDQDSKDY 179
QY 181 LSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
Db 180 MSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREK 219

RESULT 7
PC4203

Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C:Accession: PC4203
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996

A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody Maba34
A:Reference number: PC4203; MUID:97082978; PMID:8964510
A:Molecule type: mRNA
A:Residues: 1-219 <KWA>
A:Cross-references: GB:U29147; NID:gl594225; PIDN:AAC52821.1; PID:g1594226
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density lipoprotein (HDL) and is involved in the regulation of lipid metabolism.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-219/Domain: C region #status predicted <CRG>

Query Match 68.3%; Score 782.5; DB 2; Length 219;
Best Local Similarity 66.8%; Pred. No. 1.7e-48;
Matches 147; Conservative 32; Mismatches 40; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGOSPQLLIYSGSHRA 60
Db 1 DVLMTQTPSLSPVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGOSPQLLIYKVSNR 60
QY 61 SGVPDRFSGSVGDTFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 120
Db 61 SGVPDRFSGSGGDTFTLRISRVEAEDLVGYVFCQSHVPTFTGGGTNLEIKRAD-AA 119
QY 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 180
Db 120 VSIFPPSDEQLTSGGASVVCFLNFFPKDINVKWKIDGSRQNGVLNSWTDQDSKDY 179
QY 181 LSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
Db 180 MSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREK 219

RESULT 8
S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75336; NID:g414143; PIDN:CAA53226.1; PID:g414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 777.5; DB 2; Length 217;
Best Local Similarity 67.9%; Pred. No. 3.9e-48;
Matches 148; Conservative 27; Mismatches 42; Indels 1; Gaps 1;

QY 3 VLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGOSPQLLIYSGSHRAS 62
Db 1 VMTQSPSLSPVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGOSPQLLIYKVSREF 60
QY 63 VPDPRFSGSVGDTFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 122
Db 61 VPDPRFSGSGGDTFTLRISRVEAEDLVGYVFCQSHVPTFTGGGTNLEIKRAD-AA 119
QY 123 IFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 182
Db 120 IFPPSDEQLTSGGASVVCFLNFFPKDINVKWKIDGSRQNGVLNSWTDQDSKDY 179
QY 183 LSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
Db 180 MSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREK 217

RESULT 9
S16112

Ig kappa chain V region (G2a) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16112
R:Vaesen, M.; Froesch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.
Biochem. J. 251, 451-453, 1991
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha 2-macroglobulin
A:Reference number: S16112; MUID:92000313; PMID:1910583
A:Accession: S16112
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-219 <BIT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 777.5; DB 2; Length 219;
Best Local Similarity 66.8%; Pred. No. 3.9e-48;
Matches 147; Conservative 31; Mismatches 41; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGOSPQLLIYSGSHRA 60
Db 1 DVVMTQTPSLSPVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGOSPQLLIYKVSNR 60
QY 61 SGVPDRFSGSVGDTFTLRISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKRGTVAA 120
Db 61 SGVPDRFSGSGGDTFTLRISRVEAEDLVGYVFCQSHVPTFTGGGTNLEIKRAD-AA 119
QY 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDY 180
Db 120 VSIFPPSDEQLTSGGASVVCFLNFFPKDINVKWKIDGSRQNGVLNSWTDQDSKDY 179
QY 181 LSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
Db 180 MSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNREK 219

RESULT 10

S38865

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001

C:Accession: S38865

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of an

A:Reference number: S38864

A:Accession: S38865

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-219 <KIP>

A:Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 67.1%; Score 769.5; DB 2; Length 219;

Best Local Similarity 67.3%; Pred. No. 1.4e-47;

Matches 148; Conservative 29; Mismatches 42; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNGYTYLDWYLOKPGQSPOLLIYSGSHRA 60

D 1 ELVMTQSPISLSVSLGDAQASISCRSSQSLVHTNGNTYLHWYLOKPGQSPKLLIYVSNRF 60

QY 61 SGVPDRFSGSVSGTDTLRLSRVEADGVVYCMQGLQSPFTFGCTKVDIKRGTVAAAPS 120

D 61 SGVPDRFSGSGSGTDTLRLSRVEADGLGVYFCSTQVHPWTFGGGTKEIKRAD-AAPT 119

QY 121 VFIFPPSDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYTS 180

D 120 VSIFPPSDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYTS 179

QY 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

D 180 MSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 11

JL0029

Ig kappa chain precursor (RP93) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000

C:Accession: JL0029

R:Chien, N.C.; Pollock, R.R.; Desaynard, C.; Scharff, M.D.

J. Exp. Med. 167, 954-973, 1988

A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor

A:Reference number: JL0029; MUID:88171315; PMID:3127529

A:Accession: JL0029

A:Molecule type: mRNA

A:Residues: 1-225 <CHI>

A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell

A:Note: the authors translated the codon CCG for residue 106 as Pro, ACC for residue 132

A:Note: the nucleotide sequence shown is inconsistent with authors' translation because

ect except for four positions shown above

C:Comment: The protein is an anti-phosphorylcholine antibody.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:7-223/Product: Ig kappa chain #status predicted <IILC>

F:7-106/Domain: V region #status predicted <VAR>

F:107-119/Domain: J region #status predicted <JIR>

F:120-225/Domain: C region #status predicted <COR>

Query Match 65.5%; Score 750.5; DB 2; Length 225;

Best Local Similarity 64.5%; Pred. No. 3.3e-46;

Matches 142; Conservative 31; Mismatches 46; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNGYTYLDWYLOKPGQSPOLLIYSGSHRA 60

D 7 DVLMTQIPSLPVLGDAQASISCRSSQSLVHTNGNTYLHWYLOKPGQSPNLLIYKISNRF 66

QY 61 SGVPDRFSGSVSGTDTLRLSRVEADGVVYCMQGLQSPFTFGCTKVDIKRGTVAAAPS 120

D 61 SGVPDRFSGSGSGTDTLRLSRVEADGLGVYFCSTQVHPWTFGGGTKEIKRAD-AAPT 125

QY 121 VFIFPPSDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYTS 180

D 120 VSIFPPSDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYTS 185

QY 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

D 186 MSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 225

RESULT 12

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S06084

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain c

A:Reference number: S06084; MUID:90016888; PMID:2508067

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 <CRO>

A:Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-240/Product: Ig kappa chain #status predicted <MAT>

F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 63.3%; Score 725; DB 2; Length 240;

Best Local Similarity 63.3%; Pred. No. 2.2e-44;

Matches 140; Conservative 31; Mismatches 48; Indels 2; Gaps 2;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHLS-NGYTYLDWYLOKPGQSPOLLIYSGSHR 59

D 21 DFMVTQSPSSLAIVAGETVTINCKSSQSLFSGNOKNYLAWYQKPGQSPKLLIYWASTR 80

QY 60 ASGVDPDRFSGSVSGTDTLRLSRVEADGVVYCMQGLQSPFTFGCTKVDIKRGTVAAAP 119

D 81 QSGVPDRFSGSGSGTDTLRLSRVEADGLAIYCYQYETPTFGAGTKLEKLRAD-AAP 139

QY 120 SYFIFPPSDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSY 179

D 140 TVSIFFPPSTEQLATGGASVCLMNNFYPRDISVKKWIDGTERDRGVLDSDVTDQDSKDSY 199

QY 180 SLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

D 200 SMSSTLSLKADYESHNLTYCEVHKTSSSPVVKSFNRNEC 240

RESULT 13

A31790

Ig kappa chain V region (17/9) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C:Accession: A31790

R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A

J. Biol. Chem. 263, 17100-17105, 1988

A:Title: Preliminary crystallographic data, primary sequence, and binding data for an

A:Reference number: A92686; MUID:89034213; PMID:3182835

A:Accession: A31790

A:Molecule type: mRNA

A:Residues: 1-220 <SCH>

A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

60.2%; Score 690; DB 2; Length 220;

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:44 ; Search time 5.01901 seconds
(without alignments)
1818.046 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSLPLSVTPGEPAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	47.8	106	1	KAC_HUMAN
2	527	46.0	117	1	KV2E_HUMAN
3	500	43.6	113	1	KV2D_HUMAN
4	478.5	41.8	112	1	KV2C_HUMAN
5	467.5	40.8	115	1	KV2A_HUMAN
6	455	39.7	113	1	KV2B_HUMAN
7	444	38.7	133	1	KV2F_HUMAN
8	432	37.7	113	1	KV2E_MOUSE
9	429	37.4	113	1	KV2G_MOUSE
10	423	36.9	113	1	KV2F_MOUSE
11	402	35.1	112	1	KV2D_MOUSE
12	394.5	34.4	108	1	KV1_CANFA
13	394	34.4	113	1	KV2C_MOUSE
14	387	33.8	112	1	KV2A_MOUSE
15	370	32.3	129	1	KV3L_HUMAN
16	369	32.2	129	1	KV3M_HUMAN
17	368.5	32.2	114	1	KV4A_HUMAN
18	367	32.0	106	1	KACB_RAT
19	366.5	32.0	134	1	KV3B_HUMAN
20	366	31.9	109	1	KV3D_HUMAN
21	366	31.9	109	1	KV3D_MOUSE
22	362	31.6	120	1	KV3A_MOUSE
23	359	31.3	106	1	KACA_RAT
24	357	31.2	109	1	KV3E_HUMAN
25	357	31.2	109	1	KV3G_HUMAN
26	354	30.9	133	1	KV4B_HUMAN
27	351	30.6	108	1	KV3A_HUMAN
28	350	30.5	106	1	KAC_MOUSE
29	349.5	30.5	128	1	KV3K_HUMAN
30	343.5	30.0	111	1	KV3M_MOUSE
31	340.5	29.7	111	1	KV3L_MOUSE
32	340	29.7	109	1	KV3F_HUMAN
33	338.5	29.5	111	1	KV3O_MOUSE

34	338.5	29.5	111	1	KV3U_MOUSE
35	338	29.5	129	1	KV3H_HUMAN
36	336.5	29.4	111	1	KV3S_MOUSE
37	335.5	29.3	111	1	KV3N_MOUSE
38	334.5	29.2	111	1	KV3R_MOUSE
39	333.5	29.1	111	1	KV3H_MOUSE
40	332	29.0	110	1	KV3P_MOUSE
41	331.5	28.9	111	1	KV3Q_MOUSE
42	326.5	28.5	111	1	KV3J_MOUSE
43	326.5	28.5	111	1	KV3T_MOUSE
44	324.5	28.3	111	1	KV3C_MOUSE
45	324.5	28.3	131	1	KV3I_MOUSE

P01673	mus musculu
P04207	homo sapien
P01671	mus musculu
P01666	mus musculu
P01670	mus musculu
P01660	mus musculu
P01668	mus musculu
P01669	mus musculu
P01662	mus musculu
P01672	mus musculu
P01656	mus musculu
P01661	mus musculu

ALIGNMENTS

RESULT 1					
ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.	
AC	P01834;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Ig kappa chain C region.				
GN	IGKC.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE (MYELOMA PROTEIN EU)				
RX	MEDLINE=71064023; PubMed=5489770;				
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";				
RL	Biochemistry 9:3155-3161(1970).				
RN	[2]				
RP	DISULFIDE BONDS.				
RX	MEDLINE=71064027; PubMed=4923144;				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";				
RL	Biochemistry 9:3188-3196(1970).				
RN	[3]				
RP	SEQUENCE (BENCE-JONES PROTEIN TI).				
RX	MEDLINE=72188439; PubMed=5027703;				
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;				
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";				
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81042304; PubMed=6775818;				
RA	Hietor P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;				
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";				
RL	Cell 22:197-207(1980).				
RN	[5]				
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).				
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;				
RL	(In) Fraenkel F., Shugar D. (eds.);				
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).				
RN	[6]				
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).				
RX	MEDLINE=68242259; PubMed=5585923;				
RA	Hilschmann N.;				
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";				

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RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RX SEQUENCE (BENCE-JONES PROTEIN AG).
RP MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1.2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
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CC -----
CC EMBL; J00241; AAA58989.1; -.
DR EMBL; V00557; CAA23823.1; -.
DR PIR; A02116; K3HU.
DR HSP; P01842; 7FAB.
DR Genew; HGNC:5716; IGKC.
DR MIM; 147200; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 26 86
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1.2) MARKER).
FT /FTid=VAR_003897.
FT CONFLICT 14 14
FT CONFLICT 57 57
FT CONFLICT E -> Q (IN REF. 5 AND 6).
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ
Query Match 47.8%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.9e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 115 TVAAPSVFIIPPSDEQLKSGTASVCLLNFFPRAKVQWKVDNALSGNSQESVTEQDS 174
D 1 TVAAPSVFIIPPSDEQLKSGTASVCLLNFFPRAKVQWKVDNALSGNSQESVTEQDS 60
QY 175 KDSYLSLSLTLSKADYKHKYACEVTHQGLSPVTKSFNRGEC 220
D 61 KDSYLSLSLTLSKADYKHKYACEVTHQGLSPVTKSFNRGEC 106
RESULT 2
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
```

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RN SEQUENCE FROM N.A.
RP MEDLINE=84191506; PubMed=6325927;
RX Klobeck H.G., Solomon A., Zachau H.G.;
RA "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00009; -. NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117
FT DOMAIN 5 27
FT DOMAIN 28 43
FT DOMAIN 44 58
FT DOMAIN 59 65
FT DOMAIN 66 97
FT DOMAIN 98 106
FT DOMAIN 107 116
FT DISULFID 27 97
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
SQ
Query Match 46.0%; Score 527; DB 1; Length 117;
Best Local Similarity 89.4%; Pred. No. 3.4e-38;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 1 EIVLTQSPLSLPVTGPGPASISCRSSQSLHSGNYVLDWYLOKPGQSPOLLIIYSGSHRA 60
D 5 DIVMTQSPLSLPVTGPGPASISCRSSQSLHSGNYVLDWYLOKPGQSPOLLIIYSGSRA 64
QY 61 SGVPDRFSGSGVGTFTLRSRVEAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
D 65 SGVPDRFSGSGVGTFTLRSRVEAEADVGVYCMQGLQSPFTFGPGTKVDIKR 117
RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis.";
RL Biochemistry 12:3763-3780(1973).
[2]
RN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
```

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RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis."
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR; A01885; K2HUTW.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 43.68; Score 500; DB 1; Length 113;
Best Local Similarity 82.38; Pred. No. 6.4e-36;
Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTYLDWYLOKPGSPQLLIYSGSHRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHSGDFLWYLYLQKPGSPQLLIYALSRA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPDRFSGSGGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPDRFSGSGGTDFTLKISRVAEDGVVYCMZALQAPITFGGQTRLEIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
KV2C_HUMAN
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01885; K2HUCM.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 40.88; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.88; Pred. No. 3.8e-33;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTYLDWYLOKPGSPQLLIYSGSHR 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DIVMTQSPSLPVTPGEPASISCRSSQSLDGDGNTLNWYLYLQKPGSPQLLIYLSYR 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 ASGVPDRFSGSGGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 ASGVPDRFSGSGGTDFTLKISRVAEDGVVYCMQRLQLEIPYTFGGQTKLEIRR 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
KV2B_HUMAN
```

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FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 41.88; Score 478.5; DB 1; Length 112;
Best Local Similarity 78.88; Pred. No. 4.2e-34;
Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTYLDWYLOKPGSPQLLIYSGSHRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVLTQSPSLPVTPGEPASISCRSSQSLZSBG-DYLDWYLYLQKPGSPZLLIYLGSNRA 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPDRFSGSGGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 SGVPDRFSGSGGTDFTLKISRVAZBVGYYCMQALQTPLTFGGNTNVEIKR 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
KV2A_HUMAN
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01885; K2HUCM.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 40.88; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.88; Pred. No. 3.8e-33;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTYLDWYLOKPGSPQLLIYSGSHR 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DIVMTQSPSLPVTPGEPASISCRSSQSLDGDGNTLNWYLYLQKPGSPQLLIYLSYR 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 ASGVPDRFSGSGGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 ASGVPDRFSGSGGTDFTLKISRVAEDGVVYCMQRLQLEIPYTFGGQTKLEIRR 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
KV2B_HUMAN
```

```
ID KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
RL with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
CC PIR; A01886; K2HUPR.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT CHAIN 1 20
FT SIGNAL 21 133
FT DOMAIN 21 43
FT DOMAIN 44 59
FT DOMAIN 60 74
FT DOMAIN 75 81
FT DOMAIN 82 113
FT DOMAIN 114 122
FT DOMAIN 123 132
FT DISULFID 43 113
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 38.7%; Score 444; DB 1; Length 133;
Best Local Similarity 75.2%; Pred. No. 4.5e-31;
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60
DB 1 DVNMTQSPFLPVTGLQGPASISCRSSQSLVYSDGNTLYLNMFQRPQSPRLIYKVSNRD 80
QY 61 SGVPDRSGSGVSGTDFTLKISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113
DB 81 SGVPDRSGSGVSGTDFTLKISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 133

RESULT 8
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=85128968; PubMed=6441768;
RA Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57BL/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Sevler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -I- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
CC PIR; A01912; KVM517.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT NON_TER 93 93
SQ SEQUENCE 93 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 39.7%; Score 455; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 4.2e-32;
Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60
DB 1 DVNMTQSPFLPVTGLQGPASISCRSSQSLVYREGTLYLWYLOKPGQSPQLLIYLSYRD 60
QY 61 SGVPDRSGSGVSGTDFTLKISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113
DB 61 SGVPDRSGSGVSGTDFTLKISRVAEADVGVYCMQGLQSPFTFGPTGKVDIKR 113

RESULT 7
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Weindl A., Combriato G., Solomon A., Zachau H.G.;
RT "Human Immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match
Best Local Similarity 37.7%; Score 432; DB 1; Length 113;
Matches 85; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLVTPGEPASISCRSSQSLHSHNGTYLDWYLRKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQTAPSVNLTGTSASISCRSSKSLHSHNGTYLDWYLRKPGQSPQLLIYQMSNLA 60

QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGYYCMQGLSPFTFGPTKVDIKR 113
Db 61 SGVPRFSGSGTDFTLIRSRVEADVGYYCAINLELPYTFGGTKLEIKR 113

RESULT 9
KV2G_MOUSE
ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83178921; PubMed=6404298;
RA Chang J.-Y., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KVM526.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match
Best Local Similarity 37.4%; Score 429; DB 1; Length 113;
Matches 82; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLVTPGEPASISCRSSQSLHSHNGTYLDWYLRKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQTAPSVNLTGTSASISCRSSKSLHSHNGTYLDWYLRKAGQSPKLLIYKVSNRF 60

QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGYYCMQGLSPFTFGPTKVDIKR 113
Db 61 SGVPRFSGSGTDFTLIRSRVEADLGIYFCSTHTVPTFGGKLEIKR 113

RESULT 10
KV2F_MOUSE
ID KV2F_MOUSE STANDARD; PRT; 113 AA.
AC P01630.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83055101; PubMed=7141411;
RA Herbst H., Chang J.-Y., Abersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
the group A streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match
Best Local Similarity 36.9%; Score 423; DB 1; Length 113;
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLVTPGEPASISCRSSQSLHSHNGTYLDWYLRKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQTAPSVNLTGTSASISCRSSKSLHSHNGTYLDWYLRKPGQSPQLLIYRMSNLA 60

QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGYYCMQGLSPFTFGPTKVDIKR 113
Db 61 SGVPRFSGSGTDFTLIRSRVEADVGYYCMQREYPTFGGKLEIKR 113

RESULT 11
KV2D_MOUSE
ID KV2D_MOUSE STANDARD; PRT; 112 AA.
AC P01629.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region 2S1.3.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83055101; PubMed=7141411;
RA Herbst H., Chang J.-Y., Abersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
the group A streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KVM526.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;
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CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
CC PIR: A01911; KVM51.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; BD5EF5E6D789FBEC CRC64;

Query Match 35.1%; Score 402; DB 1; Length 112;
Best Local Similarity 72.3%; Pred. No. 1.3e-27;
Matches 81; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQAAFNPVTLTGTSASCRSSKLSQSKGITYLYWYLQKPGQSPQLLIYQMSNLA 60

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPTGKVDIKR 112
DB 61 SGVPDRFSGSGTDFTLIRISRVEAEDGVVYCANLQELPYTFGGTKLEIK 112

RESULT 12
KV1_CANFA
ID KV1_CANFA STANDARD; PRT; 108 AA.
AC P01618;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region GOM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Flissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE
RX MEDLINE=79026193; PubMed=100411;
RA Wasserman R.L., Capra J.D.;
RT "The amino acid sequence of the light chain variable region of a
RT canine myeloma immunoglobulin: evidence that the VK subgroups
RT predated mammalian speciation.";
RL Immunochimistry 15:303-305(1978).
CC -!- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
CC CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF
CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR PIR: A01907; K2DGM.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
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SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 34.4%; Score 394.5; DB 1; Length 108;
Best Local Similarity 69.0%; Pred. No. 5.5e-27;
Matches 78; Conservative 13; Mismatches 17; Indels 5; Gaps 1;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQTPISLSVSGEPASISCRSSQSNL----DYLNMVYLQKAGOSPRLLPQDSQRA 55

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPTGKVDIKR 113
DB 56 SGVPDRFSGSGTDFTLIRIGRVEAEDAGIYCMQGRSFYPTFGQGRLEVR 108

RESULT 13
KV2C_MOUSE
ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A01910; KVM551.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 34.4%; Score 394; DB 1; Length 113;
Best Local Similarity 69.0%; Pred. No. 6.4e-27;
Matches 78; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVITQDELSPVTSGESVSISSCRSSKSLYKDGKTYLNMFLQGPQSPRLIYLMSTRA 60

QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPTGKVDIKR 113
DB 61 SGVSDRFSGSGSGTDFTLISIRKAEADVGVVYCOQLVEYPLTFGAGTKLEIKR 113

RESULT 14
KV2A_MOUSE
ID KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   Immunoglobulin_v region; Signal.
FT   SIGNAL      1
FT   CHAIN       20
FT   CHAIN       21 129
FT   DOMAIN      21 43
FT   DOMAIN      44 55
FT   DOMAIN      56 70
FT   DOMAIN      71 77
FT   DOMAIN      78 109
FT   DOMAIN      110 118
FT   DOMAIN      119 129
FT   DISULFID    43 109
FT   NON_TER     129 129
SQ   SEQUENCE    129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match      32.3%; Score 370; DB 1; Length 129;
Best Local Similarity 66.4%; Pred. No. 8.3e-25;
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

QY   1  EIVLTQSPLESLPVTPGQASISCRSSQSLHNSGYTYLDHWYLOKPGQSPQLLIYSGSRA 60
      |||||...:|||||:|||||:|||||: 1  || || |||||:||||| 1 ||
Db    21  EIVLTQSPGLTSLSPGERATLSCRASVSQSS---YLAWYQQKPGQAPRLIYIGASSRA 76

QY   61  SGVPDRFSGSVSGTDFLTRISRVAEADVGVVYCMQGLQSPFTFGPGKPVDIR 113
      :|||...|||...|||:||||| 1  || || |||||:||||| 1 ||
Db    77  TGIPTDRFSGSGSGTDFLTRISLRLEPEDEVAVYVCOQYCTSPRTFGQGTKEIKR 129

Search completed: March 14, 2003, 11:48:07
Job time : 5.01901 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:09 ; Search time 16.3118 seconds
(without alignments)
2778.994 Million cell updates/sec

Title: US-09-822-698A-24
Perfect score: 1146
Sequence: 1 EIVLTQSPVLPVTGPAS.....EVTHQGLSPVTKSENRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	973.5	84.9	239	4	Q8TCD0	Q8Tcd0 homo sapien
2	795.5	69.4	238	11	Q9M37	Q9m37 mus musculu
3	782.5	68.3	239	11	Q8VC55	Q8vc55 mus musculu
4	776.5	67.8	238	11	Q8VC16	Q8vc16 mus musculu
5	648	56.5	234	11	Q8VCF0	Q8vcp0 mus musculu
6	635	55.4	214	11	Q9VIA5	Q9ria5 mus musculu
7	624.5	54.5	235	11	Q91W12	Q91w12 mus musculu
8	621	54.2	234	11	Q91WF8	Q91wf8 mus musculu
9	615	53.7	234	11	Q8R062	Q8r062 mus musculu
10	609	53.1	233	11	Q91WS9	Q91ws9 mus musculu
11	590	51.5	234	11	Q8R028	Q8r028 mus musculu
12	437.5	38.2	233	4	Q8TBC9	Q8tbc9 homo sapien
13	433.5	37.8	237	4	Q8WTU6	Q8wtu6 homo sapien
14	431.5	37.7	237	4	Q8WUK4	Q8wuk4 homo sapien
15	428.5	37.4	114	4	Q9UL80	Q9ul80 homo sapien
16	407	35.5	236	4	Q96E61	Q9ee61 homo sapien

17	406	35.4	104	11	Q9JL82	Q9jl82 mus musculu
18	377	32.9	240	4	Q8WUK3	Q8wuk3 homo sapien
19	376.5	32.9	235	11	Q99M11	Q99m11 mus musculu
20	373	32.5	109	4	Q9UL78	Q9ul78 homo sapien
21	369	32.2	109	4	Q9UL86	Q9ul86 homo sapien
22	364.5	31.8	233	4	Q96I69	Q96i69 homo sapien
23	351.5	30.7	108	4	Q9UL83	Q9ul83 homo sapien
24	340.5	29.7	111	11	Q920B9	Q920b9 mus musculu
25	325.5	28.4	107	11	Q9ER29	Q9er29 mus musculu
26	322	28.1	107	4	Q9UL81	Q9ul81 homo sapien
27	322	28.1	109	4	Q9UL85	Q9ul85 homo sapien
28	316.5	27.6	108	4	Q9UL77	Q9ul77 homo sapien
29	316	27.6	116	4	Q96PF6	Q96pf6 homo sapien
30	313	27.3	106	5	Q904I0	Q9u4i0 schistosoma
31	309.5	27.0	108	4	Q9UL79	Q9ul79 homo sapien
32	308	26.9	107	4	Q96SA9	Q96sa9 homo sapien
33	307.5	26.8	298	11	Q9QVF0	Q9qvf0 mus musculu
34	306.5	26.7	108	4	Q9UL70	Q9ul70 homo sapien
35	299.5	26.1	134	11	Q8VDD0	Q8vdd0 mus musculu
36	295.5	25.8	108	11	Q8VIJ0	Q8vij0 mus musculu
37	293.5	25.6	109	11	Q920B6	Q920b6 mus musculu
38	284.5	24.8	103	11	Q9JL80	Q9jl80 mus musculu
39	283.5	24.7	99	11	Q9JL74	Q9jl74 mus musculu
40	276.5	24.1	101	11	Q9JL78	Q9jl78 mus musculu
41	265.5	23.2	97	11	Q9JL76	Q9jl76 mus musculu
42	255.5	22.3	127	11	Q925S9	Q925s9 mus musculu
43	249.5	21.8	109	6	Q9N0W5	Q9n0w5 oryctolagus
44	240.5	21.0	107	11	Q9JL84	Q9jl84 mus musculu
45	234	20.4	130	11	Q9D8W4	Q9d8w4 mus musculu

ALIGNMENTS

RESULT 1

Q8TCD0	PRELIMINARY;	PRT;	239 AA.
ID	Q8TCD0		
AC	Q8TCD0:		
DT	01-JUN-2002 (Tremblrel. 21, Created)		
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)		
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)		
DE	Hypothetical 26.2 kDa protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LUNG;		
RA	Strausberg R.;		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC022362; AAH22362.1; -.		
KW	Hypothetical protein.		
SQ	SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;		

Query Match	84.9%	Score 973.5;	DB 4;	Length 239;
Best Local Similarity	85.5%	Pred. No. 1.5e-84;		
Matches	188;	Conservative	18;	Mismatches 13;
Indels	1;	Gaps	1;	
Qy	1	EIVLTQSPVLPVTGPASISCRSSQSLHNSGYTLDWYLRKPGQSPQLLIYSGSHR	60	
Db	21	DVMTQSPVLPVLTGQPASISCRSTQSLVYSDGNTVLTNNFQQRPQSPRLIYKVNRD	80	
Qy	61	SGVPRFSGSGVSGDFTLRISREAEDGVGYCHQGLQSPFTFGPGVKVDIKRGTVAAPS	120	
Db	81	SGVPRFSGSGSGDFTLRISREAEDGVGYCHQGLQSPFTFGPGVKVDIKRGTVAAPS	139	
Qy	121	VFIPPPDEQLKSGTASVVCVLLNFFPREAKVQKVDNALQSGNSQESVTEQDSKSTYS	180	
Db	140	VFIPPPDEQLKSGTASVVCVLLNFFPREAKVQKVDNALQSGNSQESVTEQDSKSTYS	199	
Qy	181	LSSTLTLSKADYEKHKH YACEVTHQGLSSPVTKSFNRGEC	220	

Db 200 LSSTLTLSKADYEKKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 2

Q99M37

ID Q99M37 PRELIMINARY; PRT; 238 AA.

AC Q99M37;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical 26.3 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX [1]

RN R1

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC002035; AAH02035.1; -

DR HSSP; P01679; 2FEJ.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003600; Ig_like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00409; Ig; 2.

DR SMART; SM00407; IGC1; 1.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; Ig_like; 1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

QO SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 69.4%; Score 795.5; DB 11; Length 238;

Best Local Similarity 67.7%; Pred. No. 1.3e-67;

Matches 149; Conservative 31; Mismatches 39; Indels 1; Gaps 1;

Qy 1 EIVLTSPSLPVTGCEPASISCRSSQSLHNSGYTLDMVLQKPGQSPOLLIVSGSHRA 60

Db 20 DVMTQTPLSLPVSLGDAQSISCRSSQIVHSNGTYLEWYLQKPGQSPKLLIYKYSNRF 79

Qy 61 SGVPDRFSGSGCTDFTLRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120

Db 80 SGVPDRFSGSGCTDFTLRISRVEAEDGLGVYCYCGSHVPYTFGSGTKLEIKRAD-AAPT 138

Qy 121 VFIPTPSDEQLKSGTASVYCLLNNEYPREAKVQMKVDNALQSGNSQSVTEQDSKDSYTS 180

Db 139 VSIPTSPSDEQLKSGGASVYCLLNNEYPREAKVQMKVDNALQSGNSQSVTEQDSKDSYTS 198

Qy 181 LSSTLTLSKADYEKKVYACEVTHQGLSSPVTKSFNRGEC 220

Db 199 MSSTLTLTKEDEYRHSNYTCEATHTSTSPVKSFNREC 238

RESULT 3

Q8VC55

ID Q8VC55 PRELIMINARY; PRT; 239 AA.

AC Q8VC55;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Hypothetical 26.3 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX [1]

RN R1

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL TISSUE-COLON;

RA submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DB 80 SGVDFRSGSGGDFTLKISRVEADLGVFCQSOTHPPTFGGTGLEIKRAD-AAPT 138
 QY 121 VFIFPPDEQLKSTASVVCCLNPNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180
 DB 139 VSIFPPSEQIQTGGASVVCFLNNFPYDKINVKWKIDGSERQNGVLNSWTDQSDSKSTYS 198
 QY 181 LSSITLTLSKADYEKKHKYACEVTHOGLSSPVTKSFNRGEC 220
 DB 199 MSSTLTLTCKDEVERHNSYTCEATHKTSTSPIVKSFRNEC 238

RESULT 5
 QBVCP0 PRELIMINARY; PRT; 234 AA.
 AC QBVCP0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 25.7 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL EMBL: BC019474; RAH19474.1; -.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; Igcl; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 56.5%; Score 648; DB 11; Length 234;
 Best Local Similarity 56.4%; Pred. No. 1.3e-53;
 Matches 124; Conservative 34; Mismatches 56; Indels 6; Gaps 2;

QY 1 EIVLTQSPSLPVTGPETASISCRSQSLLHSNGTYTLDWYLQKPGQSPOLLYYSGSHRA 60
 DB 21 DIQLTQSPASLASVGFTVITCRASENI-----YSYLAWYQQKQGKSPOLLVYNKATLA 75
 QY 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
 DB 76 DGVPSRFSGSRSGTQFSLKINSIQPEDPGSYCYQHSGIPFTFGSGTKLEIKRAD-AAPT 134
 QY 121 VFIFPPSDRLQKSTASVVCCLNPNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180
 DB 135 VSIFPPSSQLTSGGASVVCFLNNFPYDKINVKWKIDGSERQNGVLNSWTDQSDSKSTYS 194
 QY 181 LSSITLTLSKADYEKKHKYACEVTHOGLSSPVTKSFNRGEC 220
 DB 199 MSSTLTLTCKDEVERHNSYTCEATHKTSTSPIVKSFRNEC 234

RESULT 6
 Q9RIA5 PRELIMINARY; PRT; 214 AA.
 ID Q9RIA5;
 AC Q9RIA5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Kappa light chain of Mab7 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db 194 MSSTLTITKDEYERHNSYTCETHKSTSPIVKSFNRNEC 233

RESULT 11

Q8R028
ID Q8R028 PRELIMINARY; PRT; 234 AA.
AC Q8R028 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028540; AAH28540.1; -
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0AEE CRC64;

Query Match 51.5%; Score 590; DB 11; Length 234;
Best Local Similarity 52.7%; Pred. No. 4.4e-48;
Matches 116; Conservative 29; Mismatches 69; Indels 6; Gaps 2;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLOKPGSQPOLLIYSGSHRA 60
Db 21 ETTVTQSPASLSVATGKVTIRCTITDIDD-----MNYQKQGPPEPKLLISEGNTLR 75
QY 61 SGVPDRFSGSVGTDTFLTRISRVEAEDVGYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 76 PGVPSRFSSSGYGTDFVTIENTLSEADVYCLQSDNNPLTFCAGTKLELRAD-AAPT 134
QY 121 VFIFPPSDEQLKSGTASVCLLNFFPREAKVQWKVDNALQNSQESVTEQDSKSDSTYS 180
Db 135 VSIFPPSDEQLKSGTASVCLLNFFPREAKVQWKVDNALQNSQESVTEQDSKSDSTYS 194
QY 181 LSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 220
Db 195 MSSTLTITKDEYERHNSYTCETHKSTSPIVKSFNRNEC 234

RESULT 12

Q8RBC9
ID Q8RBC9 PRELIMINARY; PRT; 233 AA.
AC Q8RBC9 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028283; AAH28283.1; -
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BF6D6F4DF92 CRC64;

Query Match 38.2%; Score 437.5; DB 4; Length 233;
Best Local Similarity 44.5%; Pred. No. 1.4e-33;
Matches 98; Conservative 40; Mismatches 69; Indels 13; Gaps 8;

QY 4 LTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLOKPGSQPOLLIYSGSHRASGV 63
Db 23 LTQPP-SVSGAPGORVITSCGSSNIGA-GYD-VHYYQQLPGTAPKLLIYGSNRPSPG 76

QY 64 PDRESGSVGTDTFLTRISRVEAEDVGYCMQGLQSP--FTFGPGTKVDIKRGTVAAPSV 121
Db 77 PERFGSSSGTAVTITISGVQAEADADYYCQADSSGTYVWFGGKTKLTVLGQPKAAAPSV 136
QY 122 FIFPPSDEQLKSGTASVCLLNFFPREAKVQWKVDNA--LQSGNSQESVTEQDSKSDSTYS 180
Db 137 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG--VETTPSKQSNKYA 194
QY 181 LSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 220
Db 195 ASSYLSTLTPQWKSHKSYSCQVTHGEG--STVEKTVAPTEC 232

RESULT 13

Q8WTU6
ID Q8WTU6 PRELIMINARY; PRT; 237 AA.
AC Q8WTU6 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022098; AAH22098.1; -
DR InterPro; IPR003599; Ig_c1
DR InterPro; IPR003597; Ig_c1
DR InterPro; IPR003596; Ig_MHC
DR Pfam; PF00047; Ig_2
DR SMART; SM00409; Ig_2
DR SMART; SM00407; Igc1; 1
DR SMART; SM00406; Igc1; 1
DR PROSITE; PS00290; Igc_MHC; UNKNOWN_1
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;

Query Match 37.8%; Score 433.5; DB 4; Length 237;
Best Local Similarity 43.2%; Pred. No. 3.4e-33;
Matches 96; Conservative 43; Mismatches 72; Indels 11; Gaps 7;

QY 3 VLTQSPSLPVTGPEPASISCRSSQSLHNSGYTLDWYLOKPGSQPOLLIYSGSHRASG 62
Db 22 VLTQPP-SVSGAPGORVITSCGSSNIGA-GYD-VHYYQQLPGTAPKLLIYGSNRPSPG 78
QY 63 VDRFSGSVGTDTFLTRISRVEAEDVGYCMQ---GLQSPFTFGPGTKVDIKRGTVAAAP 119
Db 79 VDRFSGSKSGTASLAITGLQAEADADYYCQSDYSLASGVEGSGTKLTVLGQPKAAP 138
QY 120 SVEIFPPSDEQLKSGTASVCLLNFFPREAKVQWKVDNA--LQSGNSQESVTEQDSKSDST 178
Db 139 SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAG--VETTPSKQSNK 196
QY 179 YLSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 220
Db 197 YAASSYLSTLTPQWKSHRSYSCQVTHGEG--STVEKTVAPTEC 236
RESULT 14
Q8WUK4
ID Q8WUK4 PRELIMINARY; PRT; 237 AA.
AC Q8WUK4 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020233; AAH20233.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 37.4%; Score 428.5; DB 4; Length 114;
Best Local Similarity 73.7%; Pred. No. 3.7e-33;
Matches 84; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLSPLVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db :||:||||||| :||||||| :||: ||| :|:||||| :||| :|
1 DVVMTQSPVLSPLVTLRQPASISCRSSQSPVYSDGNTYLNWFQORPGSPRLIYKVSNRD 60
QY 61 SGVPDRFSGSVSGTDFTLRISRYVEAEDVGYYCMQGLQ-SPTEGPGTKVDIKR 113
Db ||||||| :||||| :||||| :||||| :||||| :||||| :||| :|||
61 SGVPDRFSGSVSGTDFTLRISRYVEAEDVGYYCMQGLQ-SPTEGPGTKVDIKR 114

Search completed: March 14, 2003, 11:49:36
Job time : 17.3118 secs

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020233; AAH20233.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 37.7%; Score 431.5; DB 4; Length 237;
Best Local Similarity 43.2%; Pred. No. 5.3e-33;
Matches 96; Conservative 42; Mismatches 73; Indels 11; Gaps 7;

QY 3 VLTQSPVLSPLVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRASG 62
Db ||||| :| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
22 VLTQPP-SVSGAPGQGVITISCTGSSNIGA-GYD-VHVIQQLPGTAPKLLIYGNSNRPSG 78
QY 63 VPDFSGSVSGTDFTLRISRYVEAEDVGYYCM--QGLOSPFTFGPGTKVDIKRGTVAAP 119
Db ||||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
79 VPDFSGSKSGTSASIAITGLQAEADYCYQSYDSSLSGFWFGGKTLVLGPKAAP 138
QY 120 SVFIPTPDSDEQLKSTASVWCLLNFFYPREAKVQWKVDNA-LQSGNSQESVTEQDSKDST 178
Db || :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
139 SVTLFPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG--VETTTPSKQSNKK 196
QY 179 YSLSTLTLSKADYKHKHYACENTHOGLSPPVTKSFNRGEC 220
Db | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
197 YAASSYLSLTPEQWKSRSYSCQVTHEG--STVEKTVAPTEC 236

RESULT 15
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; RAD56270.1; -.
DR HSP; F80362; 1WTU.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:04 ; Search time 41.1559 Seconds
(without alignments)
1460.205 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 OVQLVGGGLVPGGSLRL.....MHEALHNYTKSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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	5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
	6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
	7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
	8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
	9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
	10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
	11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
	12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
	13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
	14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
	15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
	16:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
	17:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
	18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
	19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
	20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
	21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
	22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
	23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2411	100.0	451	22	AAE12715 Human recombinant
2	2270	94.2	449	21	AAV68810 A rat heavy chain
3	2257	93.6	474	23	AAO14065 Heavy chain protei
4	2236.5	92.8	461	22	AAU07745 Humanised monoclon
5	2229.5	92.5	477	22	AAU14288 Human novel protei
6	2228.5	92.4	475	13	AAZ20057 Heavy chain of 3D6
7	2216	91.9	582	22	AAZ81987 Ganglioside GD3 sp
8	2211.5	91.7	452	20	AAZ29458 Recombinant immuno
9	2211.5	91.7	452	21	AAZ30322 Humanised anti-IL-
10	2211.5	91.7	452	21	AAV77766 Humanised anti-IL-

11	2207.5	91.6	459	14	AAZ42066 Human anti-HBs hea
12	2202.5	91.4	452	19	AAW69316 Anti-IL-8 humanise
13	2190	90.8	477	15	AAZ47453 chiT84.12 H3 heavy
14	2186	90.7	466	13	AAZ24812 Sequence encoded b
15	2177	90.3	453	14	AAZ33311 Humanised MaE11 ve
16	2177	90.3	453	21	AAZ85199 Heavy chain amino
17	2174	90.2	461	14	AAZ42162 Anti-HIV-1 recombi
18	2172.5	90.1	444	21	AAZ32263 Humanised anti-CD2
19	2171	90.0	582	22	AAZ81991 Ganglioside GD3 sp
20	2169	90.0	451	20	AAW95659 Mus musculus anti-
21	2169	90.0	451	20	AAW95661 Mus musculus anti-
22	2169	90.0	451	21	AAZ85201 Light chain amino
23	2169	90.0	451	22	AAZ47088 Anti-IgE antibody,
24	2169	90.0	451	22	AAZ76948 Full length heavy
25	2169	90.0	451	22	AAZ76950 Full length heavy
26	2168	89.9	451	20	AAZ50031 Human E27 anti-IgE
27	2168	89.9	451	20	AAW95663 Mus musculus anti-
28	2168	89.9	451	21	AAZ07473 Amino acid sequenc
29	2168	89.9	451	22	AAZ74212 E27 anti-IgE antib
30	2168	89.9	451	22	AAZ76952 Full length heavy
31	2165.5	89.8	470	7	AAZ60351 Chimeric human-mou
32	2165.5	89.8	470	8	AAZ70547 Sequence of novel
33	2160	89.6	478	19	AAW63763 Macaque primatized
34	2160	89.6	478	23	AAU11644 Protein sequence o
35	2154	89.3	478	18	AAW01820 Primatized anti-hu
36	2118	87.8	481	13	AAZ24442 Sequence of antibo
37	2116	87.8	449	14	AAZ43339 Completely humanis
38	2116	87.8	449	19	AAW49816 Amino acid sequenc
39	2114.5	87.7	519	23	AAZ81993 Human secreted pro
40	2113.5	87.7	731	22	AAZ52156 Humanised HMFG-1 h
41	2113.5	87.7	741	22	AAZ52159 Humanised HMFG-1 h
42	2112.5	87.6	581	22	AAZ81972 Ganglioside GD2 sp
43	2109.5	87.5	465	22	AAZ72228 Humanised 323/A3 (
44	2109.5	87.5	467	13	AAZ22758 Reshaped CD4 antib
45	2109.5	87.5	467	13	AAZ22759 Reshaped CD4 antib

ALIGNMENTS

RESULT 1
AAE12715
ID AAE12715 standard; Protein; 451 AA.

AC AAE12715;

XX
DT 04-JAN-2002 (first entry)

XX Human recombinant immunoglobulin (Ig) heavy chain region.

XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
KW heavy chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; immunoglobulin; Ig.

XX Homo sapiens.

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX N-PSDB; AAD20745.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Claim 12; Page 106-108; 126pp; English.
 PS
 XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human recombinant immunoglobulin
 CC (Ig) heavy chain region (variable VH and CH constant heavy chain).
 XX Sequence 451 AA;

Query Match 100.0%; Score 2411; DB 22; Length 451;
 Best Local Similarity 100.0%; Pred. No. 6.3e-136;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60
 Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60
 QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGQGLTVTS 120
 Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGQGLTVTS 120
 QY 121 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180
 Db 121 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180
 QY 181 SGLYSLSVTVVPSSSLGDTQYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELIG 240
 Db 181 SGLYSLSVTVVPSSSLGDTQYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELIG 240
 QY 241 GPSVFLPPPKDFTLMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQY 300
 Db 241 GPSVFLPPPKDFTLMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQY 300
 QY 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
 Db 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
 QY 361 ELTRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
 Db 361 ELTRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
 QY 421 WQOQNVFSCVMHEALHNHYTQKSLSLSPGK 451
 Db 421 WQOQNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 2
 AAY68810
 ID AAY68810 standard; Protein; 449 AA.
 XX
 AC AAY68810;
 XX
 XX 16-MAY-2000 (first entry)
 XX
 DE A rat heavy chain region and a human hinge region.
 XX
 KW CD3 antigen complex; chimeric antibody; immunosuppression; heavy chain;
 KW CD3 antigen-T-cell receptor complex; graft rejection; cancer.

XX Synthetic.
 OS Rattus sp.
 OS Homo sapiens.
 XX WO200005268-A1.
 XX 03-FEB-2000.
 XX 21-JUL-1999; 99WO-GB02380.
 XX 21-JUL-1998; 98GB-0015909.
 XX (BTGI-) BTG INT LTD.
 XX Waldmann H, Frewin M;
 DR WPI; 2000-182655/16.
 DR N-PSDB; AAZ60599.
 XX New humanized anti-CD3 antibodies, used for treating cancer or for
 PT immunosuppression and preventing graft rejection -
 XX Disclosure; Page 45-47; 56pp; English.
 XX The present sequence represents the heavy chain variable region of a rat
 CC immunoglobulin G (IgG) antibody which is specific for the CD3 antigen
 CC complex, and the human CHI-hinge-aglycosylCH2CH3. The specification
 CC describes chimeric human/rodent anti-CD3 antibodies, which have a
 CC rodent CD3 light chain variable region and a human heavy chain variable
 CC region. The anti-CD3 antibodies can render T-cells non-functional by
 CC antibody blockade of the CD3 antigen-T-cell receptor (TCR) complex.
 CC They can be used for immunosuppression, particularly for the control
 CC of graft rejection. The antibodies can also enhance or re-direct T-cell
 CC responses to antigens. They can be used in the treatment of cancer.
 XX Sequence 449 AA;
 Query Match 94.2%; Score 2270; DB 21; Length 449;
 Best Local Similarity 94.9%; Pred. No. 1.6e-127;
 Matches 431; Conservative 5; Mismatches 10; Indels 8; Gaps 2;
 QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60
 Db 1 EQVLESGLVQPGGSLRLSCAASGFTFSSPMAVWRQAPGKLEWVSTISTSGRTYY 60
 QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYCAK---HTGGGVWDPIDYWGQGLTV 117
 Db 61 RDSVKGRTISRDNKNTLYLQMNLSRAEDTAVYCAKFRQYSGG----FDYWGQGLTV 115
 QY 118 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 177
 Db 116 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175
 QY 178 LQSSGLYSLSVTVVPSSSLGDTQYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPE 237
 Db 176 LQSSGLYSLSVTVVPSSSLGDTQYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPE 235
 QY 238 LLGGPSVFLPPPKDFTLMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPRE 297
 Db 236 LLGGPSVFLPPPKDFTLMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPRE 295
 QY 298 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 357
 Db 296 EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
 QY 358 SRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 417
 Db 356 SRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 415
 QY 418 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
 Db 416 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

Db	196	TFPAVLQSGSLKSLSSVTVFSSSLGQTGYICNVNHNKPSITKVDKRVKPSCDKTHTCPP	255
QY	233	CPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK	292
Db	256	CPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK	315
QY	293	TKPREEQNSTYRVVSVLTVLHODWLNAGEYKCKVSNKALPAPIEKTIISKAKGQPREQV	352
Db	316	TKPREEQNSTYRVVSVLTVLHODWLNAGEYKCKVSNKALPAPIEKTIISKAKGQPREQV	375
QY	353	YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS	412
Db	376	YTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS	435
QY	413	KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	451
Db	436	KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	474
RESULT 4			
AAU07745			
ID	AAU07745 standard; Protein; 461 AA.		
XX	AC AAU07745;		
DT	04-DEC-2001 (first entry)		
XX	Humanised monoclonal antibody Hu266, heavy chain.		
DE			
XX			
XX	Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;		
KW	Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;		
KW	gene therapy.		
XX			
XX			
OS	Mus sp.		
OS	Homo sapiens.		
OS	Synthetic.		
XX			
XX	Location/Qualifiers		
FF	1..19		
FT	Peptide		
FT	/label= Signal_peptide		
FT	20..461		
FT	/label= Mature_Hu266_heavy_chain		
FT	/note= "This sequence is specifically claimed in		
FT	claim 17"		
XX			
XX	WO200162801-A2.		
PN			
XX			
PD	30-AUG-2001.		
XX			
PF	26-FEB-2001; 2001WO-US06191.		
XX			
XX	24-FEB-2000; 2000US-0184601.		
PR	08-DEC-2000; 2000US-0254465.		
PR	08-DEC-2000; 2000US-0254498.		
XX			
XX			
PA	(UNIW) UNIV WASHINGTON.		
PA	(ELIL) LILLY & CO ELI.		
XX			
XX			
PI	Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;		
PI	Vasquez M;		
XX			
XX			
DR	WPI; 2001-550087/61.		
XX			
XX			
PT	New humanised antibody for the treatment of Alzheimer's comprises the		
PT	inhibition and reduction of the formation of amyloid plaques -		
XX			
XX	Example 13; Fig 5; 63pp; English.		
XX			
CC	The invention relates a humanised antibody that specifically binds		
CC	an epitope contained within positions 13-28 of amyloid beta peptide,		
CC	Abeta. The antibody is useful to inhibit and reduce the formation of		
CC	amyloid plaques or the effects of toxic soluble Abeta species in humans		
CC	their fragments are used for the manufacture of a medicament. This includes		

Db	377	QVYTLPSREMTKQVSLTCLVKGFVPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL	436
QY	411	YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQKSLSLSPGK	451
Db	437	YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQKSLSLSPGK	477
RESULT 6			
AAR20057	ID	AAR20057 standard; Protein; 475 AA.	
XX	AC	AAR20057;	
XX	DT	25-MAR-1992 (first entry)	
XX	XX	Heavy chain of 3D6 anti-HIV antibody.	
XX	DE	Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;	
KW	KW	complementarity determining region.	
XX	XX	Homo sapiens.	
OS	XX		
Key		Location/Qualifiers	
FH	FT	Peptide	1..19
FT	FT	/label= signal	
FT	FT	Region	20..49
FT	FT	/label= Framework_1	
FT	FT	Region	50..54
FT	FT	/label= CDR-1	
FT	FT	Region	55..68
FT	FT	/label= Framework_2	
FT	FT	Region	69..85
FT	FT	/label= CDR_2	
FT	FT	Region	86..117
FT	FT	/label= Framework_3	
FT	FT	Region	118..134
FT	FT	/label= CDR_3	
FT	FT	Region	135..145
FT	FT	/label= Framework_4	
FT	FT	Region	146..475
FT	FT	/label= Constant_region	
XX	XX	WO9118983-A.	
XX	XX	12-DEC-1991.	
XX	XX	28-MAY-1991;	91WO-1000067.
XX	XX	29-MAY-1990;	90AT-0001178.
XX	PA	(JUNG/) JUNGBAUER A.	
XX	PI	Felgenhauer M, Himmeler G, Kohl J, Steindl F;	
XX	PI	WPI; 1992-007468/01.	
XX	DR	N-PSDB; AAQ20066.	
XX	XX	Recombinant protein which binds to complex viral antigen and	
PT	PT	Hiv-1 - contains variable region of antibody derived from 3D6	
PT	PT	cell line, used for detecting HIV-1 antigen	
XX	XX	Claim 2; Page 24; 52pp; German.	
XX	XX	The variable region of the heavy chain is used in a recombinant	
CC	CC	protein with the variable region from the kappa light chain of 3D6,	
CC	CC	the two V regions being joined by a linker. The recombinant protein	
CC	CC	binds to HIV gp160.	
CC	CC	See also AAQ20067 and AAQ20068.	
XX	XX	Sequence	475 AA;
SQ			
Query Match		92.4%;	Score 2228.5; DB 13; Length 475;
Best Local Similarity		92.8%;	Pred. No. 4.9e-125;

Query Match	92.4%	Score 2228.5;	DB 13;	Length 475;
Best Local Similarity	92.8%	Pred. No. 4.9e-125;		

CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention.

XX
SQ Sequence 582 AA;
Query Match 91.9%; Score 2216; DB 22; Length 582;
Best Local Similarity 92.7%; Pred. No. 3.4e-124;
Matches 418; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 QVLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGMVROAPKGLWVSGIGSGGGSTYY 60
DB 1 EVQLVSGGGDFVQPGGSLRVSCAASGFAFSHYAMSVROAPKGLWVAYISSGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIIDYWGQGLTVTS 120
DB 61 SDSVKGRFTISRDNKNTLYLQMNLSRAEDSAVYFCTRVKLGTY--FDVWGQGLTVTS 118
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQS 180
DB 119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQS 178
QY 181 SGLYSLSVVTPVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLG 240
DB 179 SGLYSLSVVTPVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLG 238
QY 241 GPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREQY 300
DB 239 GPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREQY 298
QY 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
DB 299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 420
DB 359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 418
QY 421 WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 419 WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

RESULT 8
AAV29458
ID AAV29458 standard; Protein; 452 AA.
XX
AC AAV29458;
XX
XX 05-OCT-1999 (first entry)
XX Recombinant immunoglobulin SEQ ID NO:71.
XX
XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
XX diagnosis; inflammatory disorder; conjugate; immunoglobulin;
XX fusion protein.
XX Synthetic.
XX
XX WQ9937779-A1.
XX
XX 29-JUL-1999.
XX
XX 19-JAN-1999; 99WO-US01081.
XX
XX 24-JUL-1998; 98US-0122513.
XX 22-JAN-1998; 98US-0012116.
XX 20-FEB-1998; 98WO-US03337.
XX 24-JUL-1998; 98US-0121952.
XX
XX (GETH) GENENTECH INC.

PI Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;
PI Zapata GA;
XX
DR WPI; 1999-469134/39.
XX
XX New conjugates of nonproteinaceous polymers with antibody fragments,
XX used for treating inflammatory disorders
XX
XX Disclosure; Page 354-355; 360pp; English.

XX The present invention describes a novel conjugate having one or more
XX antibody fragments covalently attached to one or more nonproteinaceous
XX polymer molecules, where the apparent size of the conjugate is at least
XX about 500 kDa. Conjugates of antibody fragments which bind the human
XX interleukin (IL) 8 with a nonproteinaceous polymer can be used for
XX treating inflammatory disorders e.g. acute lung injury, ischaemic
XX reperfusion disorder, and autoimmune diseases. They can also be used
XX for treating e.g. inflammatory skin diseases including psoriasis and
XX atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
XX diseases. The conjugates can also be used as reagents in an animal
XX model system for in vivo study of the biological functions of the
XX antigen recognised by the conjugate. The present sequence represents
XX a recombinant immunoglobulin protein from the present invention.

XX Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 20; Length 452;
Best Local Similarity 92.5%; Pred. No. 4.8e-124;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGMVROAPKGLWVSGIGSGGGSTYY 60
DB 1 EVQLVQSGGGILVQPGGSLRLSCAASGYSFSSHYMHWVROAPKGLWVGYIDPSNGETTY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK--HTGGGVWDPIIDYWGQGLTVT 118
DB 61 NQKFGRTLSRDNSKNTAYLQMNLSRAEDTAVYYCARGDYRYNGDW- FQVWGQGLTVT 119
QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVL 178
DB 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVL 179
QY 179 QSSGLYSLSVVTPVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
DB 180 QSSGLYSLSVVTPVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 239
QY 239 LGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREE 298
DB 240 LGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREE 299
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
DB 300 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 418
DB 360 REMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 419
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 9
AAB30322
ID AAB30322 standard; Protein; 452 AA.
XX
XX AAB30322;
XX
XX 12-FEB-2001 (first entry)
XX
XX Humanised anti-IL-8 antibody related protein SEQ ID NO: 71.

Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
 adult respiratory distress syndrome; multiple organ failure;
 bacterial pneumonia; inflammatory bowel disease.

Unidentified.

US6133426-A.

17-OCT-2000.

20-FEB-1998; 98US-0026985.

21-FEB-1997; 97US-0038664.

22-JAN-1998; 98US-0074330.

(GETH) GENENTECH INC.

Presta LG, Leong SR, Gonzalez TN;

WPI; 2000-686027/67.

Humanized anti-interleukin 8 monoclonal antibody variant useful for
 treating inflammatory disorders, such as adult respiratory distress
 syndrome, hypovolemic shock and ulcerative colitis -

Disclosure; Column 199-202; 240pp; English.

The present invention provides a number of humanised monoclonal anti-IL-8
 antibodies which can be used in the diagnosis and treatment of
 inflammatory disorders, including adult respiratory distress syndrome,
 septic shock, multiple organ failure, bacterial pneumonia and
 inflammatory bowel disease. The present sequence comprises one of the
 antibodies of the invention.

Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 21; Length 452;
 Best Local Similarity 92.5%; Pred. No. 4.8e-124;
 Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSIGSGGSTYY 60

DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVWVQAPGKLEWGYIDPSNGETTY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAK--HTGGGVMDPIDYWGQGLT 118

DB 61 NQKFKGRFTLSRDNSKNTAVYLMNSLRAEDTAVYYCARGDYRYNGDWF-FDVWGQGLT 119

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

DB 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179

QY 179 QSSGLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238

DB 180 QSSGLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 239

QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTPREE 298

DB 240 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTPREE 299

QY 299 QYNSTYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

DB 300 QYNSTYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 418

DB 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 419

QY 419 SRWQGGNVFSCVNVHEALHNHYTQKSLSLSPGK 451

DB 420 SRWQGGNVFSCVNVHEALHNHYTQKSLSLSPGK 452

RESULT 10

AA77766

XX AAY77766 standard; Protein; 452 AA.

XX AC AAY77766;

XX DT 06-JUN-2000 (first entry)

XX DE Humanised anti-IL-8 antibody related protein seq ID No:71.

XX KW Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6GAV1IN35A;

XX KW inflammatory disorder; adult respiratory distress syndrome;

XX KW affinity purification.

XX OS Homo sapiens.

XX PN US6025158-A.

XX PD 15-FEB-2000.

XX PF 20-FEB-1998; 98US-0027449.

XX PR 21-FEB-1997; 97US-0038664.

XX PR 22-JAN-1998; 98US-0074330.

XX PA (GETH) GENENTECH INC.

XX PI Presta LG, Leong SR, Gonzalez TN;

XX DR WPI; 2000-181809/16.

XX PT New nucleic acid molecule encodes a polypeptide which is an
 anti-interleukin-8 monoclonal antibody or antibody fragment useful for
 the production of anti-interleukin-8 monoclonal antibodies or fragments

Examples; Columns 199-202; 189pp; English.

The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
 (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs
 (complementarity determining regions) of the humanized anti-IL-8
 6G4.2.5V1IN35A light chain; and amino acids 24-253 of the humanized
 anti-IL-8 6G4.2.5V1IN35A heavy chain. The anti-IL-8 MAb and fragments
 can be used in diagnosis, for affinity purification of IL-8 from
 recombinant cell culture or natural sources and for the treatment of
 inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic
 acids encoding the anti-IL-8 MAb can be associated in a vector with
 another gene encoding another protein or protein fragment to produce a
 fusion protein which can make isolation and/or purification of the
 protein an easier process.

Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 21; Length 452;
 Best Local Similarity 92.5%; Pred. No. 4.8e-124;
 Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSIGSGGSTYY 60

DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVWVQAPGKLEWGYIDPSNGETTY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAK--HTGGGVMDPIDYWGQGLT 118

DB 61 NQKFKGRFTLSRDNSKNTAVYLMNSLRAEDTAVYYCARGDYRYNGDWF-FDVWGQGLT 119

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

DB 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179

QY 179 QSSGLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238

DB 180 QSSGLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 239

```
QY 239 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
|||||
Db 240 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299
|||||
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPS 358
|||||
Db 300 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPS 359
|||||
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
|||||
Db 360 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 419
|||||
QY 419 SRWQGNVFSCSVMHREALNHHYTKQSLSPGK 451
|||||
Db 420 SRWQGNVFSCSVMHREALNHHYTKQSLSPGK 452
|||||

RESULT 11
AAR42066
ID AAR42066 standard; Protein; 459 AA.
XX
AC AAR42066;
XX
DT 29-APR-1994 (first entry)
DE Human anti-HBs heavy chain.
XX
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..9
FT Protein /label= sig_peptide
FT /label= mat_protein

W09320205-A.
XX
PD 14-OCT-1993.
XX
PF 30-MAR-1993; 93WO-JP00396.
XX
PR 30-MAR-1992; 92JP-0074678.
XX
PA (SUNR ) SUNTORY LTD.
XX
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;
XX
DR WPI; 1993-336913/42.
XX
DR N-PSDB; AAQ49944.
XX
PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity
XX
PS Disclosure; Fig 6-8; 46pp; Japanese.
XX
CC Polynucleotides encoding the L and H chains of human anti-HBs
CC Ab are given in AAQ49943-Q49944. The Ab can be easily produced in
CC large quantities for therapeutic use.
XX
SQ Sequence 459 AA;

Query Match 91.6%; Score 2207.5; DB 14; Length 459;
Best Local Similarity 92.7%; Pred. No. 8.4e-124;
Matches 418; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLEWVSGISGGSTYY 60
|||||
Db 10 QVQLVESGGGVQPGRLSRSLSCAASGFTFSSNMHWVROAPGKGLEWVAVILYDGNHKEY 69
|||||
QY 61 ADSVKGRFTISRDNKNTLYLEKSLQTDITGVYICRDQTYGV-HRPDSWGOGTLTVTS 120
|||||
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Db 70 ADSVKGRFTISRDNKNTLYLEKSLQTDITGVYICRDQTYGV-HRPDSWGOGTLTVTS 128
|||||
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 180
|||||
Db 129 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 188
|||||
QY 181 SGLYSLSVTVTPSSISGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPCPAPELLG 240
|||||
Db 189 SGLYSLSVTVTPSSISGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPCPAPELLG 248
|||||
QY 241 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
|||||
Db 249 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 308
|||||
QY 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRD 360
|||||
Db 309 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRD 368
|||||
QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 420
|||||
Db 369 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 428
|||||
QY 421 WQGNVFSCSVMHREALNHHYTKQSLSPGK 451
|||||
Db 429 WQGNVFSCSVMHREALNHHYTKQSLSPGK 459
|||||

RESULT 12
AAW69316
ID - AAW69316 standard; Protein; 452 AA.
XX
AC AAW69316;
XX
DT 15-FEB-1999 (first entry)
DE Anti-IL-8 humanised antibody 6G4V1N35A.choSD.9.
XX
KW Humanised antibody; chimeric antibody; monoclonal antibody; mouse;
KW human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW ischaemic reperfusion; adult respiratory distress syndrome;
KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
KW rheumatoid arthritis; Sjogren's syndrome; vasculitis;
KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
KW therapy; 6G4V1N35A.choSD.9.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN W09837200-A2.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-US03337.
XX
PR 22-JAN-1998; 98US-0012116.
PR 21-FEB-1997; 97US-0804444.
XX
PA (GETH ) GENENTECH INC.
XX
PI Hsai V, Koumenis I, Leong SR, Presta LR, Shahrokh Z;
PI Zapata GA;
XX
DR WPI; 1998-467563/40.
DR N-PSDB; AAV44956.
XX
PT New conjugates of antibody fragments - having covalently attached
PT non-proteinaceous polymer molecules, particularly polyethylene
PT glycol, for improving the residence time in the circulation.
XX
```


PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
XX disorders e.g. allergies
PS
XX Example 4; Fig 3; 113pp; English.
CC Residues were selected from MaE11 and inserted or substituted into
CC a human Fab antibody background (Vh region Kabat subgroup III and VI
CC region kappa subgroup I). A first version, humaeli1 or version 1 is
CC given below. The affinity of version 1 was assayed and found to be
CC ca. 100 times lower than that of the donor antibody MaE11.
CC Therefore, further modifications in the sequence of version 1
CC were made.
XX
XX
SQ Sequence 453 AA;
Query Match 90.3%; Score 2177; DB 14; Length 453;
Best Local Similarity 91.6%; Pred. No. 5.4e-122;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLWVSGISGSGSTY 59
Db :||||:||||:||||:||||:| : : :||||:||||:| : |||
1 EVQLVESGGGLVQPGGSLRLSCAVSYITSGYSWNIHQAPGKGLWVASIT-YDGSIN 59
QY 60 YADSVKGRFTISRDNKNTFLQNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGT 118
Db :||||:||||:||||:||||:||||:| : | |||||
60 YADSVKGRFTISRDNKNTFLQNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQGT 118
QY 119 VSSAST--KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 176
Db :||||:||||:||||:||||:||||:||||:| : |||||
119 VSSASTKGGKPSVFPPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 178
QY 177 VLQSSGLYSLSVTVPSSSLGTQTYICNVNHPKSNFKVDKVEPKSCDKTHTCPPCPAP 236
Db :||||:||||:||||:||||:||||:||||:||||:| : |||||
179 VLQSSGLYSLSVTVPSSSLGTQTYICNVNHPKSNFKVDKVEPKSCDKTHTCPPCPAP 238
QY 237 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
Db :||||:||||:||||:||||:||||:||||:||||:||||:| : |||||
239 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
QY 297 EQYINSTRYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:| : |||||
299 EQYINSTRYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358
QY 357 PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT 416
Db :|||:|:||||:||||:||||:||||:||||:||||:||||:| : |||||
359 PSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT 418
QY 417 DKSRWQQGNVFCSVNHEALHNHYTQKSLSLSPGK 451
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:| : |||||
419 DKSRWQQGNVFCSVNHEALHNHYTQKSLSLSPGK 453

Search completed: March 14, 2003, 11:47:40
Job time : 43.1559 secs

Db 300 NSTYRVVSVLTVLHODWLNKGVCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 359
Qy 361 ELTKNOVSLTCLVKGFPYSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
Db 360 EMTKNQVSLTCLVKGFPYSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 419
Qy 421 WQGNVFCSCVMHEALHNHYTKQSLSPG 450
Db 420 WQGNVFCSCVMHEALHNHYTKQSLSPG 449

RESULT 2
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BASEY, CAROL D.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D1
; CURRENT APPLICATION NUMBER: US/09/680,148
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
US-09-680-148-2

Query Match 91.8%; Score 2214.5; DB 4; Length 449;
Best Local Similarity 92.7%; Pred. No. 4.5e-167;
Matches 417; Conservative 12; Mismatches 20; Indels 1; Gaps 1;
Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWVWVQAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYHWVRQAPGKGLWVARIYPTNGTRY 60
Qy 61 ADSVKGRFTTISDRNSKNTLYIQMNSLRAEDTAVVYCAKHTGGGVWDPIDYWGOGTLTVS 120
Db 61 ADSVKGRFTTISADTSKNTAYLQMNSLRAEDTAVVYCSRWGGDGY-AMDYWGOGTLTVS 119
Qy 121 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
Db 120 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 179
Qy 181 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 240
Db 180 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 239
Qy 241 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Db 240 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 299
Qy 301 NSTYRVVSVLTVLHODWLNKGVCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
Db 300 NSTYRVVSVLTVLHODWLNKGVCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 359
Qy 361 ELTKNOVSLTCLVKGFPYSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
Db 360 EMTKNQVSLTCLVKGFPYSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 419
Qy 421 WQGNVFCSCVMHEALHNHYTKQSLSPG 450
Db 420 WQGNVFCSCVMHEALHNHYTKQSLSPG 449

RESULT 3
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-71

Query Match 91.7%; Score 2211.5; DB 3; Length 452;
Best Local Similarity 92.5%; Pred. No. 7.7e-167;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;
Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWVWVQAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGSYFSFSSHYMHWVWVQAPGKGLWVYIDPSNGTTY 60
Qy 61 ADSVKGRFTTISDRNSKNTLYIQMNSLRAEDTAVVYCAK--HTGGGVWDPIDYWGOGTLTV 118
Db 61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVVYCARGDVRYNGDWF-FDWVGOGTLTV 119
Qy 119 VSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
Db 120 VSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179
Qy 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
Db 180 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 239
Qy 239 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
Db 240 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299
Qy 299 QYNSTYRVVSVLTVLHODWLNKGVCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 358 QYNSTYRVVSVLTVLHODWLNKGVCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359

Db 300 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPTEKTISKAKQPREPOVYTLPPS 359
QY 359 RDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFSLYSLKLTVDK 418
Db 360 REEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFSLYSLKLTVDK 419
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 4
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-71

Query Match 91.7%; Score 2211.5; DB 4; Length 452;
Best Local Similarity 92.5%; Pred. No. 7.7e-167;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLVSGGGLVQPGGSLRSLCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 1 EVOLVSGGGLVQPGGSLRSLCAASGYSFSSHYMHVWRQAPGKLEWGYIDPSNGETTY 60

QY 61 ADSVKGRTLSRDNSKNTLYLQMNLSRAEDTAVYYCAK--HTGGGVWDPIDYWGOGTLVT 118
Db 61 NQFKGRFTLSRDNSKNTLYLQMNLSRAEDTAVYYCARGDYRYNGDNF-FDVGOGTLVT 119

QY 119 VSSASTKGPSVFFLAPSSKTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAYL 178
Db 120 VSSASTKGPSVFFLAPSSKTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAYL 179

QY 179 QSSGLISLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDTHHTCCPCPAPEL 238
Db 180 QSSGLISLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDTHHTCCPCPAPEL 239

QY 239 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Db 240 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299
QY 299 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPTEKTISKAKQPREPOVYTLPPS 358
Db 300 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPTEKTISKAKQPREPOVYTLPPS 359
QY 359 RDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFSLYSLKLTVDK 418
Db 360 REEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFSLYSLKLTVDK 419

QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-121-952A-71

Query Match 91.7%; Score 2211.5; DB 4; Length 452;
Best Local Similarity 92.5%; Pred. No. 7.7e-167;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLVSGGGLVQPGGSLRSLCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 1 EVOLVSGGGLVQPGGSLRSLCAASGYSFSSHYMHVWRQAPGKLEWGYIDPSNGETTY 60

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;
;
; 61 ADSVKGRTISRNSKNTLYLQMSLRADTAAYYCAK--HTGGGVWDPIDYWGQGLT 118
;
; 61 NQKFKGRFTLSRNSKNTAYLQMSLRADTAAYYCARGDYRYNGDWF-FDWGQGLT 119
;
; 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
;
; 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 179
;
; 179 QSSGLYSLSSVTVPSSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
;
; 180 QSSGLYSLSSVTVPSSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 239
;
; 239 LGGPSVFLFPKPKDFTLMSRTPETVCVVVDVSHEDPEVKFNWYDGVGEVHNKTKPREE 298
;
; 240 LGGPSVFLFPKPKDFTLMSRTPETVCVVVDVSHEDPEVKFNWYDGVGEVHNKTKPREE 299
;
; 299 QYNSTYRVSVLTVLHQDLNGKEYCKKVSNNKALPAIEKTIISKAKGQPREPQVYTLPPS 358
;
; 300 QYNSTYRVSVLTVLHQDLNGKEYCKKVSNNKALPAIEKTIISKAKGQPREPQVYTLPPS 359
;
; 359 RDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
;
; 360 REEMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 419
;
; 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
;
; 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452
;
RESULT 6
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
```

```
;
;
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-234-340A-71
;
Query Match 91.7%; Score 2211.5; DB 4; Length 452;
Best Local Similarity 92.5%; Pred. No. 7.7e-167;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;
;
Qy 1 QVLVQSGGGLVQPGSLRLSCLASGFTFRSNAGWVRQAPGKLEWVSGISGGSTYY 60
Db 1 EVQLVQSGGGLVQPGSLRLSCLASGYFSFSHYMHVWRQAPGKLEWVGYIDPSNGETTY 60
;
Qy 61 ADSVKGRTISRNSKNTLYLQMSLRADTAAYYCAK--HTGGGVWDPIDYWGQGLT 118
Db 61 NQKFKGRFTLSRNSKNTAYLQMSLRADTAAYYCARGDYRYNGDWF-FDWGQGLT 119
;
Qy 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
Db 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 179
;
Qy 179 QSSGLYSLSSVTVPSSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
Db 180 QSSGLYSLSSVTVPSSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 239
;
Qy 239 LGGPSVFLFPKPKDFTLMSRTPETVCVVVDVSHEDPEVKFNWYDGVGEVHNKTKPREE 298
Db 240 LGGPSVFLFPKPKDFTLMSRTPETVCVVVDVSHEDPEVKFNWYDGVGEVHNKTKPREE 299
;
Qy 299 QYNSTYRVSVLTVLHQDLNGKEYCKKVSNNKALPAIEKTIISKAKGQPREPQVYTLPPS 358
Db 300 QYNSTYRVSVLTVLHQDLNGKEYCKKVSNNKALPAIEKTIISKAKGQPREPQVYTLPPS 359
;
Qy 359 RDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
Db 360 REEMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 419
;
Qy 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452
;
RESULT 7
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
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; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARIANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-157-101A-7

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Query Match 91.6%; Score 2207.5; DB 1; Length 459;
Best Local Similarity 92.7%; Pred. No. 1.6e-166;
Matches 418; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

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QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGETFRSNAMGWVQAPGKLEWVSGISGGSTYY 60
DB 10 QVQLVESGGGVQPGSLRLSCAASGETFRSNAMGWVQAPGKLEWVSGISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAKHTG-GVWDPIDYWGQGLTVTS 120
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAKHTG-GVWDPIDYWGQGLTVTS 120
QY 70 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAKHTG-HRFDSWGQGLTVTS 128
DB 70 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAKHTG-HRFDSWGQGLTVTS 128
QY 121 SASTKGVSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVLIQS 180
DB 121 SASTKGVSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVLIQS 180
QY 129 SASTKGVSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVLIQS 188
DB 129 SASTKGVSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVLIQS 188
QY 181 SGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPAPPELLG 240
DB 181 SGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPAPPELLG 240
QY 189 SGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPAPPELLG 248
DB 189 SGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPAPPELLG 248
QY 241 GPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
DB 241 GPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
QY 249 GPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 308
DB 249 GPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 308
QY 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
DB 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
QY 309 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 368
DB 309 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 368
QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
DB 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420
QY 421 WQOGNPFSCSVMHREALNHYTKQSLSPGK 451
DB 421 WQOGNPFSCSVMHREALNHYTKQSLSPGK 451

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RESULT 8
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-8

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Query Match 90.3%; Score 2177; DB 3; Length 453;
Best Local Similarity 91.6%; Pred. No. 4.1e-164;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

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QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGETFRSN-AMGWVQAPGKLEWVSGISGGSTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSYITSGYSWNIRQAPGKLEWVASIT-YDGSIN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAKHTG-GVWDPIDYWGQGLTVT 118
DB 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAKHTG-HRFDSWGQGLTVT 118
QY 119 VSSAST--KGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 176
DB 119 VSSASTKGVSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFP 178
QY 177 VLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPAP 236
DB 177 VLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPAP 238
QY 237 ELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
DB 237 ELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
QY 297 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356
DB 297 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358
QY 357 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT 416
DB 357 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT 418
QY 417 DKSRWQOGNPFSCSVMHREALNHYTKQSLSPGK 451
DB 417 DKSRWQOGNPFSCSVMHREALNHYTKQSLSPGK 453

```

RESULT 9

US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64

SEQ ID NO 8

LENGTH: 453

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: humanized mae11, version 1 heavy chain

US-08-466-163B-8

Query Match 90.3%; Score 2177; DB 4; Length 453;

Best Local Similarity 91.6%; Pred. No. 4,1e-164;

Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTSRN-AMGWVROAPGKGLVWVSGISGGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNWIRQAPGKGLWVASIT-YDGSIN 59
Qy 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDVWGQGLT 118
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDVWGQGLT 118
Qy 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 176
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Qy 177 VLASGGYLSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAP 236
Db 179 VLQSSGLYLSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAP 238
Qy 237 ELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPR 296
Db 239 ELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPR 298
Qy 297 EEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTL 356
Db 299 EEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTL 358
Qy 357 PSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 416
Db 359 PSREMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 418
Qy 417 DKSRWQGNVFCSCVMHEALHNHYTQKLSLSPCK 451
Db 419 DKSRWQGNVFCSCVMHEALHNHYTQKLSLSPCK 453

RESULT 10

US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-14

Query Match 90.0%; Score 2169; DB 2; Length 451;

Best Local Similarity 91.4%; Pred. No. 1.8e-163;

Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTSRN-AMGWVROAPGKGLVWVSGISGGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNWIRQAPGKGLWVASIT-YDGSIN 59
Qy 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDVWGQGLT 118
Db 60 YNPSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQGLT 118
Qy 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Qy 179 QSSGLYLSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAP 238
Db 179 QSSGLYLSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAP 238
Qy 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 298
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 298
Qy 299 QNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTL 358
Db 299 QNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTL 358
Qy 359 RDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 418
Qy 419 SRWQGNVFCSCVMHEALHNHYTQKLSLSPCK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKLSLSPCK 451

RESULT 11

US-08-887-352B-16

Sequence 16, Application US/08887352B

Patent No. 5994511

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
 TITLE OF INVENTION: Improving Polypeptides
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/887,352B
 FILING DATE: 03-Jul-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P1123
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 451 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-887-352B-16

```

: Sequence 65, Application US/08466151
: Patent No. 6037453
: GENERAL INFORMATION:
: APPLICANT: Jardieu, Paula M.
: APPLICANT: Presta, Leonard G.
: TITLE OF INVENTION: Immunoglobulin Variants
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,151
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/466163
: FILING DATE: 06-Jun-1995
: APPLICATION NUMBER: 08/405617
: FILING DATE: 15-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/185899
: FILING DATE: 26-JAN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/879495
: FILING DATE: 07-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/744768
: FILING DATE: 14-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Svoboda, Craig G.
: REGISTRATION NUMBER: 39,044
: REFERENCE/DOCKET NUMBER: P0718P2C1D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-1489
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 65:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 451 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-08-466-151-65

Query Match          90.0%; Score 2169; DB 3; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps

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Db      1  EVQLVESGGGLVPGGSLRLSCAASGYSYISGYSWNIROAPGKLEWVASIT-YDGSIN 59
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      60  YADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAKHTG-GGVMDPTDYYWGQGTFLT 118
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      60  YNPVKGRITISRDSDKNTFLQMSLRRAEDTAVYYCARGSHYFGHH-FAVWGQGTFLT 118
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      119  VSSASTKGPVFPLAPSKSTSGGTAALGCLVKDYPPPEVTVSWNSGALTSGVHTFPAVL 178
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Db      119  VSSASTKGPVFPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
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QY      179  QSSGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKYDKKVEPKSCDKTHTCPCPAPEL 238
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Db      179  QSSGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKYDKKVEPKSCDKTHTCPCPAPEL 238
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      239  LGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNRYVDGVEVHNAAKTPREE 298
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Db 239 LGGPSVFLFPPPKDQTLMSRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 298
Qy 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358
Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Qy 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 13
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

Qy 1 QVQLVQSGGGLVQPQGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPQGGSLRLSCAVSYISYGSYNNIRQAPGKGLWVASIT-YDGSN 59
Qy 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGVMDPIDYWGQGLTV 118
Db 60 YNPVKGRITISRDDSKNTFYLMNSLRAEDTAVYICARGSHYFGHHW-FAYWGQGLTV 118
Qy 119 VSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 178
Qy 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPCPAPEL 238
Qy 239 LGGPSVFLFPPPKDQTLMSRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 298
Db 239 LGGPSVFLFPPPKDQTLMSRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 298
Qy 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358
Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Qy 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352

RESULT 14
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

Qy 1 QVQLVQSGGGLVQPQGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPQGGSLRLSCAVSYISYGSYNNIRQAPGKGLWVASIT-YDGSN 59
Qy 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGVMDPIDYWGQGLTV 118
Db 60 YNPVKGRITISRDDSKNTFYLMNSLRAEDTAVYICARGSHYFGHHW-FAYWGQGLTV 118
Qy 119 VSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 178
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Qy 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPCPAPEL 238
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Qy 239 LGGPSVFLFPPPKDQTLMSRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 298
Db 239 LGGPSVFLFPPPKDQTLMSRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 298
Qy 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358
Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Qy 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352

; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.8e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;
QY 1 QVLVQSGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLEWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASIT-YDGS 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGLTV 118
Db 60 YNPVKGRITISRDSKNTLYLQMNSLRAEDTAVYYCARGSHYFGWH-FAVWGQGLTV 118
QY 119 VSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPEL 238
Db 179 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPEL 238
QY 239 LGGPSVLEPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPRE 298
Db 239 LGGPSVLEPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPRE 298
QY 299 QYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSKLTVDK 418
QY 419 SRWQOGNVFSCSVMHREALNHYTKSLSPCK 451
Db 419 SRWQOGNVFSCSVMHREALNHYTKSLSPCK 451

Search completed: March 14, 2003, 11:50:19
Job time : 16.1473 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:47:44 ; Search time 13.7186 Seconds
(without alignments)
1515.277 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALNHYTKQSLSPCK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2270	94.2	449	10	US-09-736-371B-21
3	2211.5	91.7	452	9	US-09-726-258-71
4	2177	90.3	453	9	US-09-925-179-8
5	2177	90.3	453	10	US-09-802-077-8
6	2177	90.3	453	10	US-09-802-096-8
7	2169	90.0	451	9	US-09-925-179-65
8	2169	90.0	451	10	US-09-920-171-14
9	2169	90.0	451	10	US-09-920-171-16
10	2168	89.9	451	10	US-09-920-171-18
11	2166	89.8	451	9	US-09-925-179-66
12	2160	89.6	451	9	US-09-925-179-68
13	2160	89.6	478	9	US-10-124-905-8
14	2160	89.6	478	9	US-09-948-429B-8
15	2113.5	87.7	731	10	US-09-825-012-46
16	2113.5	87.7	741	10	US-09-825-012-55
17	2108.5	87.5	729	10	US-09-825-012-52
18	2108.5	87.5	739	10	US-09-825-012-61
19	2102.5	87.2	730	10	US-09-825-012-49

20	2102.5	87.2	740	10	US-09-825-012-58	Sequence 58, Appl
21	2092	86.8	476	10	US-09-747-669-3	Sequence 3, Appl
22	2090	86.7	443	10	US-09-917-410-4	Sequence 4, Appl
23	2066	85.7	476	9	US-10-124-905-12	Sequence 12, Appl
24	2066	85.7	476	9	US-09-948-429B-12	Sequence 12, Appl
25	2044	84.8	476	9	US-10-124-905-4	Sequence 4, Appl
26	2044	84.8	476	9	US-09-948-429B-4	Sequence 4, Appl
27	2038	84.5	470	10	US-09-859-053-32	Sequence 32, Appl
28	2038	84.5	470	10	US-09-859-053-36	Sequence 36, Appl
29	2026.5	84.1	475	10	US-09-740-002-27	Sequence 27, Appl
30	2021.5	83.8	475	10	US-09-740-002-25	Sequence 25, Appl
31	2019.5	83.8	450	9	US-09-996-288-216	Sequence 216, Appl
32	2019.5	83.8	450	9	US-09-996-288-218	Sequence 218, Appl
33	2019.5	83.8	450	9	US-09-996-288-250	Sequence 250, Appl
34	2019.5	83.8	450	10	US-09-796-848A-43	Sequence 43, Appl
35	2019.5	83.8	450	10	US-09-796-848A-49	Sequence 49, Appl
36	2017.5	83.7	450	9	US-09-996-288-222	Sequence 222, Appl
37	2017.5	83.7	450	9	US-09-996-288-224	Sequence 224, Appl
38	2017.5	83.7	450	10	US-09-796-848A-39	Sequence 39, Appl
39	2017.5	83.6	450	10	US-09-796-848A-41	Sequence 41, Appl
40	2015.5	83.6	450	9	US-09-996-288-220	Sequence 220, Appl
41	2015.5	83.6	450	10	US-09-796-848A-37	Sequence 37, Appl
42	2012.5	83.5	450	9	US-09-996-288-212	Sequence 212, Appl
43	2012.5	83.5	450	9	US-09-996-288-214	Sequence 214, Appl
44	2012.5	83.5	450	9	US-09-996-288-226	Sequence 226, Appl
45	2012.5	83.5	450	9	US-09-996-288-252	Sequence 252, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DIX-015.1 US
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PHI-IgG1
US-09-822-698A-26

Query Match	100.0%	Score 2411;	DB 10;	Length 451;
Best Local Similarity	100.0%	Pred. No. 6.1e-116;		
Matches 451;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db 1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRS	NAMGWVRQAPGKLEWVSGSGSTYY	60	
Qy 61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDT	AVYCAKHTGGGVWDPIDYWGOGTLVTVS	120	
Db 61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDT	AVYCAKHTGGGVWDPIDYWGOGTLVTVS	120	
Qy 121	SASTKGPSVFPLAPSSKSTSGGTAALGCLVK	DYFPEPTVSWNSGALTSGVHFFPAVLQS	180	
Db 121	SASTKGPSVFPLAPSSKSTSGGTAALGCLVK	DYFPEPTVSWNSGALTSGVHFFPAVLQS	180	
Qy 181	SGLYSLSSVTVFSSSLGTQTYICNVNHKPS	NTKVOKKPEKSCDKTHTCPPCPAPPELLG	240	
Db 181	SGLYSLSSVTVFSSSLGTQTYICNVNHKPS	NTKVOKKPEKSCDKTHTCPPCPAPPELLG	240	

Qy 241 GPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Db 241 GPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Qy 301 NSTYRVSVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360
Db 301 NSTYRVSVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360
Qy 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSR 420
Db 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSR 420
Qy 421 WOOGNVFSCVMHEALHNHYTQKSLSLSPGK 451
Db 421 WOOGNVFSCVMHEALHNHYTQKSLSLSPGK 451
RESULT 2
US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US2002013198A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736,371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-371B-21
Query Match 94.2%; Score 2270; DB 10; Length 449;
Best Local Similarity 94.9%; Pred. No. 8.9e-109;
Matches 431; Conservative 5; Mismatches 10; Indels 8; Gaps 2;
Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSFPMWVROAPGKGLWVSTISGGRTYY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK---HTGGGVMDPIDYWGQGLTV 117
Db 61 RDSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKFRQYSGG----FDYWGQGLTV 115
Qy 118 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 177
Db 116 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175
Qy 178 LQSSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPE 237
Db 176 LQSSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPE 235
Qy 238 LLGGPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 297
Db 236 LLGGPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
Qy 298 EQYNSTYRVSVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 357
Db 296 EQYASTYRVSVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 355
Qy 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD 417
Db 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD 415

Qy 418 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 416 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
RESULT 3
US-09-726-258-71
; Sequence 71, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.; Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 09/234,182
; APPLICATION NUMBER:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-726-258-71
Query Match 91.7%; Score 2211.5; DB 9; Length 452;
Best Local Similarity 92.5%; Pred. No. 8.4e-106;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;
Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVROAPGKGLWVGYIDPSNGETTY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK--HTGGGVMDPIDYWGQGLTV 118
Db 61 NQKFKGRFTISRDNKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWF--FDVWGQGLTV 119
Qy 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Db 120 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 179
Qy 179 QSSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 238

Db 180 QSGSLSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPeL 239
 QY 239 LGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
 Db 240 LGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 299
 QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
 Db 300 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
 QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
 Db 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 419
 QY 419 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451
 Db 420 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 452

RESULT 4
 US-09-925-179-8
 ; Sequence 8, Application US/09925179
 ; Publication No. US20030044858A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardieu, Paula M.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
 ; FILE REFERENCE: P07182C1D1US
 ; CURRENT APPLICATION NUMBER: US/09/925,179
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: US 08/466,163
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860
 ; PRIOR FILING DATE: 1992-08-14
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 68
 ; SEQ ID NO 8
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: humanized mae11, version 1 heavy chain
 US-09-925-179-8

Query Match 90.3%; Score 2177; DB 9; Length 453;
 Best Local Similarity 91.6%; Pred. No. 4.8e-104;
 Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;
 QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGGSTY 59
 Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYITSGYSWNIHQAPGKGLWVASIT-YDGS 59
 QY 60 YADSVKGRFTISRDNKNTLYIQMNSLRADETAIVYCAKHTG-GGVWDPIDYWGQGLTV 118
 Db 60 YADSVKGRFTISRDNKNTLYIQMNSLRADETAIVYCAKHTG-GGVWDPIDYWGQGLTV 118
 QY 119 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 176
 Db 119 VSSASTKKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 178
 QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAP 236
 Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAP 238
 QY 237 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
 Db 239 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
 QY 297 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
 Db 299 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298

Db 239 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
 QY 297 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
 Db 299 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
 QY 357 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 416
 Db 359 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
 QY 417 DKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451
 Db 419 DKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 453

RESULT 5
 US-09-802-077-8
 ; Sequence 8, Application US/09802077
 ; Patent No. US20010033842A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardieu, Paula M.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
 ; FILE REFERENCE: P0718P2C2US
 ; CURRENT APPLICATION NUMBER: US/09/802,077
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860
 ; PRIOR FILING DATE: 1992-08-14
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 64
 ; SEQ ID NO 8
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: humanized mae11, version 1 heavy chain
 US-09-802-077-8

Query Match 90.3%; Score 2177; DB 10; Length 453;
 Best Local Similarity 91.6%; Pred. No. 4.8e-104;
 Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;
 QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGGSTY 59
 Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYITSGYSWNIHQAPGKGLWVASIT-YDGS 59
 QY 60 YADSVKGRFTISRDNKNTLYIQMNSLRADETAIVYCAKHTG-GGVWDPIDYWGQGLTV 118
 Db 60 YADSVKGRFTISRDNKNTLYIQMNSLRADETAIVYCAKHTG-GGVWDPIDYWGQGLTV 118
 QY 119 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 176
 Db 119 VSSASTKKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 178
 QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAP 236
 Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAP 238
 QY 237 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
 Db 239 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
 QY 297 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
 Db 299 ELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298


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US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14
Query Match          90.0%; Score 2169; DB 10; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.2e-103;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;
QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFSN-AMGWVROAPGKGLWVSGISGGSTY 59
Db 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIROAPGKGLWVASIT-YDGSN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICAKHTG-GGVWDPIIDYWGQGLT 118
Db 60 YNPSVKGRITISRDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHWH-FAVMGQGLT 118
QY 119 VSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
QY 239 LGGPSVFLEPPPKDPTLMISRPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
Db 239 LGGPSVFLEPPPKDPTLMISRPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLV 418
Db 359 REEMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLV 418
QY 419 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451
Db 419 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451
RESULT 9
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
```

: ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

```

Query Match	89.9%;	Score 2168;	DB 10;	Length 451;
Best Local Similarity	91.4%;	Pred. No. 1.4e-103;		
Matchee 41A. Conservative		12. Mismatches 23;		
Matchee 41B. Conservative				Gaps 4;

[illegible]

QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGWDPIDYWGQGLVT 118

Qy 119 VSSASTKGPSVFPLAPSSKSTSGCTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy 179 QSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKKEVPKSCDKTHTCTCPCPAPEL 238

QY	LGGPSYFLFPXPKDTLMI	SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	298
QY	239		

DD	239	LOGPSVLEFFNCRDIEMLGKIFEVACVVDVSHDDIEVRLNMIIDOTVYHNRNIRKEE
QY	299	QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS

299 QYNSTIRVSVSLTVLHQDWLNGKEIKVCKSNKALFAPIERILLNRASQGFKEFQVILLFFS
359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

359 REEMTRNQVSLTCLVKGFFPSDIAVENESGQPPENNYKTTTPVLDSDGSFFLYSALVDK 411

Db

419 SRWQQGNVFCVMHEALHNHYTQKSLSPGK 451

QY

Db 419 SRWQGNVFSCSYMHEALHNHYTQKSLSLSPGK 451

US-09-925-179-66
; Sequence 66, Application US/09925179
. Publication NO. US2003004485A1

; INVENTOR: JARDIEU, PAULA M.
 ; APPLICANT: JARDIEU, PAULA M.
 ; APPLICANT: PRESTA, LEONARD G.
 ; TITLE OF INVENTION: ANTI-IGF ANTIBODIES (AS AMENDED)

```

; FILE REFERENCE: F0/16F2C1D1C105
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; CREDIT INFORMATION NUMBER: 00/465,152

```

; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15

; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860
 ; PRIOR FILING DATE: 1992-08-14

; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14

```

; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 66
; LENGTH: 451
;

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```

; ORGANISM: ARTIFICIAL sequence
;
; FEATURE:
;
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F
;

```

Query Match 89.8%; Score 2166; DB 9; Length 451;
Best Local Similarity 91.2%; Pred. No. 1.7e-103;
Matches 413; Conservative 14; Mismatches 22; Indels

a

1 QVQLVQSGGGLVPGGSLRLSCAASGFTFSN-AMGWVRQAPGKLEWVSGLSGGSGSY 59
: : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : :

b

1 EVQLVESGGGLVPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASIT-YDGSSTN 59

60 YADSVKGRETIISRDNSKNTLYLQMNSLRAEDTAVVYCAKHTG-GGWDPIDYWGQGLTVT 118

60 YNPSLKGRITISRDDSKNTFTYLOMNSLRAEDTAVVYCAKSHYEGHHW-FAVWGQGLTVT 118

y	119	VSSASTKGPVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSCALTSGVHTFPAVL	178
b	119	VSSASTKGPVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSCALTSGVHTFPAVL	178

179 QSSGLYSLSSVVTVPPSSSLGQTYYICNVNHPNSTKVDDKVEPKSCDKTHTCPCPAPEL 238
 |||||
 170 QSSGLYSLSSVVTVPPSSSLGQTYYICNVNHPNSTKVDDKVEPKSCDKTHTCPCPAPEL 238
 |||||

239 LGGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE

299 QYNSTYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS

359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNCPENNYKTTTPVLDSDGSFFLYSKLTVDK 410

419 SRWQGGVFCSVNHEALHNHYTQKSLSPGK 451

[illegible]

US-09-925-179-68
Sequence 68, Application US/09925179
Publication No. US20030044858A1

APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-IgE Antibodies (as amended)

CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 08/466,163

PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1994-01-20
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879 495

PRIOR FILING DATE: 1992-03-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14

```

; SEQ ID NO 68
; LENGTH: 451
; TYPE: PRT

```

;
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to
US-09-925-179-68

Query Match	89.6%;	Score 2160;	DB 9;	Length 451;
Best Local Similarity	90.5%;	Pred. No. 3.5e-103;		
Matches 410:	Conservative 16;	Mismatches 23;	Indels 4;	Gaps

```
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-8

Query Match      89.6%; Score 2160; DB 9; Length 478;
Best Local Similarity 89.8%; Pred. No. 3.6e-103;
Matches 412; Conservative 12; Mismatches 27; Indels 3;

QY 1 QVOLVQSGGLVQPGSLRLSCAASGFTFRSN-AMGWVRQAPGKLEWVSGISGGSTY 59
Db 1 EVOLVESGGLVQPGSLRLSCAVSGYSITSGYSNWTIRQAPGKLEWMSGIT-YDGSIN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTG-GGVNDPIDYWGQGLVT 118
Db 60 YNDSLKGRITVSRDSDSKNTFYQLNSARAEDTAVYICARGSHYFCHWH-FAVWQGGFLVT 118

QY 119 VSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSQVHTFPAVL 178
Db 119 VSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSQVHTFPAVL 178

QY 179 QSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238

QY 239 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPR 298
Db 239 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPR 298

QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKTIISKAKGQPREPQVYITLPPS 358
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKTIISKAKGQPREPQVYITLPPS 358

QY 359 RDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSEFFLYSKLTVDK 418
Db 359 RESMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSEFFLYSKLTVDK 418

QY 419 SRVQGNVFSCSVMHREALNHYTKLSLSPGK 451
Db 419 SRVQGNVFSCSVMHREALNHYTKLSLSPGK 451

RESULT 13
US-10-124-905-8
; Sequence 8, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
```

```
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-8

Query Match      89.6%; Score 2160; DB 9; Length 478;
Best Local Similarity 89.8%; Pred. No. 3.6e-103;
Matches 412; Conservative 12; Mismatches 27; Indels 3;

QY 1 QVOLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISG--SGST 58
Db 20 EVOLVESGGLVQPGSLRLSCAVSGFTFSDHYWYFRQAPGKPEWVGFRNKPNGGTT 79

QY 59 YVADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCA----KHTGGV--WDPIDYWG 112
Db 80 EVAASVKDRFTISRDDSKSIAYLQMSLKIETAVYICTSYISHCRGGVCYGYFEFWG 139

QY 113 QGTLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSQVH 172
Db 140 QGALVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSQVH 199

QY 173 TPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPP 232
Db 200 TPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKAEKPKSCDKTHTCPP 259

QY 233 CPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVINAK 292
Db 260 CPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVINAK 319

QY 293 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKTIISKAKGQPREPQV 352
Db 320 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKTIISKAKGQPREPQV 379

QY 353 YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSEFFLYS 412
Db 380 YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSEFFLYS 439

QY 413 KLTVDKSRVQGNVFSCSVMHREALNHYTKLSLSPGK 451
Db 440 KLTVDKSRVQGNVFSCSVMHREALNHYTKLSLSPGK 478

RESULT 14
US-09-948-429B-8
; Sequence 8, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-948-4298-8

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Query Match      89.6%; Score 2160; DB 9; Length 478;
Best Local Similarity 89.8%; Pred. No. 3 6e-103;
Matches 412; Conservative 12; Mismatches 27; Indels 8; Gaps 3;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGTFTRSNAMGWVROAPGKLEWVSGISG--SGGST 58
Db 20 EVQLVESGGGLVQPGGSLRVSCAVSGTFTSDHYMYWFRQAPGKPEWVGFI RNKPNGGTT 79

Qy 59 YYADSVKGRFTISRDNKNTLYIQMNSLRADDTAVYCA---KHTGGGV--WDPIDYWG 112
Db 80 EYAAASVKDRFTISRDNKNTLYIQMNSLRADDTAVYCA---KHTGGGV--WDPIDYWG 139

Qy 113 QGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 172
Db 140 QGALTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199

Qy 173 TFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCTPP 232
Db 200 TFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCTPP 259

Qy 233 CPAPELLGGPSVFLFPPKPKDRLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 292
Db 260 CPAPELLGGPSVFLFPPKPKDRLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319

Qy 293 TKPREEQYNSTYRVVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 352
Db 320 TKPREEQYNSTYRVVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379

Qy 353 YLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY 412
Db 380 YLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY 439

Qy 413 KLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK 451
Db 440 KLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK 478

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RESULT 15
US-09-825-012-46
; Sequence 46, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46

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; LENGTH: 731
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
; US-09-825-012-46

Query Match      87.7%; Score 2113.5; DB 10; Length 731;
Best Local Similarity 88.2%; Pred. No. 1.2e-100;
Matches 398; Conservative 20; Mismatches 30; Indels 3; Gaps 2;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGTFTRSNAMGWVROAPGKLEWVSGISGSGSTFY 60
Db 20 QVQLVQSGAEEVKPKGASVKSCASGYTFSAYIEWRQAPGKLEWVSGEILPGSNNSRY 79

Qy 61 ADSYKGRFTISRDNKNTLYIQMNSLRADDTAVYCAKHTGGVMDPIDYWGQGLTVTVS 120
Db 80 NEKFKGRVTVTRDTSTNTAYMELSLRSEDVAVYCAR-SYDFAW--FAYWGQGLTVTVS 136

Qy 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180
Db 137 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 196

Qy 181 SGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPELLG 240
Db 197 SGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPELLG 256

Qy 241 GPSVFLFPPKPKDRLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Db 257 GPSVFLFPPKPKDRLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 316

Qy 301 NSTYRVVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
Db 317 NSTYRVVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 376

Qy 361 ELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSR 420
Db 377 ELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSR 436

Qy 421 WQGNVFCSCVMHEALHNHYTOKSLSLSPGK 451
Db 437 WQGNVFCSCVMHEALHNHYTOKSLSLSPGK 467

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Search completed: March 14, 2003, 11:51:51
Job time : 14.7186 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:54 ; Search time 18.4344 Seconds
(without alignments)
2351.940 Million cell updates/sec

Title: US-09-822-698A-26
Perfect score: 2411
Sequence: 1 QVOLVQSGGLVQPGSLRL.....MHEALHNHYTKLSLSLSPGK 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1767	73.3	330	1 GHU	Ig gamma-1 chain C
2	1630.5	67.6	377	2 A23511	Ig gamma-3 chain C
3	1628.5	67.5	377	2 A60764	Ig gamma-3 chain C
4	1604	66.5	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	66.0	327	1 G4HU	Ig gamma-4 chain C
6	1513	62.8	470	2 S22080	Ig heavy chain pre
7	1499.5	62.2	444	2 PC4436	monoclonal antibod
8	1451.5	60.2	469	2 S37483	Ig gamma-2a chain
9	1435	59.5	446	2 S40295	Ig gamma-2a chain
10	1430	59.4	374	2 S69339	Ig gamma-2a chain
11	1430	59.3	472	2 S31459	Ig heavy chain V r
12	1382	57.3	474	1 G2MS11	Ig gamma-1 chain -
13	1376.5	57.1	475	2 S01321	Ig gamma-2b chain
14	1263	52.4	328	2 I47159	Ig gamma-2a chain
15	1260	52.3	255	4 S31866	Ig gamma-1 chain C
16	1257	52.1	328	2 I47160	Ig gamma 2b chain
17	1254	52.0	234	2 P70207	Ig gamma 2b chain
18	1231	51.1	328	2 I47158	Ig gamma chain C r
19	1230.5	51.0	323	1 GHRB	Ig gamma 1 chain c
20	1227	50.9	328	2 I47161	Ig gamma chain C r
21	1216.5	50.5	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	48.2	308	2 C30554	Ig gamma-2 chain C
23	1152	47.8	326	2 PS0017	Ig heavy chain C r
24	1151	47.7	289	1 G3HUI	Ig gamma-1 chain C
25	1146.5	47.6	333	2 PS0018	Ig gamma-3 heavy c
26	1142	47.4	324	1 GIMS	Ig gamma-2b chain
27	1141	47.3	329	1 G3MSC	Ig gamma-1 chain C
28	1137	47.2	393	1 G1MSC	Ig gamma-3 chain C
29	1130	46.9	398	1 G3MSM	Ig gamma-3 chain C

30 1126 46.7 330 1 G2MSA
31 1123.5 46.6 335 1 G2MSAB
32 1121 46.5 399 1 G2MSAM
33 1118.5 46.4 329 2 S00847
34 1112 46.1 322 2 PS0019
35 1093 45.3 548 2 S38864
36 1092.5 45.3 327 2 S06611
37 1082 44.9 405 1 G2MSBM
38 1066 44.2 277 2 I47162
39 891.5 37.0 249 2 S69340
40 881.5 36.6 572 2 B46529
41 866.5 35.9 549 2 S04845
42 842 34.9 218 2 A36040
43 814 33.8 220 2 A49444
44 792.5 32.9 241 2 S69131
45 779 32.3 627 2 S14683

ALIGNMENTS

RESULT 1

GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S36861; S38887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, R',98-135 <CUN>
A:Note: this sequence has the G1m(3) marker, 97-ArG
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q',156-165, 'Q',167-176, 'Q',178-194, 'N',196-197, 'D',199-238, 'E',2
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

Query Match 67.5%; Score 1628.5; DB 2; Length 377;
 Best Local Similarity 82.0%; Pred. No. 1.6e-86;
 Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 122 ASTKGPSVPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
 DB 1 ASTKGPSVPLAPSKSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKKY----- 219
 DB 61 GLYSLSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKRELTKNOVSLTCLVK 120

QY 220 -----EPKSCDKTHTCCPPAPPELLGGPSVFLFPPPKPKDT 254
 DB 121 DTPPPCPKPEPKSCDTPPCPCPEPKSCDTPPCPCPEPKSGVFLFPPPKPKDT 180

QY 255 LMSRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNATKPREQYNSTYRVSVLTFLH 314
 DB 181 LMSRTPEVTCVVVDVSHEDPEVKFYVDGVEVHNATKPREQYNSTYRVSVLTFLH 240

QY 315 ODWLNGKEYCKVSNKALPAPKEKTSKAKGPPEQVYTLPPSRDELTKNOVSLTCLVK 374
 DB 241 ODWLNGKEYCKVSNKALPAPKEKTSKAKGPPEQVYTLPPSRDELTKNOVSLTCLVK 300

QY 375 GFYPSDIAEVESNGOPENNYKTPPVLDSDGSLFLYSLTKVDKSRQGNVFCVSMHE 434
 DB 301 GFYPSDIAEVESNGOPENNYKTPPVLDSDGSLFLYSLTKVDKSRQGNVFCVSMHE 360

QY 435 ALHNHYTKSLSLSPGK 451
 DB 361 ALHNHYTKSLSLSPGK 377

RESULT 4
 G2HU
 Ig gamma-2 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
 C:Accession: A93906; A92809; A90752; A93132; A02148
 R:Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
 A:Reference number: A93906; MUID:82137621; PMID:6804948
 A:Accession: A93906
 A:Molecule type: DNA
 A:Residues: 1-326 <ELL>
 A:Cross-references: GB:V00554; GB:J00230; NID:q32759; PIDN:CAB58438.1; PID:96066056
 A:Note: Lys-326 is probably removed posttranslationally
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
 A:Reference number: A92809; MUID:81007873; PMID:6774012
 A:Contents: myeloma protein Til
 A:Accession: A92809
 A:Molecule type: protein
 A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A:Note: Trp-156 is at or near the complement-binding site
 R:Connell, J.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a
 A:Reference number: A90752; MUID:80001357; PMID:113060
 A:Contents: myeloma protein Zie
 A:Accession: A90752
 A:Molecule type: protein
 A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
 A:Note: this sequence has since been revised
 R:Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
 A:Reference number: A93132; MUID:80114419; PMID:118920
 A:Contents: Zie
 A:Accession: A93132

A:Molecule type: protein
 A:Residues: 238-275 <HOF>
 R:Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A:Reference number: A94591
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
 ned
 R:Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
 A:Reference number: A90253; MUID:72033500; PMID:4940472
 A:Contents: annotation; myeloma protein Sa, disulfide bonds
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124; PMID:5782707
 A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG2
 A:Cross-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:133-202/Domain: immunoglobulin homology <IM2>
 F:239-306/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.5%; Score 1604; DB 1; Length 326;
 Best Local Similarity 91.2%; Pred. No. 3.5e-85;
 Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 122 ASTKGPSVPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
 DB 1 ASTKGPSVPLAPSKSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPPAPPELLGG 241
 DB 61 GLYSLSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKVERKCCVE--CPPCPAPP-VAG 116

QY 242 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNATKPREQYN 301
 DB 117 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVEVHNATKPREQFN 176

QY 302 STYRVSVTLTLHODWLNGKEYCKVSNKALPAPKEKTSKAKGPPEQVYTLPPSRDE 361
 DB 177 STYRVSVTLTLHODWLNGKEYCKVSNKALPAPKEKTSKAKGPPEQVYTLPPSRDE 236

QY 362 LTKNQVSLTCLVKGFYPSDIAEVESNGOPENNYKTPPVLDSDGSLFLYSLTKVDKSRW 421
 DB 237 MTKNQVSLTCLVKGFYPSDIAEVESNGOPENNYKTPPVLDSDGSLFLYSLTKVDKSRW 296

QY 422 QQGNVFCVSMHEALHNHYTKSLSLSPGK 451
 DB 297 QQGNVFCVSMHEALHNHYTKSLSLSPGK 326

RESULT 5
 G4HU
 Ig gamma-4 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
 R:Ellison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two identical heavy (lambda) chains. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.0%; Score 1590.5; DB 1; Length 327;
Best Local Similarity 90.9%; Pred. No. 2.1e-84;
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

Qy 122 ASYKGVFPLPSSKSTSGTAAAGLVKDYPPVTVSNWNGALTSVHFPVAVLQSS 181
Db 1 ASYKGVFPLPSSKSTSGTAAAGLVKDYPPVTVSNWNGALTSVHFPVAVLQSS 60
Qy 182 GLYSLSVWTVPPSSSLGTQTYICNVNHPKSTKVDKVKVEPKSCDKTHCTCPCPAPPELLGG 241
Db 61 GLYSLSVWTVPPSSSLGTQTYICNVNHPKSTKVDKVKVEPKSCDKTHCTCPCPAPPELLGG 117
Qy 242 PSVFLPFPKPKDNLMTSRTEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 301
Db 118 PSVFLPFPKPKDNLMTSRTEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 177
Qy 302 STYRWVSVLTVLHODWLNGLNGEYKCKVSNKALPAPIETKTSKAGQPREQVYTLPSRDE 361
Db 178 STYRWVSVLTVLHODWLNGLNGEYKCKVSNKALPAPIETKTSKAGQPREQVYTLPSRDE 237
Qy 362 LTKNQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTTPPVLDSDGFFLYSKLTVDKSRW 421
Db 238 MTKNQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTTPPVLDSDGFFLYSKLTVDKSRW 297
Qy 422 OQGNVFCVSNHEALHNHYTKSLSPGK 451
Db 298 OQGNVFCVSNHEALHNHYTKSLSPGK 327

RESULT 6
S22080
Ig heavy chain precursor (B/Mt.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g
A:Reference number: S06610; MUID:90097956; PMID:2513487
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.8%; Score 1513; DB 2; Length 470;
Best Local Similarity 64.2%; Pred. No. 8.9e-80;
Matches 292; Conservative 55; Mismatches 100; Indels 8; Gaps 6;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSTYY 60
Db 20 QVQLRESGFLVLPKPSQTLSTCTVSGFSLSYALTWVRQAPGKALEWVGGIT-SGGTTY 78
Qy 61 ADSVKGRTTISRDNKNTLYLQMSLRADETAVIYCAKHTGGVWDP--IDYWGQGTILVT 118
Db 79 NPALKSRLSITKENSQSVLSVSVTPEDTATYTCARSTYGEYGDGAIADAMGOGLLVT 138
Qy 119 VSSASTKGPSVFPLAPSSKSTSGGTAAAGLVKDYPPVTVSNWNGALTSVHFPVAVL 178
Db 139 VSSASTTAPKVPYSSCCGCGSSSTVTLGCLVSSYMEPVTWNSGALKSGVHTFFAVL 198
Qy 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSTKVDKVKVEPKSCDKTHCTCPCPAPEL 238
Db 199 QSSGLYSLSSVTVPPSGTSG-QTFTCNVAHPASSTKVDKAVDP-TC-KPSPCDCCPPEL 255
Qy 239 LGGPSVFLEFPKPKDNLMTSRTEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
Db 256 LGGPSVFLEFPKPKDNLMTSRTEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 315
Qy 299 QYNSYRVVSVLTVLHODWLNGLNGEYKCKVSNKALPAPIETKTSKAGQPREQVYTLPPS 358
Db 316 QYNSYRVVSVLTVLHODWLNGLNGEYKCKVSNKALPAPIETKTSKAGQPREQVYTLPPS 375
Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEMESNQ--ENNYKTTTPPVLDSDGFFLYSKLTVD 416
Db 376 QEELSKSTVSLTCMVTSEFVPDYIAVEMQRPESDEKYGTTTPQLDADSSYFLYSLKRV 435
Qy 417 DKSRNQGNVFCVSNHEALHNHYTKSLSPGK 451
Db 436 DRNSWQEGDTYTCVVMHEALHNHYTKSKTSKAGK 470

RESULT 7
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, N.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp
A:Reference number: J05810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase activity. It is directed ag
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:251-320/Domain: immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 62.2%; Score 1499.5; DB 2; Length 444;
Best Local Similarity 61.0%; Pred. No. 5e-79;
Matches 278; Conservative 73; Mismatches 88; Indels 17; Gaps 7;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGIS--GSGGST 58
DB 1 EQVAVETGGGLVVRGNSLKSLTSGFTFSNYRMHLVQPPGKRLEWIAVITVKSNDYGA 60
QY 59 YYADSVKGRFTISRDNKNTLYIQMNSLRAEDTAVYYCAKHTGGVW-DPIDYWGQGLTV 117
DB 61 KYAESVGRGFTISRDSKSSVYLQMNRLREEDTATYYCCRTP---WVYAMDWGQGTGV 116
QY 118 TVSNASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSCVHTFP 177
DB 117 IVSSAKTTPPSVFLPAPGSAQAQNTSMVTLGCLVKGYFPEPTVTWNSGLSSGVHTFP 176
QY 178 LQSSGLYSLSSVWTPVSSSLGTQYICNVNHPKSNTKVDKKVPEPKSCDKTHTCPP--CPA 235
DB 177 LQSD-LYTLSSSVTPSSWSEITVCNVAHPASSTKVDKKIVPRDGC---CKPCICTV 231
QY 236 PELGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTP 295
DB 232 PEV---SSVTFPPKPKDVLITITPKVTCVVDVSHEDPEVKFNWYVDGVEVHTAQTQ 288
QY 296 REQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAGQPREPOVYTL 355
DB 289 REQENSTFRSVSELPINHQDWLNKKEYCKRVNSAAPPAPIETKISKGRKAPQVYTI 348
QY 356 PPSDELTKNQVSLTCLVKGYPSDIAVWESNGQPENNYKTPPVLDSDGSFELYSKIT 415
DB 349 PPKQMAKDKVSLTCDITDFPEPDIVWQWNGQPAENYKNTQIMTDGVSFVYSKLN 408
QY 416 VDKSPWQGNVPSGVNHEALHNHYTOKSLSLSPGK 451
DB 409 VQKSNWEAGNTFTCSVLHLEGLHNHTTKSLSHSPGK 444

RESULT 8
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Duccancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 60.2%; Score 1451.5; DB 2; Length 469;
Best Local Similarity 59.8%; Pred. No. 3e-76;
Matches 271; Conservative 71; Mismatches 106; Indels 5; Gaps 4;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGISGGSTY 60
DB 20 QIQLOQSGPELVKPCASVKISKASGYFTFDYIHWVKQPGQGLKWIWYFASGNTKY 79
QY 61 ADSVKGRTISRDNKNTLYIQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
DB 80 NENFKGKATLVDTSSSTAYMQLSSLTSEDVAVYFCARMGATA-TLLDYWGQGLTVTS 138
QY 121 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSCVHTFPV 180
DB 139 SAKTAPSVFLPAPCGDITGSSVTLGCLVKGYFPEPTVLTWNSGLSSGVHTFPV 198
QY 181 SGLYSLSSVWTPVSSSLGTQYICNVNHPKSNTKVDKKVPEPKSCDKTHTCPP--CPA 238
DB 181 SGLYSLSSVWTPVSSSLGTQYICNVNHPKSNTKVDKKVPEPKSCDKTHTCPP--CPA 238

DB 199 D-LYTLSSSVTPSSWTPSOSITCNVAHPASSTKVDKKIIEPRG-PTIKPCPPCKCAPNL 256
QY 239 LGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPRE 298
DB 257 LGGPSVFLPAPKPKDTLMISLPLIVTCVVDVSHEDPEVKFNWYVDGVEVHTAQTQTHRE 316
QY 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAGQPREQVYTLPPS 358
DB 317 DYNSTLRVWSALPIHQDWMSGKEFKCKVNNKDLPAPIETKISKPGSVRAPQVYVLP 376
QY 359 RDELTKNQVSLTCLVKGYPSDIAVWESNGQPENNYKTPPVLDSDGSFELYSKITV 418
DB 377 EEMTKKQVLTICNVTFPEPDIVWNTNKGKTELNYKNTPEVLDSDGSFELYSKLRVEK 436
QY 419 SRWQGNVPSGVNHEALHNHYTOKSLSLSPGK 451
DB 437 KNWERNYSYSCVVHLEGLHNHTTKSFSTRPGK 469

RESULT 9
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CH>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbonyl group (Asn) {covalent} #status experimental

Query Match 59.5%; Score 1435; DB 2; Length 446;
Best Local Similarity 60.0%; Pred. No. 2.5e-75;
Matches 271; Conservative 69; Mismatches 104; Indels 8; Gaps 5;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGISGGSTY 60
DB 1 QIQLOQSGPELVKPCASVKISKASGYFTFDYIHWVKQPGQGLKWIWYFASGNTKY 60
QY 61 ADSVKGRTISRDNKNTLYIQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
DB 61 NEFKGKATLVDTSSSTAYMQLSSLTSEDVAVYFCAR---GGKF-AMDYWGQGLTVTS 116
QY 121 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSCVHTFPV 180
DB 117 SAKTAPSVFLPAPCGDITGSSVTLGCLVKGYFPEPTVLTWNSGLSSGVHTFPV 176
QY 181 SGLYSLSSVWTPVSSSLGTQYICNVNHPKSNTKVDKKVPEPKSCDKTHTCPP--CPA 238
DB 177 D-LYTLSSSVTPSSWTPSOSITCNVAHPASSTKVDKKIIEPRG-PTIKPCPPCKCAPNL 234
QY 239 LGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPRE 298
DB 235 LGGPSVFLPAPKPKDTLMISLPLIVTCVVDVSHEDPEVKFNWYVDGVEVHTAQTQTHRE 294

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A:Reference number: A02157; MUID:80120716; PMID:6766534
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A:Cross-references: GB:J00461
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A:Reference number: A26235; MUID:80081501; PMID:117548
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
A:Reference number: A26232; MUID:80081502; PMID:117549
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>
R:Oillo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
A:Reference number: A26233; MUID:82173203; PMID:6803173
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
A:Cross-references: GB:J00461
R:Kim, H.; Yanaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
J. Biol. Chem. 269, 12345-12350, 1994
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359; PMID:7512967
A:Accession: A53598
A>Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
C:Genetics:
A:Introns: 139/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:157-222/Domain: immunoglobulin homology <IMI>
F:236-257/Region: hinge
F:281-350/Domain: immunoglobulin homology <IM2>
F:387-454/Domain: immunoglobulin homology <IM3>
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220, 288-348, 394-452/Disulfide bonds: #status predicted
F:247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 57.3%; Score 1382; DB 1; Length 474;
Best Local Similarity 56.8%; Pred. No. 3e-72;
Matches 260; Conservative 73; Mismatches 115; Indels 10; Gaps 3;
QY 1 QVOLQSGGGLVOPGGSRLRSCAASGFTFRSNAMGWVRQAPKGLWVSGISGGSTYY 60
DB 20 EVOLQSGPELVNPGASVSKSCASGYFTIYVHWVQKPGGLEWIGVINPKDGTGF 79
QY 61 ADSVKGRTISRNSKNTLYLQNSLRADTAIVYCAKHTGGVWDPIYWGQGLTVTVS 120
DB 80 NEFKGKATLTDKSNATMEUSLTSSEDSAVIYCARDYD---YDFWYWGQGLTVTVS 136
QY 121 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNMSGALTSGVHFFPAVLQS 180

DB 137 AAKTTPPSVYPLAPGCGDITGSSVTSGCLVKGYPESVTVTWNSGSLSSVHTLSQALLQ 196
QY 181 SGLYSLSSVVTPSSSLGHTQFTICNVNHNKPSNTKVDKKVPEKSCDKT-HTCPP-----C 233
DB 197 SGLYTMSSSVTPSSSTWPSQTVCVAHPASSTTVDKLEPSPGISTINPCPPCKECHKC 256
QY 234 PAPELGGPSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
DB 257 PAPNLEGGSVFIFPPNIDKLVMLISLTPKVTQVYVDVSEDDPDVQISFVNNVEVHTAQT 316
QY 294 KPREEQNSTYRVSVSLTVLHQDLWNGKEYCKVSKNKAIPAPIEKTIKAKAQPREPOVY 353
DB 317 QTHREDYNSTIRVSVLTPHQDWMGSGKEFKCKVNNKOLPSPIERTISKIKGLVRAPQVY 376
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413
DB 377 ILPPPAEQLSRKDVSLTCLVGFNCPDISVEWTSNGHTEENYKDTAPVLDSDGSFYIYSK 436
QY 414 LTVDKSRMOQGNVFCSCVMHEALHNYTKQSLSPGK 451
DB 437 LNKTSKWEKTSFSCNVRHEGLKYYLTKTISRSPGK 474
RESULT 13
S01321
.. Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475 <DEI>
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>
Query Match 57.1%; Score 1376.5; DB 2; Length 475;
Best Local Similarity 57.2%; Pred. No. 6.1e-72;
Matches 262; Conservative 71; Mismatches 116; Indels 9; Gaps 4;
QY 1 QVOLVOSGGLVOPGGSRLRSCAASGFTFRSNAMGWVRQAPKGLWVSGISGGSTYY 60
DB 20 QVOLQSGAELARPGASVKLSCKASGYLTISYGISWVKQRTQGLEWIGEIVPGSGNSYF 79
QY 61 ADSVKGRTISRNSKNTLYLQNSLRADTAIVYCAKHTGGVWDPIYWGQGLTVTVS 120
DB 80 NEFKGKATLTVDKSSSTAYLHLSLTSSEDSAVYFCAGPRQVGLL-PFGYWGQGLTVTVS 138
QY 121 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNMSGALTSGVHFFPAVLQS 180
DB 139 AAKTTPPSVYPLAPGCGDITGSSVTLCGLVKGFPEPTVTSNMSGSLSSVHTFPALLQ- 197
QY 181 SGLYSLSSVVTPSSSLGHTQFTICNVNHNKPSNTKVDKKVPEKSCDKT-HTCPP-----C 233
DB 198 SGLYTMSSSVTPSSSTWPSQTVCVAHPASSTTVDKLEPSPGISTINPCPPCKECHKC 257
QY 234 PAPELGGPSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
DB 258 PAPNLEGGPSVIFPPNIDKLVMLISLTPKVTQVYVDVSEDDPDVQISFVNNVEVHTAQT 317
QY 294 KPREEQNSTYRVSVSLTVLHQDLWNGKEYCKVSKNKAIPAPIEKTIKAKAQPREPOVY 353
DB 318 QTHREDYNSTIRVSVSLTPHQDWMGSGKEFKCKVNNKOLPSPIERTISKIKGLVRAPQV 377
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413

F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match	52.3%;	Score 1260;	DB 4;	Length 255;
Best Local Similarity	97.5%;	Pred. No. 1.5e-65;		
Matches 233;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

Qy 213 TKVDKKVEPKSCDKTHTCPPCPAPELGGPSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSH 272
Db 17 TVAQADVESKCDKTHTCPPCPAPELGGPSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSH 76

Qy 273 EDPEVKENWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKAL 332
Db 77 EDPEVKENWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKAL 136

Qy 333 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 392
Db 137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196

Qy 393 NNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 197 NNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 255

Search completed: March 14, 2003, 11:51:09
Job time : 19.4344 secs

Db 378 ILSPPEQLSRKDVSLTCLAVGSPEDISVETSTNGHTEENYKDTAPVLDSDGSGFYISK 437

Qy 414 LVVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

Db 438 LNMKTSKWEKTFSCNVNRHGEGLKNYLUKKTIISRSPGK 475

RESULT 14

I47159

Ig gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47159

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124

C:Genetics:

A:Gene: IgG2a

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMM>

Query Match	52.4%;	Score 1263;	DB 2;	Length 328;
Best Local Similarity	69.6%;	Pred. No. 1.3e-65;		
Matches 231;	Conservative 43;	Mismatches 52;	Indels 6;	Gaps 2;

Qy 122 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 181

Db 1 APTATSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTWNSGALSSVHTFPAVLQPS 60

Qy 182 GLYSLSVVTVSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPELGG 241

Db 61 GLYSLSVMVTPASSLSKSYTCNVNHPATTTKVDKRVGKTKPPCPCPACESP---G 116

Qy 242 PSVFLEPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 301

Db 117 PSVFLEPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 176

Qy 302 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 361

Db 177 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPHAE 236

Qy 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSEFFLYSKLTVDKS 419

Db 237 LSRKSVISITCLVTGFPDIDVWQRNGQPEPEGNVRTTPQQDVGDTYFLYSKFSVDKA 296

Qy 420 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

Db 297 SWGGGIFQCAVMHEALHNHYTQKSLSKTPGK 328

RESULT 15

S31866

Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C>Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C:Accession: S31866

R:Filpula, D.

submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene products

A:Reference number: S31866

A:Accession: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <FIL>

A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

C:Keywords: immunoglobulin

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:44 ; Search time 10.289 Seconds
(without alignments)
1818.046 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLSPK 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1767	73.3	330	1 GCL_HUMAN	P01857 homo sapien
2	1604	66.5	326	1 GCL_HUMAN	P01859 homo sapien
3	1590.5	66.0	327	1 GCA_HUMAN	P01861 homo sapien
4	1230.5	51.0	323	1 GC_RABIT	P01870 oryctolagus
5	1216.5	50.5	329	1 GC2_CAVPO	P01862 cavia porce
6	1156	47.9	290	1 GC3_HUMAN	P01860 homo sapien
7	1152	47.8	326	1 GCL_RAT	P20759 rattus norv
8	1146.5	47.6	333	1 GCB_RAT	P20761 rattus norv
9	1142	47.4	324	1 GCL_MOUSE	P01868 mus musculu
10	1141	47.3	329	1 GC3_MOUSE	P22436 mus musculu
11	1137	47.2	393	1 GC1M_MOUSE	P01869 mus musculu
12	1130	46.9	398	1 GC3M_MOUSE	P03987 mus musculu
13	1126	46.7	330	1 GCNA_MOUSE	P01863 mus musculu
14	1123.5	46.6	335	1 GCAB_MOUSE	P01864 mus musculu
15	1121	46.5	339	1 GCAM_MOUSE	P01865 mus musculu
16	1118.5	46.4	329	1 GCC_RAT	P20762 rattus norv
17	1112	46.1	322	1 GCA_RAT	P20760 rattus norv
18	1087	45.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1082	44.9	405	1 GCBM_MOUSE	P01867 mus musculu
20	492	20.4	428	1 EPC_HUMAN	P01854 homo sapien
21	483.5	20.1	429	1 EPC_RAT	P01855 rattus norv
22	471	19.5	117	1 HV3C_HUMAN	P01764 homo sapien
23	468	19.4	421	1 EPC_MOUSE	P06336 mus musculu
24	466.5	19.3	114	1 HV3B_HUMAN	P01763 homo sapien
25	456.5	18.9	122	1 HV3G_HUMAN	P01768 homo sapien
26	450.5	18.7	122	1 HV3A_HUMAN	P01762 homo sapien
27	449.5	18.6	116	1 HV3T_HUMAN	P01781 homo sapien
28	447	18.5	121	1 HV3J_HUMAN	P01771 homo sapien
29	444	18.4	454	1 MUC_HUMAN	P01871 homo sapien
30	440	18.2	455	1 MUC_MOUSE	P01872 mus musculu
31	439	18.2	458	1 MUC_RABIT	P03988 oryctolagus
32	438.5	18.2	116	1 HV05_CARAU	P19181 carassius a
33	437.5	18.1	122	1 HV3H_HUMAN	P01769 homo sapien

34	437.5	18.1	126	1 HV3K_HUMAN	P01772 homo sapien
35	435.5	18.1	136	1 HV16_MOUSE	P01783 mus musculu
36	435	18.0	115	1 HV3D_HUMAN	P01765 homo sapien
37	432	17.9	117	1 HV02_CANFA	P01785 canis famil
38	430	17.8	476	1 MUCM_MOUSE	P01873 mus musculu
39	429	17.8	479	1 MUCM_RABIT	P04221 oryctolagus
40	428	17.8	119	1 HV3I_HUMAN	P01770 homo sapien
41	427	17.7	115	1 HV3F_HUMAN	P01767 homo sapien
42	422.5	17.5	120	1 HV3U_HUMAN	P01782 homo sapien
43	422	17.5	457	1 MUC_SUNMU	P20768 suncus muri
44	419.5	17.4	119	1 HV3M_HUMAN	P01774 homo sapien
45	419	17.4	120	1 HV3E_HUMAN	P01766 homo sapien

ALIGNMENTS

RESULT 1
GCL_HUMAN
ID GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -|- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)
 CC MARKER & THE GLM (NON-1) MARKERS.
 CC -|- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -|- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -|- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 CC EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR Genex; HGNC:5525; IGHL1.
 DR MIM; 147100; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 98
 FT DOMAIN 1 98
 FT CH1.
 FT HINGE.
 FT 99 110
 FT DOMAIN 111 223
 FT CH2.
 FT 224 330
 FT DOMAIN 27 83
 FT DISULFID 103 103
 FT INTERCHAIN (WITH LIGHT CHAIN).
 FT 109 109
 FT DISULFID 109 109
 FT INTERCHAIN (WITH HEAVY CHAIN).
 FT 112 112
 FT DISULFID 144 204
 FT INTERCHAIN (WITH HEAVY CHAIN).
 FT 250 308
 FT DISULFID 180 180
 FT CARBOHYD
 FT 330 330
 FT MOD_RES
 FT 97 97
 FT VARIANT
 FT 239 239
 FT N-LINKED (GLCNAC. . .).
 FT REMOVED POST-TRANSLATIONALLY.
 FT K -> R (IN GLM(3) MARKER).
 FT /FTId=VAR_003886.
 FT D -> E (IN GLM(NON-1) MARKER).
 FT /FTId=VAR_003887.
 FT 241 241
 FT VARIANT
 FT L -> M (IN GLM(NON-1) MARKER).
 FT /FTId=VAR_003888.
 FT 123 126
 FT STRAND

FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
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 FT STRAND 183 190
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 FT STRAND 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 73.3%; Score 1767; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.4e-114;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 122 ASTKGPSVFPLAPSKSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 181
 Db 1 ASTKGPSVFPLAPSKSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60
 Qy 182 GLYSLSSVVTVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 241
 Db 61 GLYSLSSVVTVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Qy 242 PSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 301
 Db 121 PSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
 Qy 302 STYRVVSVLTVQLHQLNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 361
 Db 181 STYRVVSVLTVQLHQLNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 Qy 362 LFNKQVSLTCLVKGYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 421
 Db 241 LFNKQVSLTCLVKGYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
 Qy 422 QQGNVFSCVMHEALHNHYTOKLSLSLSPGK 451
 Db 301 QQGNVFSCVMHEALHNHYTOKLSLSLSPGK 330
 RESULT 2
 GC2_HUMAN STANDARD; PRT; 326 AA.
 ID GC2_HUMAN
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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Db 176 QYNTTRFVSVLPFIQHDWLRGKFKCKYVYNKALPAPIEKTISKTKGAPRMPDVYTLPPS 235
QY 359 RDELTKNOVSLTCLVGFYPSDIAVWESNGOP--ENNKTTPPVLDSDGSFFLYSKLTV 416
Db 236 RDELSKSKSVTCLLIINFADPHVWASNRVPVSEKEYKNTPTPIEDADGSLYSLKTV 295
QY 417 DKSRWQOQNVFSCVMHEALHNHYTKSLSLSPG 450
Db 296 DKSANDQGTVTCTVMHEALHNHVTKAISRSPG 329

RESULT 6
GC3_HUMAN STANDARD; PRT; 290 AA.
ID GC3_HUMAN
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
RL Biochemistry 19:4304-4308(1980).
RN [2]
RP REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; PubMed=402363;
RA Michaelen T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:883-889(1977).
RN [3]
RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
Structure of the FC fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS: IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
REF.2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALL OF THE CHI REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
SEGMENT (12-28).
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AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ig gamma-1 chain C region.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=80045036; PubMed=6769752;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 RN [2]
 RN SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=80202559; PubMed=6769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seldman J.G., Peterlin B.M., Leder P., Honjo T.; sequences
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
 cloned in a bacterial plasmid.";
 RL Gene 9:87-97(1980).
 RN [3]
 RN SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RP MEDLINE=80012837; PubMed=113776;
 RX Rogers J., Clarke P., Salsler W.;
 RA "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
 heavy chain.";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RN SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RP MEDLINE=78242288; PubMed=98524;
 RA Adetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 murine myeloma gamma1 chain.";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RN DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
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 CC EMBL; V00793; CAA24172.1; -
 DR EMBL; V00793; CAA24173.1; -
 DR EMBL; V00793; CAA24174.1; -
 DR EMBL; V00793; CAA24175.1; -
 DR EMBL; V00795; CAA24176.1; -
 DR PIR; A02159; GIMS.
 DR HSSP; P01842; 7FAB.
 DR GlycoSuiteDB; P01868; -
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003597; Iq-cl.
 DR Pfam; PF00047; Iq; 3.
 DR SMART; SM00407; Igc1; 2.
 DR PROSITE; PS00290; Iq_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1 97
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.

FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT /FTID=CAR_000055.
 FT DISULFID 244 302
 FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
 FT CONFLICT 276 276 N -> D (IN REF. 3).
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3DF2C93 CRC64;
 Query Match 47.4%; Score 1142; DB 1; Length 324;
 Best Local Similarity 62.0%; Pred. No. 1.3e-71;
 Matches 206; Conservative 56; Mismatches 60; Indels 10; Gaps 4;
 QY 122 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 181
 DB 1 AKTTPPSVYPLAPSGAAQTNSMVTGLCLVKGYRPEPVTVTWNSGSLSSGVHTFPAVLQSD 60
 QY 182 GLYSLSSVTVPSLSGLTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 239
 DB 61 -LYTLSSVTVPSPPRPSSETVTCNVAHPASSTKVDKKIVPRDCG-----CKPCICTVPEV- 114
 QY 240 GGPSVFLPFPKPKDTLMTSRTPETCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
 DB 115 --SSVFIIPPFPKDKVLTITLTPKVTCTVVDLISKDDPEVQFSWFDVDEVHTAQTQPREEQ 172
 QY 300 YNSTYRVSVLTIVLHQDLNGKEYCKKYSNKKALPAPIETKISKAKGQPREPQVYTLPPSR 359
 DB 173 FNSITFRSVSELPIMHQDLNGKEYCKRVNSAFAPIETKISKGRPKAPQVYTIPTPK 232
 QY 360 DELTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419
 DB 233 EQMAKDKVSLTCMITDFPEPDITVEQWNGQPAENYKNTQPIIMNTNGSYFVYSKLVQKS 292
 QY 420 RWOOGNVEFSCVMHEALNHYTQKSLSLSPGK 451
 DB 293 NWEAGNTFTCSVLHSEGLNHHNTEKSLSHSPCK 324
 RESULT 10
 GC3_MOUSE STANDARD; PRT; 329 AA.
 ID GC3_MOUSE
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-3 chain C region, secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RL EMBO J. 3:2041-2046(1984).
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DR EMBL; J00451; -, NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 47.3%; Score 1141; DB 1; Length 329;
Best Local Similarity 64.0%; Pred. No. 1.5e-71;
Matches 212; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

QY 123 STKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSSG 182
Db 1 ITTAPSVIPLVPGCDSTSGSSVTLGCLVKGYPPEPTVKWNYGALSSGVRTSSVLQ-SG 59
QY 183 LYSLSVVTVPPSSSLGTQTYICNNVNHKPSNTKVDKVEPKSCDKTHTCP--PCPAPELLG 240
Db 60 FYSLSLVTVPPSSVTPSQTYICNVHPASTELIKRIEPR-IPKSTPPGSSCPPGNILG 118
QY 241 GPSVLEFPFKPKDTLMTSRPTVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Db 119 GPSVFIEFPFKPKDMLSLTPKVCVVVDVSEDDPDVHVSWEVDNKEVHTAWTPQREAOY 178
QY 301 NSTVRVSVLTVLHODLNCKEYKCKVSNKALPAPKEITLSKAKGQPREPQVYTLPPSRD 360
Db 179 NSTFRVVSALPIQHQDMRKEKCKVSNKALPAPKEITLSKPKGRAQTPQVYTIPTPPRE 238
QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGPENNYKTTTPVLDSGSEFELYSKLTVDKSR 420
Db 239 QMSKKVSLTCLVNTFSESAISVEWERNGELEGQDYKNTPEILDSDGTFLYSKLTVDTS 298
QY 421 WQGNVPSCSVMHEALHNHYTQKSLSLSPGK 451
Db 299 WLOGEIFTCSVWHEALHNHHTQKLSRSPGK 329

RESULT 11
GC1M_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82221190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
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DR EMBL; V00793; CAA24172.1; -.
DR EMBL; V00793; CAA24173.1; -.
DR EMBL; V00793; CAA24174.1; -.
DR PIR; B02159; GLMSM.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102
FT DISULFID 104 104
FT DISULFID 107 107
FT DISULFID 109 109
FT DISULFID 138 198
FT CARBOHYD 174 174
FT DISULFID 244 302
FT TRANSMEM 340 357
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 47.2%; Score 1137; DB 1; Length 393;
Best Local Similarity 61.9%; Pred. No. 3.6e-71;
Matches 205; Conservative 56; Mismatches 60; Indels 10; Gaps 4;

QY 122 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 181
Db 1 AKTTPSVVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSSLSGSGVHTFPAVLQSD 60
QY 182 GLYSLSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCP--CPAPELL 239
||:||||| ||||| :|| ||| | 1:||||| :| | | | |

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Db 61 -LYTLSSSVTPSSPRPSETVTCNVAHPASSTKVDDKIVPRDCG----CKPCICTVPEV- 114
Oy 240 GGPVSFLFPPKPKDPLMSRPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPREEQ 299
Db 115 --SSVFIEPPKPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFVDVVEVHTAQTPREEQ 172
Oy 300 YNSTRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTIKSKAKGQPREPOVYTLPPSR 359
Db 173 FNSTRVSSELPIMHODWLNGKEFKCRVNSAFAPIEKTIKSKTKGRKAPQVYTIIPPK 232
Oy 360 DELTKNOVSLTCLVGFYPSDIAVWESNGQPENNYKTTTPVLDSGDSFFLYSLKTVDKS 419
Db 233 EQWADKVSLLCMTDFPEDITVWQNGQPAENYKNTQIPMTNGSYFYYSKLVQKS 292
Oy 420 RWOQNVFSCSVMHALNNHYTKQSLSLSPG 450
Db 293 NNEAGNTFTCSVLHEGLHHHTKSLSHSPG 323

RESULT 12
GC3M_MOUSE STANDARD; PRT; 398 AA.
ID GC3M_MOUSE AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00451; AAB59655.1;
DR EMBL: V01526; CAA24767.1; ALT_SEQ.
DR PIR: A02155; G3MSM.
DR HSSP: P01857; 1FC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; IG1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 98 113 CH1.
FT DOMAIN 114 223 HINGE.
FT DOMAIN 224 327 CH2.
FT
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FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7264B50A41B95 CRC64;

Query Match 46.9%; Score 1130; DB 1; Length 398;
Best Local Similarity 63.8%; Pred. No. 1.1e-70;
Matches 210; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

Oy 123 STKGPSVFPPPLAPSSTSGTGAALGLVXDYFPEPVTVVSNWNSGALTSGVHTTTPAVLQSSG 182
Db 1 TTTAPSVVPLVPGCDSTSGSVTLGLVKGYPPEPVTVKWNYGALSSGVRTVSSVLQ-SG 59

Oy 183 LYSLSVVTVTPSSSLGTQTQYICNVNHPKSNKTKVDKVEPKSCDKHTCP--PCPAPELLG 240
Db 60 FYSLSLVTVTPSSWPSQTVICNVNHPASKTELIIKRIEPR-IPKSTPPGSSCPPGNIIG 118

Oy 241 GPSVFLFPPKPKDPLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPREEQ 300
Db 119 GPSVFIEPPKPKDPLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPREEQ 178

Oy 301 NSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTIKSKAKGQPREPOVYTLPPSRD 360
Db 179 NSTFRVVSALPIQHDMMRGKEFKCKVNNKALPAPIERTISKPKRAQTPQVYTIIPPRE 238

Oy 361 ELTKNOVSLTCLVGFYPSDIAVWESNGQPENNYKTTTPVLDSGDSFFLYSLKTVDKSR 420
Db 239 QMSKKKVSLLTCLVNFSEALSVEWERNGEQDYKNTPFILDSDGTGYFLYSLKTVDTDS 298

Oy 421 WQGNVFCSCVMHEALNNHYTKQSLSLSP 449
Db 299 WLQGEITCSVWHEALNNHTQKNLSRSP 327

RESULT 13
GCAA_MOUSE STANDARD; PRT; 330 AA.
ID GCAA_MOUSE AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollio R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
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RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RL for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RP [5]
RN DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
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DR EMBL; V00798; CAA24178.1; -
DR PTR; A02152; G2MSA.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cI.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGcI; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 46.7%; Score 1126; DB 1; Length 330;
Best Local Similarity 63.6%; Pred. No. 1.6e-70;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 122 ASTKGPSVRPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
Db 1 AKTAPSVPLPVCVGGTGGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAVLQSD 60

QY 182 GLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPK-----SCDKTHTCPCPA 239
Db 61 -LVTLSSTVTSSTWPSQSIICNVNHPASSKTKVDKIEPRG-PITKPCPCCKCAPNLL 118

QY 240 GGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNKYVDGVEVHNKTKPREBQ 299
Db 119 GGSVFIFPKIKDVLMLISPLIVTCVVDVSDDDPDQVQISFVNNVHTAQTQTHRED 178

QY 300 YNSTYRVSVLTVLHODWLNKGYCKVSKNKPAPTEKTSKAKGQPREPOVYILPPSR 359
Db 179 YNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPIAPERTISKPGSVRAPQVYILPPPE 238

QY 360 DELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 419
Db 239 EEMTKQVLTLCMTVDMPEDIVVETWNTNGKTELKNTPEVLDSDGSFYFMYSKLRVEK 298

QY 420 RWOQGNVFCSSVMHEALHNYTKQSLSPGK 451
Db 299 NWVERNSYSCVWVHEGLNHHHTTKSFRTPGK 330

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RESULT 14
GCAB_MOUSE
ID GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IGG2a and IGG2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -! MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cI.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGcI; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 46.6%; Score 1123.5; DB 1; Length 335;
Best Local Similarity 61.3%; Pred. No. 2.5e-70;
Matches 206; Conservative 53; Mismatches 70; Indels 7; Gaps 2;

QY 122 ASTKGPSVRPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
Db 1 AKTAPSVPLPVCVGGTGGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAVLQ-S 59

QY 182 GLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPK-----SCDKTHTCPCPA 235
Db 60 GLYTLSSSTVTSNTWPSQTITCNVHPASSKTKVDKIEPRVPIQNCPHPQVRPCAA 119

QY 236 PELGGGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNKYVDGVEVHNKTKP 295
Db 120 PDLGGGSVFLFPKPKIKDVLMLISPLIVTCVVDVSDDDPDQVQISFVNNVHTAQTQT 179

QY 296 REEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKPAPTEKTSKAKGQPREPOVYTL 355
Db 180 HREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNRALSPIEKTISKPRGPVRAQVYVL 239

QY 356 PPSDELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT 415

```


GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:09 ; Search time 33.4392 Seconds
(without alignments)
2778.994 Million cell updates/sec

Title: US-09-822-698A-26
Perfect score: 2411
Sequence: 1 QVOLVQSGGLVQPGSLRL.....MHEALNHVTKLSLSPGK 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2233.5	92.6	471	Q8TC77	Q8tc77 homo sapien
2	1864	77.3	473	Q8TC63	Q8tc63 homo sapien
3	1561.5	64.8	469	Q8R3V9	Q8r3v9 mus musculus
4	1543.5	64.0	437	Q9RIA4	Q9ria4 mus musculus
5	1522.5	63.1	473	Q91Z05	Q91z05 mus musculus
6	1483.5	61.5	463	Q99LC4	Q99lc4 mus musculus
7	1481.5	61.4	473	Q9D8L4	Q9d8l4 mus musculus
8	1453	60.3	468	Q99L31	Q99l31 mus musculus
9	1429.5	59.3	473	Q99L25	Q99l25 mus musculus
10	1397	57.9	474	Q8R3H6	Q8r3h6 mus musculus
11	1266.5	52.5	337	Q95M34	Q95m34 equus caball
12	1264.5	52.4	701	Q96PQ8	Q96pq8 homo sapien
13	968.5	40.2	597	Q96BB9	Q96bb9 homo sapien
14	921	38.2	613	Q8WUK1	Q8wuk1 homo sapien
15	834	34.6	494	Q96K68	Q96k68 homo sapien
16	820.5	34.0	487	Q99KA4	Q99ka4 mus musculus

17	778.5	32.3	479	11	Q91WP5	Q91wp5 mus musculus
18	768.5	31.9	614	4	Q96GA6	Q96ga6 homo sapien
19	766	31.8	486	11	Q91Z07	Q91z07 mus musculus
20	755.5	31.3	480	11	Q91X81	Q91x81 mus musculus
21	747	31.0	278	11	Q921K1	Q921k1 mus musculus
22	738	30.6	613	11	Q8VCX7	Q8vcx7 mus musculus
23	728.5	30.2	597	4	Q9BU10	Q9bu10 homo sapien
24	725	30.1	613	4	Q96EY0	Q96ey0 homo sapien
25	722.5	30.0	597	4	Q9BQ88	Q9bqb8 homo sapien
26	721	29.9	484	11	Q8VEA0	Q8vea0 mus musculus
27	718.5	29.8	588	4	Q8WUX4	Q8wux4 homo sapien
28	718.5	29.8	618	4	Q96AA6	Q96aa6 homo sapien
29	711	29.5	573	4	Q8WU38	Q8wu38 homo sapien
30	702	29.1	496	4	Q96DK0	Q96dk0 homo sapien
31	696	28.9	496	4	Q96KX8	Q96kx8 homo sapien
32	692	28.7	500	4	Q9BRV0	Q9brv0 homo sapien
33	686.5	28.5	497	4	Q8WY24	Q8wy24 homo sapien
34	680	28.2	484	11	Q99LA6	Q99la6 mus musculus
35	675.5	28.1	482	11	Q91X92	Q91x92 mus musculus
36	673	28.0	481	11	Q91WT1	Q91wt1 mus musculus
37	661	27.4	488	11	Q91WR1	Q91wr1 mus musculus
38	655.5	27.2	416	4	Q9NPP6	Q9npp6 homo sapien
39	654.5	27.1	489	11	Q8VCX4	Q8vcx4 mus musculus
40	632.5	26.2	481	11	Q8VCV5	Q8vcv5 mus musculus
41	631.5	26.2	481	11	Q91WT3	Q91wt3 mus musculus
42	629	26.1	479	11	Q99W22	Q99w22 mus musculus
43	563.5	23.4	147	4	Q9Y509	Q9y509 homo sapien
44	536.5	22.3	426	11	Q9DCD9	Q9dcd9 mus musculus
45	507	21.0	121	4	Q9UL71	Q9ul71 homo sapien

ALIGNMENTS

RESULT 1

Q8TC77 ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAR24289.1; -
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match		92.6%	Score 2233.5;	DB 4;	Length 471;
Best Local Similarity		93.4%	Pred. No. 2.5e-174;		
Matches 423;		Conservative 9;	Mismatches 18;	Indels 3;	Gaps 2;
Qy	1	QVOLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVQAPGKGLWVSGISGGSTYY	60		
Db	20	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYNNWVQAPGKGLWVSSSSSSYY	79		
Qy	61	ADSVKGRFTISRDNKNTLYLQNSLRADDTAYVYCAKHTG--GGVWDPTDYWGQGLT	118		
Db	80	ADSVKGRFTISRDNKNTLYLQNSLRADDTAYVYCAKHTG--GGVWDPTDYWGQGLT	138		
Qy	119	VSSASTKGPSVFLAPLSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	178		
Db	139	VSSASTKGPSVFLAPLSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	198		
Qy	179	QSSGLYSLSSVTVVPSSSLGQTQYICNVNHPKSNKYDKKVEPKSCDKHTCTPCPAPEL	238		

Db 199 QSSGLYSLSSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKVKVEPKSCDKTHCTPCPAPEL 258
Qy 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDYSHEDPEVKFNWYVDGVGVHNAKTKPREE 298
Db 259 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDYSHEDPEVKFNWYVDGVGVHNAKTKPREE 318
Qy 299 QYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 319 QYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 378
Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLVTDK 418
Db 379 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLVTDK 438
Qy 419 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451
Db 439 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 471

RESULT 2
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 77.3%; Score 1864; DB 4; Length 473;
Best Local Similarity 79.2%; Pred. No. 4.2e-144; Indels 8; Gaps 4;
Matches 359; Conservative 37; Mismatches 49;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTPRSN--MGWVRQAPGKGLWVSGISGGST 58
Db 27 RLQQLSGGGLLKPSTLSLTCTVSGDSVASSSYWGVRQPPGKGLWIGTINFS-GNM 85
Qy 59 YYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGVWDIDYWGQGLTVT 118
Db 86 YSPSLRSRVTSADMSSENSFLKLDVTAADTAVYCA--AGHLVMGFGAHWGQGLVS 143
Qy 119 VSSASTKGPSVFLPAPSSKSTSGGTAALGLVKDYFPEPTVTSWNSGALTSVHTFPVAVL 178
Db 144 VSPASTKGPSVFLPAPSSKSTSGGTAALGLVKDYFPEPTVTSWNSGALTSVHTFPVAVL 203
Qy 179 QSSGLYSLSSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKVKVEPKSCDKTHCTPCPAPEL 238
Db 204 QSSGLYSLSSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKVKVEPKSCDKTHCTPCPAPEL 260
Qy 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDYSHEDPEVKFNWYVDGVGVHNAKTKPREE 298
Db 261 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDYSHEDPEVKFNWYVDGVGVHNAKTKPREE 320
Qy 299 QYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 321 QFNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 380
Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLVTDK 418
Db 381 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLVTDK 440
Qy 419 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451

Db 441 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 473

RESULT 3
Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024405; AAH24405.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 64.8%; Score 1561.5; DB 11; Length 469;
Best Local Similarity 63.5%; Pred. No. 2.3e-119; Indels 15; Gaps 6;
Matches 291; Conservative 66; Mismatches 86;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTPRSNAMGWVRQAPGKGLWVSGI--SGSGGST 58
Db 20 EVNLVESGGGLVQPGGSLRLSCAASGFTFTDYMSWVRQPPGKALEWLGFIKANKGYTT 79
Qy 59 YYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGVW--DPIDYWGQGT 115
Db 80 EYSASVKGRTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGVW--DPIDYWGQGT 139
Qy 116 LVTYSSASTKGPSVFLPAPSSKSTSGGTAALGLVKDYFPEPTVTSWNSGALTSVHTFP 175
Db 140 LVTYSSASTKGPSVFLPAPSSKSTSGGTAALGLVKDYFPEPTVTSWNSGALTSVHTFP 199
Qy 176 AVQLSSGLYSLSSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKVKVEPKSCDKTHCTPCP 233
Db 200 AVQLSSGLYSLSSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKVKVEPKSCDKTHCTPCP 254
Qy 234 PAPELLGGPSVFLPAPSSKSTSGGTAALGLVKDYFPEPTVTSWNSGALTSVHTFP 293
Db 255 TVPEV--SSVFIPPPKPKDITLMSRTPEVTCVVVDYSHEDPEVKFNWYVDGVGVHNAK 311
Qy 294 KPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQV 353
Db 312 KPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQV 371
Qy 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLK 413
Db 372 TIPPKEQMAKDKVSLTCTMITDFFPEDITVEWQWNGQPAENYKNTQPMIDTDSGFYYSK 431
Qy 414 LTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451
Db 432 LNVQKSNWEAGNTFTCSVLHDEGLHNHHTKSLSHSPGK 469

RESULT 4
Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Gamma heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD04243.1; -
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR FT NON_TER 1
FT 437
FT 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 64.0%; Score 1543.5; DB 11; Length 437;
Best Local Similarity 63.5%; Pred. No. 6.2e-118;
Matches 287; Conservative 67; Mismatches 81; Indels 17; Gaps 6;

QY 2 VQLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYYA 61
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VQLQESGGGLVKPGGSLRLSCAASGFTFSYAMSWVRQTPKRLVWVAFS-SGGIITYT 59
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICAKHTGGVWDPIDYWGQGLTVTS 121
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 DSVKGRFTYIKDRNLTSLQMSLSRSEDYAMYICAR-----GDYSAYWPGCLTVTSA 113
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 122 ASTKGPSVFPLDPSKSTSGGTAALGLVQDYFPPVTVSWNSGALTSGVHTFPAVLQSS 181
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 AKTTPPSVFLAPGSAQAQNSMTLGLVKGYFPEPTVTWNSGSSGVTGHTFPAVLQSD 173
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 182 GLYSLSVTVTPSSSLGTQTYICNVNKPSTNPKVDKVPKSCDKTHTCPP--CPAPELL 239
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 174 -LVTSSVTVPSSTPSEVTVTCNVNVAHPASSTKVDKVIYPRDGG----CKPICIVPEV- 227
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPR 299
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 228 --SSVFLFPPKPKDVLITLTPKVTCTVVDVDSKDDPEVQFSWFDVDEVHTAQTQPREQ 285
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 300 YNSTYRVVSVLTVLDHDLNGKEYKCKVSNKALPAPAEKTISKAKGQPREPQVYTLPPSR 359
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 286 FNSTERSVSELPIMHQDLNGREKFKRVNSAAPPAPAEKTIISKTKGRPAQVYTIIPPK 345
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 360 DELTKNQVSLTCLVKGFYPSDIAVEWESNGPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 346 EQMAKDKVSLTCLMIDFFEDITVEVQWNGQPAENYKNTQPIMDTDGYSFYVSKLVNQS 405
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 420 RWQOGNVFSCSVNMEALHNYTKQSLSLSPGK 451
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 406 NWEAGNTFTCSVLHEGLHHHTKLNLSHPGK 437
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN A0044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -
DR MGD; MGI:2144967; A0044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.1%; Score 1522.5; DB 11; Length 473;
Best Local Similarity 63.0%; Pred. No. 3.6e-116;
Matches 289; Conservative 64; Mismatches 93; Indels 13; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVLVESGGGLVKPGGSRKLSCAASGFTFSYGMHWRQAPGKGLVWVAYVINGSTTIY 79
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRTISRDNKNTLYLQMNSLRAEDTAVYICAKHTGGVW-DPIDYWGQGLTVTV 119
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 ADTVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICARE----LWLRIDYWGQGLTVTV 135
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 SSASTKGPSVFPLDPSKSTSGGTAALGLVQDYFPPVTVSWNSGALTSGVHTFPAVLQ 179
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SSATTPPSVFLAPGCGDTTGTSSVTLGLVKGYFPEPTVTWNSGSLSSVHTFPALLQ 195
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 180 SGLYSLSVTVTPSSSLGTQTYICNVNKPSTNPKVDKVPKSCDKT-HTCPP----- 232
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 -SGLYTMSSVTVPSSTPSEVTVTCNVNVAHPASSTVDRKLEPSPISTINCPCKCKECHK 254
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 233 CPAPPELLGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 292
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 255 CPAPNLEGGPSVFLEPPNPKDVLMLSLTPKVTCTVVDVSEDDPDVQISWFEVNNVEVHTAQ 314
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 293 TKPREQVNSTYRVSVLTVLHDLNGKEYKCKVSNKALPAPAEKTISKAKGQPREPQV 352
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 315 TQTHREDNSTIRVVSALPIQHDMMSCKEFKCKVNNKDLPSPIERTISKIKGLVRAPOV 374
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 353 YLPPEPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGPENNYKTTTPVLDSDGSFFLYS 412
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 375 YLPPAPQQLSRKDVSLCLVVGNGPGLSVIEWTSNGHTEENYKDTAPVLDSDGSFYIYS 434
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 413 KLTVDKSRWQOGNVFSCSVNMEALHNYTKQSLSLSPGK 451
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 435 KLDIKTSKWEKTDSPFCNVRHEGLKNLYLKKTKISRSPGK 473
  ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q991C4 PRELIMINARY; PRT; 463 AA.
ID Q991C4
AC Q991C4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; IGC1; 2.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IGC_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 61.5%; Score 1483.5; DB 11; Length 463;
Best Local Similarity 59.6%; Pred. No. 5.5e-113;
Matches 270; Conservative 78; Mismatches 94; Indels 11; Gaps 5;

Qy 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSTYY 60
Db 20 QVQLQSGAELARPASVLSKASGFTFTGYGVSWVKORTCGGLEWGEIYPGSGNTYY 79

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGVWDPIDYWGQGLTVTS 120
Db 80 SEKFKGKATLTDDKSSSTAYMHLSSLTSEDSAVYFCARSSYYV-YDLFAYWGQGLTVTS 138

Qy 121 SASTKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPTVTVSNAGLTSGVHTFPVAVLQS 180
Db 139 AAKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPTVTVSNAGLTSGVHTFPVAVLQS 198

Qy 181 SGLYSLSSVYVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKCDKTHTCPP--CPAPEL 238
Db 199 D-LYTSSSVYVTPSSVTPWSPSETVTCNVNHNKPSNTKVDKKVEPKCDKTHTCPP--CPAPEL 253

Qy 239 LGGPSVFLFPKPKDITMISRTPEVTCVYVVDVSHEDPEVKFNMYVDGVVHNNAKTTPRE 298
Db 254 ---SSVFIPLPKPKDITLTLPKVKVVDVSDKDPDEQVSWFVDVVDVHTAQTQPRE 310

Qy 299 QYNSTVRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 311 QFNSTFRSVSELPIMHQDWLNGKEFKRVNSAFAFPAPIEKTISKAKGQPREPQVYTLPP 370

Qy 359 RDELTKNOVSLTCLVKGFPDIAVWESNGQPNENYKTPPVLDSDGSGFFLYSKLTVDK 418
Db 371 KEQMAKDVSILTCHITDFPEDITVQWQNGQPAENYKTPQIMDTDGSFYIYSKLNQK 430

Qy 419 SRVQOQGVSCSYMHEALHNHYTKQSLSPGK 451
Db 431 SNWEAGNTFTCSVLHEGLHNHHEKSLSPGK 463

RESULT 7
Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE 1810060009RIK protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohcsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGC_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DE57A514475FBB CRC64;

Query Match 61.4%; Score 1481.5; DB 11; Length 473;
Best Local Similarity 59.5%; Pred. No. 8.2e-113;
Matches 272; Conservative 76; Mismatches 100; Indels 9; Gaps 3;

Qy 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSTYY 60
Db 20 QVQLKQSGAELVKGASVKISKASGYFTFDYINYNKQRPQGQLEWIGKIPGSGSTYY 79

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGVWDPIDYWGQGLTVTS 120
Db 80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR--SGDYDFWFAWGQGLTVTS 137

Qy 121 SASTKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPTVTVSNAGLTSGVHTFPVAVLQS 180
Db 138 AAKTTPSVYPLAPVCGGTGSSVTGLCLVKGYFPEPTVTVSNAGLTSGVHTFPVAVLQ- 196

Qy 181 SGLYSLSSVYVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPK-----SCDKTHTCPPC 234
Db 197 SGLYTLSSSVYVTPSSVTPWSPSETVTCNVNHNKPSNTKVDKKIEPRVPTQNPCLKECPPCA 256

Qy 235 APELLGSPSVFLFPKPKDITMISRTPEVTCVYVVDVSHEDPEVKFNMYVDGVVHNNAKT 294
Db 257 APDLGGSPSVFLFPKPKDITMISRTPEVTCVYVVDVSHEDPEVKFNMYVDGVVHNNAKT 316

Qy 295 PREEQYNSTVRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYT 354
Db 317 THREDYNSTLRVVSALPIQHODWNSGKKEFKCKVNNRALSPIEKTISKPRGPVRAQVYV 376

Qy 355 LPPSRDELTKNOVSLTCLVKGFPDIAVWESNGQPNENYKTPPVLDSDGSGSEFLSKL 414
Db 377 LPPPAEEMTKKEFSLTCHITDFPEDITVQWQNGQPAENYKTPQIMDTDGSFYIYSKLN 436

Qy 415 TVDKSRWQGVSCSYMHEALHNHYTKQSLSPGK 451
Db 437 RVQKSTWERSLFPACSVVHEGLHNHLLTKTISRSLGK 473

RESULT 8
Q99L31 PRELIMINARY; PRT; 468 AA.
ID Q99L31
AC Q99L31;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 60.3%; Score 1453; DB 11; Length 468;
Best Local Similarity 60.6%; Pred. No. 1.7e-110;
Matches 275; Conservative 64; Mismatches 107; Indels 8; Gaps 5;

QY 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 EVQLQQSGAELVRPGASVKLSLTASGTFNIDSLMHWKQRPQEGLEWIGWIDPEGETKY 79
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 ADSVKGREFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKH-TGGGVWDPIDYWGQGLTVT 119
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 APKFDQKATITADTSSTAYLQLSSLTSEDTAIYICARNLLGYG---DYWGQGTITV 136
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 120 SSASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 179
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 SSAKTAPSVPLAPVCGDITGSSVTLCGLVKGYFPEPTVTLTWSGSLSSGVHTFPAVLQ 196
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDKTHRCPP--CPAPE 237
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 SD-LYTLSSVTVTSWPSQITCNVAHPASSTKVDDKIEPRG-PTIKPCPCPKCAPN 254
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 LIGGPSVFLEPPPKDFTLISRPEPTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 297
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 LLGPSVFIFPPKIKDVLMIKSLSPWTCVVVDVSEDDPDVQISFWFNNVEVLTAQTQTHR 314
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 EQYNSTYRVVSVLTVTHQDWLNCKEYKCKVSNKALPAPIETKISKAKGQPREPVTLPP 357
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 EDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPQVYVLP 374
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 417
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 PEEEMTKQVTLTCMVTDMPEDIIYVETWNNKGTETLNYKNTPEVLDSDGSYFMYSKLRYE 434
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 KSRWQGNVPSVCSVMHEALNHNHYTKOKLSLSLSPGK 451
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 435 KKNWVERNSYSCSVVHEGLNHNHHTKSFSTRPGK 468
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 59.3%; Score 1429.5; DB 11; Length 473;
Best Local Similarity 59.0%; Pred. No. 1.5e-108;
Matches 270; Conservative 69; Mismatches 108; Indels 11; Gaps 5;

QY 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 QVQLQQSDAELVKPGASVKISCKVSGYTFDTHHWVKQRPQEGLEWIGYIYPRDGSYKY 79
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 ADSVKGREFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKH-TGGGVWDPIDYWGQGT 115
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSR--GGSIYYGYGLYFYDWGQGT 137
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 LVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPTVTSWNSGALTSGVHTFP 175
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 TITVSSAKTAPSVPLAPVCGDITGSSVTLCGLVKGYFPEPTVTLTWSGSLSSGVHTFP 197
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 176 AVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDKTHHTCPP--C 233
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 AVLQSD-LYTLSSVTVTSWPSQITCNVAHPASSTKVDDKIEPRG-PTIKPCPCPKC 255
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 234 PAPELLGGPSVFLPDKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKAT 293
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 PAPNLLGGPSVFIFPPKIKDVLMIKSLSPWTCVVVDVSEDDPDVQISFWFNNVEVLTAOT 315
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 294 KPREEQYNSTYRVVSVLTVTHQDWLNCKEYKCKVSNKALPAPIETKISKAKGQPREPOVY 353
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 QTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPOVY 375
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK 413
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 VLPPPEEEMTKQVTLTCMVTDMPEDIIYVETWNNKGTETLNYKNTPEVLDSDGSYFMYSK 435
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 414 LTVDKSRWQGNVPSVCSVMHEALNHNHYTKOKLSLSLSPGK 451
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 LRVEKKNWVERNSYSCSVVHEGLNHNHHTKSFSTRPGK 473
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AA025447.1; -.
DR Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

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Query Match          57.9%; Score 1397; DB 11; Length 474;
Best Local Similarity 57.6%; Pred. No. 6.7e-106;
Matches 264; Conservative 72; Mismatches 112; Indels 10; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSAAAGFTFRSNAMGWVROAPKGLGWVSGISGGSGTYY 60
DB 20 QVQLVQSGGGLVQPGGSLRLSAAAGFTFRSNAMGWVROAPKGLGWVSGISGGSGTYY 79
QY 61 ADSVKGRTISRDNSKNTLYLQMSNRAEDTAYVYCAKHTGGGVNDPIDYKQCGTLTVS 120
DB 80 SGKFGQKAKLTADKSSVTAFQLTSLTSDSAVYFCARDSDYG--DYFDWGGQATVTVS 137
QY 121 SASTKGPSVFPLAPSSKSTSGGTAAALGLVQDYFFPEPTVSNWNSGALTSGVHTFPAVLQSS 180
DB 138 SAKTTPSPVYPLAPGCGDTGSSVTLGCLVKGYPFESVTVTNWNSGSLSSVHTFPALLQ- 196
QY 181 SGLYSLSVVTVVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKT-HTCPP-----C 233
DB 197 SGLYTWSSSVTVPSSTWPSQTVTCSVAHPASSTVTDKKLEPSGPITSTINPCPKCKECHK 256
QY 234 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 293
DB 257 PAPNLEGGPSVFIFPPNPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 316
QY 294 KPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKTISKAKGQPREPQVY 353
DB 317 QTHREDYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKTISKAKGQPREPQVY 376
QY 354 TLPPSRDELTKNOVSLTCLVKGYPDSIAVEVSNQGPENNYKTPPVLDSDGSGFFLYSK 413
DB 377 ILPPPAEQLSRKDVSLTCLVKGYPDSIAVEVSNQGPENNYKTPPVLDSDGSGFFLYSK 436
QY 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 437 LDIKTSKWEATDFSCNVRHGLKNIYLAKTISRSPGK 474

RESULT 11
Q95M34 PRELIMINARY; PRT; 337 AA.
AC Q95M34 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region
DE (Fragment).
GN IGHCI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match          52.5%; Score 1264.5; DB 6; Length 337;
Best Local Similarity 69.2%; Pred. No. 2e-95;

Matches 234; Conservative 43; Mismatches 52; Indels 9; Gaps 3;

QY 122 ASTKGPSVFPLAPSSKSTSGGTAAALGLVQDYFFPEPTVSNWNSGALTSGVHTFPAVLQSS 181
DB 1 ASTTAPKVFALACGGTSDTVALGCLVSGYFPEPVKVSWSNGLTSGVHTFPAVLQSS 60
QY 182 GLYSLSVVTVVPSSSLGTQYICNVNHNKPSNTKVDKVEP-----KSCDKTHTCPPCPA 235
DB 61 GFYSLSSNMTVPASTWTSETYICNVVHAASFVKDKRIEIPDNHOKVCDMS-KCPKCPA 119
QY 236 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTP 295
DB 120 PELLGGPSVFLFPPNPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTATTP 179
QY 296 REEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKTISKAKGQPREPQVYTL 355
DB 180 KEEQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKTISKAKGQPREPQVY 239
QY 356 PPSRDELTKNOVSLTCLVKGYPDSIAVEVSNQGP--ENNYKTPPVLDSDGSGFFLYSK 413
DB 240 APHPDELKSKSVSLTCLVKGYPDSIAVEVSNQGPENNYKTPPVLDSDGSGFFLYSK 299
QY 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 300 LSVDRNRWQQQTTFTTCGMHEALHNHYTQKNVKNPKG 337

RESULT 12
Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98;12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF; 2.
DR PROSITE; PS001010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00134; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
```


GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:04 ; Search time 34.7681 Seconds
(without alignments)
1460.205 Million cell updates/sec

Title: US-09-822-698A-5

Perfect score: 1990

Sequence: 1 OVQLVSGGLVPGGSLRL.....IVEFLNRWITFCQSIISTLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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4:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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7:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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9:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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11:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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15:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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18:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1990	100.0	381	22	AAE12707
2	1289	64.8	409	22	AAU04945
3	1217	61.2	524	21	AAAY4995
4	1072.5	53.9	582	22	AAAB1987
5	1052	52.9	281	18	AAW27560
6	1027.5	51.6	582	22	AAAB1991
7	1002.5	50.4	262	23	ABP46070
8	987.5	49.6	248	22	AAAG5590
9	982	49.3	456	21	AAAY4992
10	980	49.2	450	21	AAAY4991

11	969	48.7	581	22	AAAB1972
12	943	47.4	583	22	AAAB3156
13	914.5	46.0	244	23	ABP45980
14	909	45.7	249	22	AAAB20434
15	883.5	44.4	384	22	AAAM24101
16	881	44.3	384	22	AAU14461
17	881	44.3	384	22	AAU14462
18	881	44.3	384	22	AAU14463
19	881	44.3	384	22	AAU14464
20	879	44.2	307	22	AAU14225
21	874.5	43.9	247	23	AAU09000
22	874.5	43.9	312	22	AAU14227
23	870	43.7	238	21	AAV53775
24	862	43.3	247	14	AAAB32091
25	862	43.3	249	14	AAAB32090
26	862	43.3	249	17	AAAB5213
27	860.5	43.2	240	20	AAAY02472
28	858	43.1	249	13	AAAB21262
29	849.5	42.7	240	22	AAAB46040
30	846.5	42.5	222	22	AAU04972
31	846.5	42.5	233	17	AAAB33013
32	844	42.4	253	16	AAAB72599
33	843.5	42.4	222	22	AAU04976
34	842	42.3	293	22	AAAG5715
35	840.5	42.2	240	22	AAAB46046
36	838.5	42.1	222	22	AAU04974
37	838	42.1	239	23	ABP45911
38	833.5	41.9	240	22	AAAB46038
39	832.5	41.8	240	22	AAAB46018
40	831.5	41.8	240	22	AAAB46044
41	831.5	41.8	240	22	AAAB46045
42	828.5	41.6	240	22	AAAB45999
43	828.5	41.6	240	22	AAAB46006
44	828.5	41.6	240	22	AAAB46042
45	827.5	41.6	240	22	AAAB46005

ALIGNMENTS

RESULT 1

AAE12707

ID AAE12707 standard; Protein; 381 AA.

AC AAE12707;

XX

XX

DT 04-JAN-2002 (first entry)

XX Human bivPH1-IL-2 immunocytokine protein.

DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;

KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.

XX Homo sapiens.

OS WO200175110-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US10589.

XX 30-MAR-2000; 2000US-0538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HFJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX N-PSDB; AAD20732.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member

PT for diagnosing and treating cancer, comprises mucin-1 binding domain or

PT its portion for binding to an epitope of the protein core of mucin-1

XX Claim 9; Page 95-97; 126pp; English.

PS The invention relates to an isolated tumour-associated antigen mucin-1

XX (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human biVPH1-IL-2

CC immunocytokine protein. biVPH1 is mucin specific binding portion.

XX Sequence 381 AA;

SQ

Query Match 100.0%; Score 1990; DB 22; Length 381;

Best Local Similarity 100.0%; Pred. No. 9.9e-132;

Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVQAQPGKLEWVSGISGGSGSYIY 60

DB 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVQAQPGKLEWVSGISGGSGSYIY 60

QY 61 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLPLTVTS 120

DB 61 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLPLTVTS 120

QY 121 SGGGALAEIVLTQSPSLPTPEPASISCRSSQSLHNSNGYTYLDWYLQKPGQSPQLLIY 180

DB 121 SGGGALAEIVLTQSPSLPTPEPASISCRSSQSLHNSNGYTYLDWYLQKPGQSPQLLIY 180

QY 181 SGGSHRAGVDPDRFSGSVSGTDTLRLSRVEADVGYYCMQGLQSPFTFGPGTKVDIKRG 240

DB 181 SGGSHRAGVDPDRFSGSVSGTDTLRLSRVEADVGYYCMQGLQSPFTFGPGTKVDIKRG 240

QY 241 GSGGGALAPTSSTSKTKTQLEHLLDQLMILNGINNYKNPKLTRLMTFFKYPMPKKATE 300

DB 241 GSGGGALAPTSSTSKTKTQLEHLLDQLMILNGINNYKNPKLTRLMTFFKYPMPKKATE 300

QY 301 LKHQCLEELKPLEVNLQSKNPHLRPRDLISNINVLKLGSETFMCEYADETA 360

DB 301 LKHQCLEELKPLEVNLQSKNPHLRPRDLISNINVLKLGSETFMCEYADETA 360

QY 361 TIVEFLNRWITFCQSIISTLT 381

DB 361 TIVEFLNRWITFCQSIISTLT 381

RESULT 2

AAU04945

ID AAU04945 standard; Protein; 409 AA.

XX AAU04945;

AC AAU04945;

XX 24-OCT-2001 (first entry)

DT Humanised anti-p185 antibody/IL-2 fusion protein.

XX Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;

XX cancer; tumour; adenocarcinoma; fusion protein.

XX Chimeric - Home sapiens.

OS Chimeric - Mus sp.

OS Synthetic.

Key Location/Qualifiers

Peptide 1..22 /label= Signal_peptide

Protein 23..409 /label= Mature_fusion_protein

Protein 23..259 /label= Humanised_antibody_520C9H

Region 53..57 /label= CDR

Region 72..88 /note= "Complementarity determining region"

Region 121..126 /label= CDR

Region 121..126 /note= "Complementarity determining region"

Misc-difference 123 /note= "Encoded by GGG"

Peptide 138..152 /label= Synthetic_peptide_linker

Peptide 176..186 /note= "Links the heavy chain to the light chain"

Region 202..208 /label= CDR

Region 241..249 /label= CDR

Region 261..276 /note= "Complementarity determining region"

Peptide 277..409 /label= IL_2

Protein 406 /note= "Encode by ACA"

Misc-difference 406

WO200153354-A2.

26-JUL-2001.

19-JAN-2001; 2001WO-US01919.

20-JAN-2000; 2000US-0177258.

(CHIR) CHIRON CORP.

(HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.

(HAMI-) HAMILTON REGIONAL CANCER CENT.

Austin R, Kwok CS, Ring DB;

WPI; 2001-451904/48.

N-PSDB; AAS09508.

Novel immunoconjugate useful for inhibiting tumour cell growth in vivo

comprises a humanized anti-p185 antibody linked to an Interleukin-2

polypeptide -

Claim 13; Fig 11; 74pp; English.

The sequence represents a humanised anti-p185 (520C9), single chain

antibody/human interleukin-2 (IL-2) fusion protein. The fusion protein

(or immunoconjugate) is used to inhibit the growth of tumours or cancers

particularly those characterised by overexpression of p185 e.g. human

adenocarcinomas and malignant and/or benign tumours of the breast, renal

system, salivary gland, gastrointestinal tract or gastric tumours.

Sequence 409 AA;

Query Match 64.8%; Score 1289; DB 22; Length 409;

Best Local Similarity 65.1%; Pred. No. 1.6e-82;

Matches 259; Conservative 44; Mismatches 67; Indels 28; Gaps 4;

CC chains comprises, a CH1-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CL-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (poly)peptides having different receptor or ligand functions, where further at least two of the different (poly)peptides lack an intrinsic affinity for one another and are linked via the constant domains. The heteroinhibitors have cytostatic, immunostimulatory, antileukaemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, melanomas and sarcomas.

CC The present sequence is the right chain of a heteroinhibitor comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to human Ck domain (constant domain of immunoglobulin-kappa light chain) which bears at its C-terminus the human inflammatory cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen.

CC Sequence 524 AA;

CC Query Match 61.2%; Score 1217; DB 21; Length 524;

CC Best Local Similarity 66.4%; Pred. No. 2.5e-77;

CC Matches 263; Conservative 19; Mismatches 86; Indels 28; Gaps 7;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNAMGWVRQAPGKLEWVSGTSGSGSTYY 60

DB 23 EIQLVQSGPEVKKPCASVKISCKASGYTFANYGNWKKQAPGKLEWGWINVTGGSTY 82

QY 61 ADSVKGRTISRDNKNTLYLQMSNLRADTAAYCAKHTGGVWMDIDYWGQGTLTVS 120

DB 83 ADDPKERTFTLDSTSTAHLEISLSRSEDATVFCARRE-----QFAYWGQGTLTVS 136

QY 121 -----SGGGALEIVLTQSPSLPVPVTPGEPASISCRSSQSLHSNGTYTLDWTLQK 170

DB 137 SGGGSGGGGGGGSDIQMTQSPSSLSASVGRVTITCRASQDIGN-----LTWLQOK 191

QY 171 PGQSPQLLIYSGSHRASGVPDRFSGVSGTDFTLIRISRVEADGVVYCMQGLQSPFTFG 230

DB 192 PGKTIKRLIYATSLDGSVPFRSGRSGTDYTLTISLQPEDFVYVYCLQYAIFFPTFG 251

QY 231 PGTKVDIKR-----GGSGGALAPTSSSTKTKQLQLEHLLDLQMLINGINNYKNPK 283

DB 252 QGTLKLEIFGFGGGGGGGGSGGSGMPTSSSTKTKQLQLEHLLDLQMLINGINNYKNPK 311

QY 284 LTRMLTFKFPMPKATELKHLCLEELKPLEEVNLNAQSKNHLRDLISINIVLE 343

DB 312 LTRMLTFKFPMPKATELKHLCLEELKPLEEVNLNAQSKNHLRDLISINIVLE 371

QY 344 LKGETTFMCEYADETATVIEFLNRWITFCQSIISTLT 381

DB 372 LKGETTFMCEYADETATVIEFLNRWITFCQSIISTLT 409

RESULT 3

AA44995

ID AAY44995 standard; Protein; 524 AA.

XX

AC AAY44995;

XX

DT 23-MAY-2000 (first entry)

XX

DE HD70scFv-Ck-interleukin 2.

XX

KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human; EPCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2; interleukin-2; Ck-domain; kappa light chain constant domain; heteroinhibitor; multifunctional compound; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; prevention; antiproliferative; treatment; malignant; haematopoietic cell; lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.

XX

OS Homo sapiens.

XX

PN W0200006605-A2.

XX

PD 10-FEB-2000.

XX

PF 28-JUL-1999; 99NO-EP05416.

XX

PR 28-JUL-1998; 98EP-0114082.

XX

PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.

XX

PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;

XX

DR WPI; 2000-195265/17.

XX

DR N-PSDB; AA250588.

XX

PT New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis -

XX

PS Example 10; Fig 55B; 166pp; English.

XX

CC The patent discloses heteroinhibitors which are multifunctional compounds producible in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide

CC chains comprises, a CH1-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CL-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (poly)peptides having different receptor or ligand functions, where further at least two of the different (poly)peptides lack an intrinsic affinity for one another and are linked via the constant domains. The heteroinhibitors have cytostatic, immunostimulatory, antileukaemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, melanomas and sarcomas.

CC The present sequence is the right chain of a heteroinhibitor comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to human Ck domain (constant domain of immunoglobulin-kappa light chain) which bears at its C-terminus the human inflammatory cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen.

CC Sequence 524 AA;

CC Query Match 61.2%; Score 1217; DB 21; Length 524;

CC Best Local Similarity 66.4%; Pred. No. 2.5e-77;

CC Matches 263; Conservative 19; Mismatches 86; Indels 28; Gaps 7;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNAMGWVRQAPGKLEWVSGTSGSGSTYY 60

DB 142 EVQLLESGGVPVQGRSURLSCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSNRY 201

QY 61 ADSVKGRTISRDNKNTLYLQMSNLRADTAAYCAKHTG--GGWDP-----IDYWGQ 114

DB 202 ADSVKGRTISRDNKNTLYLQMSNLRADTAAYCAKDMGWSGRFYIYMGDMVWGQ 261

QY 115 TLVTVSSG---GGALEIVLTQSPSLPVPVTPGEPASISCRSSQSLHSNGY---TYLDWYL 168

DB 262 TTVTVSSGTPGLDTHTRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQKV 321

QY 169 QKPGQSPQLLIYSGSHRASGVPDRFSGVSGTDFTLIRISRVEADGVVYVC---MQGLQS 225

DB 322 DN-----ALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYIACEVTHQGLSS 374

QY 226 PTFPGGTQVDIKRGGSGGALAPTSSSTKTKQLQLEHLLDLQMLINGINNYKNPKLT 285

DB 375 PVT-----KSFNRGECGSGGSAFTSSSTKTKQLQLEHLLDLQMLINGINNYKNPKLT 428

QY 286 RMLTFKFPMPKATELKHLCLEELKPLEEVNLNAQSKNHLRDLISINIVLELK 345

DB 429 RMLTFKFPMPKATELKHLCLEELKPLEEVNLNAQSKNHLRDLISINIVLELK 488

QY 346 GSETTFMCEYADETATVIEFLNRWITFCQSIISTLT 381

DB 489 GSETTFMCEYADETATVIEFLNRWITFCQSIISTLT 524

RESULT 4

AA81987

ID AAB81987 standard; Protein; 582 AA.

XX

AC AAB81987;

XX

DT 03-JUL-2001 (first entry)

XX

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.

XX

KW Ganglioside; GD3; complementarity determining region; CDR; antibody; cancer.

XX

OS Synthetic.

XX

PN W0200123432-A1.

XX

PD 05-APR-2001.

XX

PF 29-SEP-2000; 2000WO-JP06774..
XX
PR 30-SEP-1999; 99JP-0278291.
PR 06-APR-2000; 2000JP-0105086.
XX
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3. The antibody and its derivatives are
PT therapy of e.g. tumours, with low antigenicity, little side effects but
PT potent activity in cancer
XX
XX Claim 41; Page 168-172; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention.
XX
XX Sequence 582 AA;
SQ
Query Match 53.9%; Score 1072.5; DB 22; Length 582;
Best Local Similarity 43.5%; Pred. No. 3.8e-67;
Matches 257; Conservative 32; Mismatches 83; Indels 219; Gaps 11;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSGTY 60
DB 1 EVQLVESGGDFVQPGGSLRVSACAAGFAFASHYAMSVWRQAPGKLEWVAISSGGSGTY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPIDYWGQGLTVTVS 120
DB 61 SDSVKGRFTISRDNKNTLYLQMNLSRAEDSAVYFCTRVKLGTY--FDSWGQGLTVTVS 118
QY 121 SGGGALEIVLTQSPSLPVTPG-----EPASISCRSS----- 152
DB 119 SAS-----TKGPSVFPLAPSSKSTSGGTALGCLVKDYFPEPVTVSVNSGALTSGVIT 171
QY 153 -QSLHNSGYTYLDWYIQKPGQS--PQLLIYSGSHRAS----- 187
DB 172 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYTCNVNHRKPSNTKVDKKVEPKSCDKTHRCTPPC 231
QY 188 -----GVPD-----RFGSGVSGTD----- 201
DB 232 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 291
QY 202 -----F 202
DB 292 KPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNALPAIEKTIKAKGPREPQVY 351
QY 203 TLRISRV-----AEDGVVYCMQG-----IQSPFTFGGPK 234
DB 352 TLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSSEFLYSK 411
QY 235 VDIKRGSGSGGAL-----APTSSSTKKTQLQLEHLLLDLQ 270
DB 412 LTVDKSRWQGNVFCSVWHEALHNHYTQKSLSLSPCKAPTSSSTKKTQLQLEHLLLDLQ 471
QY 271 MILGINNKNPKLTRLTKFYPMPKATKELKHLQCLEELKPLEEVNLQAQSKNFHLRP 330
DB 472 MILGINNKNPKLTRLTKFYPMPKATKELKHLQCLEELKPLEEVNLQAQSKNFHLRP 531
QY 331 RDLISNINVLKSGSETTFMCEYADETATIVFEFLNRWITFCQSIISLT 381
DB 532 RDLISNINVLKSGSETTFMCEYADETATIVFEFLNRWITFCQSIISLT 582
RESULT 5
AAW27560

ID AAW27560 standard; Protein; 281 AA.
XX
AC AAW27560;
XX
DT 23-JAN-1998 (first entry)
XX
XX Consensus single chain fragment VH3-V-kappa-2.
XX
XX Human; antibody; preparation; library; VH3; variable region;
KW light chain; heavy chain; V-kappa-2; single chain; consensus.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1..21
FT Peptide /label= sig_peptide
FT Peptide 22..281
FT Peptide /label= mat_peptide
XX
XX WO9708320-A1.
XX
XX 06-MAR-1997.
XX
XX 19-AUG-1996; 96WO-EP03647.
XX
XX 18-AUG-1995; 95EP-0113021.
XX
XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
XX
XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
PI WPI; 1997-179277/16.
XX
XX N-PSDB; AAT87958.
XX
XX Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
XX
XX Example 2; Fig 8; 436pp; English.
XX
XX The present sequence is the consensus single chain fragment
CC VH3-V-kappa-2. VH3-V-kappa-2, which comprises the human antibody
CC heavy and light chain variable region consensus sequences VH3 and
CC V-kappa-2, was used in the preparation of a human derived antibody
CC gene library.
XX
SQ Sequence 281 AA;
Query Match 52.9%; Score 1052; DB 18; Length 281;
Best Local Similarity 81.5%; Pred. No. 4.4e-66;
Matches 207; Conservative 11; Mismatches 20; Indels 16; Gaps 2;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSGTY 60
DB 26 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVAISSGGSGTY 85
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPIDYWGQGLTVTVS 120
DB 86 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGFY-AMDYWGQGLTVTVS 144
QY 121 -----SGGGALEIVLTQSPSLPVTPGPASTISCRSSQSLHNSGYTVLD 165
DB 145 SAGGSGGGGSGGGGSDIVMTQSPSLPVTPGPASTISCRSSQSLHNSGYTVLD 204
QY 166 WYLOKPGQSPQLLIYSGSHRASGVPDRFSGVSGDFTFLRISRVEAEDGVVYCMQGLQS 225
DB 205 WYLOKPGQSPQLLIYLSNRRASGVPDRFSGVSGDFTFLKISRVEAEDGVVYCMQGHVTT 264
QY 226 PFTFGPGTKVDIKR 239
DB 265 PFTFGGQTKVEIKR 278


```
RESULT 6
AAB81991
ID AAB81991 standard; Protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP06774.
XX
PR 30-SEP-1999; 99JP-0278291.
XX
PR 06-APR-2000; 2000JP-0105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and
PT therapy of e.g. tumours, with low antigenicity, little side effects but
PT potent activity in cancer.
XX
PS Claim 39; Page 175-179; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention.
XX
SQ Sequence 582 AA;
Query Match 51.68; Score 1027.5; DA 22; Length 582;
Best Local Similarity 41.88; Pred. No. 5.5e-64;
Matches 247; Conservative 37; Mismatches 88; Indels 219; Gaps 11;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNAMGWVRQAPKGLVWVSGISGGSTYY 60
Db :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
1 EYTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSVVRQTAKRLEWVAVYSSGGSGTYY 60
QY 61 ADSVKGRTTISRDNSTNTLYLQMSLRADFTAVYCAKHTGGVWDPIYWGOGTLTVTS 120
Db :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
61 SDSVKGRFTISDNKNTLYLQMSLRSEDSAMVFCRVKLGTVY--FDSWGOGTILTVS 118
QY 121 SGGGALEIVLQSPLSLSEVTPG-----EPASISCRSS----- 152
Db :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
119 SAS-----TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHT 171
QY 153 -QSLHNSNGYTYLDWYLRKPGQS--PQLLYSGSHRAS----- 187
Db :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
172 FPAVLQSSGLYSLSVWTVVPSSSLGTQYICNVNKKPSNTKVDKKVPRKCDKTHTCPPC 231
QY 188 -----GVPD-----RFGSGVSGTD----- 201
Db :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
232 PAPELLGGPSVFLFPPPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGEVNAKT 291
QY 202 -----F----- 202
Db 292 KPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNALPAPIEKTISKAKGQPREPQVY 351
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```
QY 203 TLIRSRVE-----AEDVGYYCMQG-----LQSPFTFGPGTK 234
|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
Db 352 TLPFSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSK 411
V :|:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
QY 235 VDIKRGGSGGGAL-----APTSSTKKTKQLQLEHLLDLQ 270
:|:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
Db 412 LTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPCKAPTSSSTKTKQLQLEHLLDLQ 471
:|:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
QY 271 MILGGINNYKNPKLTRMLTEKFYMPKKATELKHLCLEELKPLEEVNLNLAQSKNFHLRP 330
|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
Db 472 MILGGINNYKNPKLTRMLTEKFYMPKKATELKHLCLEELKPLEEVNLNLAQSKNFHLRP 531
|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
QY 331 RDLISNINIVLELKGSETTFMCEYADETATIVFEFLNRWITFCQSIISTLT 381
|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
Db 532 RDLISNINIVLELKGSETTFMCEYADETATIVFEFLNRWITFCQSIISTLT 582
|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| | :|||:| |
RESULT 7
AAB46070
ID AAB46070 standard; Protein; 262 AA.
XX
AC AAB46070;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLYS binding scFv SEQ ID 2081.
XX
KW BLYS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
WPI; 2002-114799/15.
XX
Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
Claim 1; Page 2880-2881; 3148pp; English.
XX
This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
CC and so may be used to detect and quantitate the presence of BLYS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLYS. They may also be
CC administered to treat diseases associated with aberrant BLYS expression
CC and activity such as cancer, immune, and autoimmune disorders and
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CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 262 AA;
Query Match 50.4%; Score 1002.5; DB 23; Length 262;
Best Local Similarity 76.3%; Pred. NO. 1.2e-62;
Matches 200; Conservative 15; Mismatches 24; Indels 23; Gaps 3;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKH-----ID 109
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDQFQVRCVFIANPPYNYGMD 120
QY 110 YWGQGLTVTVSSGGG-----ALEIVLTQSPSLPVTGPEPASISCRSSQSLH 157
Db 121 VMKGKFTTVTVSSGGGGGGGGGSALEIVMTQSPSLPVTGPEPASISCRSSQSLH 180
QY 158 SNGYTVLDWYLPKQSPOLLIVSGSHRASGVPDRFSGSVSGTDFTLKISRVEAEDVG 217
Db 181 SNGYNLDWYLPKQSPOLLIVSGSHRASGVPDRFSGSVSGTDFTLKISRVEAEDVG 240
QY 218 YCMQGLQSPFTFGPGTKVDIKR 239
Db 241 YCMQALQTLPLTGGGTVKEIKR 262
RESULT 8
AAG65590
ID AAG65590 standard; Protein; 248 AA.
XX AAG65590;
AC
DT 07-JAN-2002 (first entry)
XX
DE Anti-hEDRF antibody e9 amino acid sequence.
XX
KW Human; erythroid differentiation related factor; hEDRF; antianemic;
KW erythrocyte deficiency; antibody e9.
XX Homo sapiens.
XX
PN EP1130030-A1.
XX
XX
PD 05-SEP-2001.
XX
PF 27-FEB-2001; 2001EP-0104821.
XX
PR 02-MAR-2000; 2000US-0517225.
XX
PA (HOFF) ROCHE DIAGNOSTICS CORP.
XX
XX Xu H, Mahoney W, Schueler P, Harriman WD;
PI
XX WPI; 2001-608195/70.
DR N-PSDB; AAH47762.
XX
XX Novel human erythroid differentiation related factor and
PT polynucleotides encoding it useful for treating anemia and other
PT erythrocyte deficiencies and for detecting expression of the factor in
PT humans
XX
XX Disclosure; Fig 4; 29pp; English.
PS
XX The invention provides a human erythroid differentiation related factor
CC (hEDRF). The hEDRF polypeptide and the encoding polynucleotide are useful
CC for treating anemias and other erythrocyte deficiencies. The hEDRF

CC protein is useful for producing antibodies, useful in screening assays to
CC identify pharmaceutical compounds of interest and compounds which bind to
CC hEDRF. The polynucleotides are useful for producing hEDRF or its related
CC polypeptides. The antibodies are useful for separating or detecting the
CC corresponding antigen e.g. for detection/quantitation of hEDRF in samples
CC taken from human subjects. Quantification of hEDRF at immunohistochemical
CC level finds value in evaluating the potential of the tissue site to
CC contribute towards the production of new erythroid cells. The present
CC sequence represents the amino acid sequence of an anti-hEDRF antibody e9.
XX
SQ Sequence 248 AA;
Query Match 49.6%; Score 987.5; DB 22; Length 248;
Best Local Similarity 78.8%; Pred. NO. 1.3e-61;
Matches 197; Conservative 16; Mismatches 24; Indels 13; Gaps 3;
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
Db 1 EVQLVSGGGLVQPGGSLRLSCAASGFTFDYAHVWROAPGKGLWVSGISWNSGIGY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHHTGGGWDPIDVWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAESSD--LESNVTWGQGLTVTVS 118
QY 121 SGGG-----ALEIVLTQSPSLPVTGPEPASISCRSSQSLHSGTYLDWYLOK 170
Db 119 SGGGGGGGGGGGSALEIVMTQSPSLPVTGPEPASISCRSSQSLHSGTYLDWYLOK 178
QY 171 PQQSPQLLIYLGSHRASGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQGLQSP-FTF 229
Db 179 PQQSPQLLIYLGSHRASGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQALQTPSLTF 238
QY 230 GPQTKVDIKR 239
Db 239 GQGTKLEIKR 248
RESULT 9
AAY44992
ID AAY44992 standard; Protein; 456 AA.
XX AAY44992;
AC
DT 23-MAY-2000 (first entry)
XX
DE M79scFv-interleukin 2-fusion protein containing tetramerisation domain.
XX
KW Murine; M79 antibody; 17-1A antigen; single-chain Fv fragment; scFv;
KW fusion construct; human; interleukin 2; IL-2; tetramerisation domain;
KW heteromimer; multifunctional compound; constant domain;
KW immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Leader_peptide
FT Region 20..126
FT /label= M79scFv_light_chain_variable_region
FT Region 127..141
FT /label= Gly-Ser_linker
FT Region 142..256
FT /label= M79scFv_heavy_chain_variable_region
FT Region 259..269
FT /note= "Human IgG3 upper hinge region with
FT additional residues"
FT Domain 270..308
FT /label= Human_p53_tetramerisation_domain
FT Peptide 309..315
FT /label= Short_peptide_linker

```
FT Domain 316..450
FT /label= Interleukin-2_domain
FT Region 451..456
FT /label= His_tag
XX
PN WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP05416.
XX
PR 28-JUL-1998; 98EP-0114082.
XX
PA (MICR-) MICROMET GES BIOMEDIKALINISCHE FORSCHUNG.
XX
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR WPI; 2000-195265/17.
DR N-PSDB; AAZ50585.
XX
XX New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis
XX
PS Example 9; Fig 48; 166pp; English.
CC The patent discloses heteroninibodies which are multifunctional compounds
CC producible in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CHI-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heteroninibodies have
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas.
CC The present sequence is a fusion protein comprising murine
CC 17-1A-antigen specific M79 single-chain Fv (scFv) fragment at the
CC N-terminus, human interleukin-2 at the C-terminus and a tetramerisation
CC domain between them. This construct was prepared to find out whether
CC an oligomerisation domain characterised in bacterial expression system
CC is applicable for expression of fully functional and secretable
CC recombinant protein in mammalian host cells. This tetrameric construct
CC was found to be expressed as secretable and fully functional protein
CC in mammalian cells.
XX
SQ Sequence 456 AA;
Query Match 49.3%; Score 982; DB 21; Length 456;
Best Local Similarity 55.18; Pred. No. 6.4e-61;
Matches 217; Conservative 27; Mismatches 50; Indels 100; Gaps 10;
QY 1 QVQLVQSGGGLVQPGGSLRLCAASGFTFRSNAMGWVRQAPGKGLEWWSGISGGSTYY 60
DB 142 QVQLQESGPGLVQPSQSLITCTVSGFSLTSGYGVHVWRQSPGKGLEWL-GVIWSGGSTDY 200
QY 61 ADSVGRFTTISRDNSKNTLYLQMNSLRAEDTAVYCAKHTGGGVMDPITYWGQGLTVTS 120
DB 201 NNAFTSRISIDKNSKQVFFKMSLQANDTAIYICARMEN---WS-FAYWGQGLTVTS 256
QY 121 SGGGALEIVLTQSPILSPVTFCEPASISCRSSQLHSNGYVLDWYLQKPGQSPQLLIY 180
DB 257 E-----FTPLG-----DTHTSG-----KP----- 271
QY 181 SGSHRASGVPDRFSGSVSGTDFLRI-----SRVEADGVYVCMQGLQSPF 227
DB 272 -----LDGEFTLQIGRERFEMFRELNEALELKA-----QAGKEP- 308
QY 228 TFGPGTKVDIKRGGSGGALAPTSSSTKTKTQLQLEHLLDLQMLNGINNKNPKLTRM 287
Db 309 -----GSGGAPAPTSSSTKTKTQLQLEHLLDLQMLNGINNKNPKLTRM 354
QY 288 LTFKFMPPKATKELKHLQCLEELKPLEEVNLNLAQSKNPHLRPRDLISINIVILELKS 347
Db 355 LTFKFMPPKATKELKHLQCLEELKPLEEVNLNLAQSKNPHLRPRDLISINIVILELKS 414
QY 348 ETTFMCEYADETATIVFELNLRWITFCQSIITLT 381
Db 415 ETTFMCEYADETATIVFELNLRWITFCQSIITLT 448
RESULT 10
AAY44991
ID AAY44991 standard; Protein; 450 AA.
XX
XX AAY44991;
XX
DT 23-MAY-2000 (first entry)
XX
DE M79scFv-interleukin 2-fusion protein containing dimerisation domain.
XX
KW Murine; M79 antibody; 17-1A antigen; single-chain Fv fragment; scFv;
KW fusion construct; human; interleukin 2; IL-2; dimerisation domain;
KW heteroninibody; multifunctional compound; constant domain;
KW immunoglobulin; cytotatic; immunostimulatory; antileukaemia; diagnosis;
KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Leader_peptide
FT Region 20..126
FT /label= M79scFv_light_chain_variable_region
FT Region 127..141
FT /label= Gly-Ser_linker
FT Region 142..256
FT /label= M79scFv_heavy_chain_variable_region
FT Region 259..268
FT /note= "murine IgG3 upper hinge region with
FT additional residues"
FT Domain 269..303
FT /label= dHLX-dimerisation_domain
FT Peptide 304..309
FT /label= Short_peptide_linker
FT Domain 310..444
FT /label= Interleukin-2_domain
FT Region 445..450
FT /label= His_tag
XX
XX WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP05416.
XX
XX 28-JUL-1998; 98EP-0114082.
XX
XX (MICR-) MICROMET GES BIOMEDIKALINISCHE FORSCHUNG.
XX
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR WPI; 2000-195265/17.
DR N-PSDB; AAZ50584.
XX
XX New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis
XX
PS Example 9; Fig 47; 166pp; English.
```

CC The patent discloses heteromimibodies which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises, a CHI-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises CL-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromimibodies have
 CC cytostatic, immunostimulatory, anticellulemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas.
 CC The present sequence is a fusion protein comprising murine
 CC 17-1A-antigen specific M79 single-chain Fv (scFv) fragment at the
 CC N-terminus, human interleukin-2 at the C-terminus and a dimerisation
 CC domain between them. This construct was prepared to find out whether
 CC an oligomerisation domain characterised in bacterial expression system
 CC is applicable for expression of fully functional and secretable
 CC recombinant protein in mammalian host cells. The dimerisation domain used
 CC in this construct proved to be not applicable in mammalian host cells.

XX Sequence 450 AA;
 SQ Query Match 49.2%; Score 980; DB 21; Length 450;
 Best Local Similarity 56.4%; Pred. No. 8.7e-61;
 Matches 215; Conservative 30; Mismatches 56; Indels 80; Gaps 10;

QY 1 QVQLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGSGSTYY 60
 DB 142 QVQLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGSGSTYY 200
 QY 61 ADSVKGRFTISRDNKNTLYLQMSNLAEDTAVYCAKHTGGVWDPIYWGQGLTVTVS 120
 DB 201 NAAFISRLSKDQNSQVFFKNSLQANDTAIYCARMEN---WS-FAYWGQGLTVTVS 256
 QY 121 SGGGALEIVLTQSPSLPVTPGPASISCRSSQSLHNSGYTYLDWYLOKPGOSPOLLIY 180
 DB 257 E-----FKPSTP-----PGSSGEL--- 271
 QY 181 SGSHRASGVDPDRSGVSGTDFTLIRSRVDAEDGVYVCMQGLQSPFTGPGTKVDIKRG 240
 DB 272 --BELLKHLKELKPKRG-----ELEEL---LKHUK-----BLLKG 303
 QY 241 GSGGGGLAPTSSTTKTQLQLEHLLDQLMILNGINNYKNPKLTRMLTFKFMPPKATE 300
 DB 304 G--SGGAPATSSSTTKTQLQLEHLLDQLMILNGINNYKNPKLTRMLTFKFMPPKATE 361
 QY 301 LKHLQCLEELKPLEEVLNLAQSKNHLRPRDLISINIVLELKGSETTFMCEYADETA 360
 DB 362 LKHLQCLEELKPLEEVLNLAQSKNHLRPRDLISINIVLELKGSETTFMCEYADETA 421
 QY 361 TIVEFLNRWTFCSIIISLT 381
 DB 422 TIVEFLNRWTFCSIIISLT 442

RESULT 11
 AAB81972
 ID. AAB81972 standard; Protein; 581 AA.
 XX AAB81972;
 AC
 XX
 XX
 DT 03-JUL-2001 (first entry)
 XX Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
 DE Ganglioside; GD2; complementation determining region; CDR; antibody;
 XX Ganglioside; GD2; complementation determining region; CDR; antibody;
 KW mouse; cancer.
 KW
 XX Synthetic.
 OS

XX WO200123573-A1.
 PN 05-APR-2001.
 XX 29-SEP-2000; 2000WO-JP06773.
 PF 30-SEP-1999; 99JP-0278290.
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 PA Hanai N, Shitara K, Nakamura K, Niwa R;
 PI WPT; 2001-266163/27.
 DR Human type complementation-determining domain transplanted antibody and
 XX derivatives against ganglioside GD2, useful in diagnosis and therapy of
 PT e.g. tumours, has low antigenicity, little side effects but potent
 PT activity in cancer -
 PS Example 3; Page 111-114; 123pp; Japanese.
 XX The present invention describes an antibody, which can react specifically
 CC with ganglioside GD2, and is transplanted with a human type
 CC complementation-determining domain (CDR), or its fragments. The antibody
 CC and its derivatives are useful in diagnosis and therapy of tumours,
 CC particularly cancer diagnosis. The present sequence is a protein
 CC used in the exemplification of the invention.
 XX Sequence 581 AA;
 SQ Query Match 48.7%; Score 969; DB 22; Length 581;
 Best Local Similarity 40.3%; Pred. No. 6.9e-60;
 Matches 238; Conservative 40; Mismatches 93; Indels 220; Gaps 12;

QY 1 QVQLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGSGSTYY 60
 DB 1 QVQLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGSGSTYY 59
 QY 61 ADSVKGRFTISRDNKNTLYLQMSNLAEDTAVYCAKHTGGVWDPIYWGQGLTVTVS 120
 DB 60 NSALMSRLTISKDQNSQVFFKNSLTAADTAVYCAKRDSDYWS--FAYWGQGLTVTVS 117
 QY 121 SGGGALEIVLTQSPSLPVTPG-----EPASISCRSS----- 152
 DB 118 SAS-----TKGPVFFPLAPSSKTSGGTAALGCLVKDYFPEPVTYSNWSGALTSGVHT 170
 QY 153 -QSLHNSGYTYLDWYLOKPGOS---PQLLIYSGSHRAS----- 187
 DB 171 FPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVHNPSTKVDKKVPEKSCDKTHTCPPC 230
 QY 188 -----GVPD-----RFGSVSGTD----- 201
 DB 231 PAPELLGGPSVFLFPPPKPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKT 290
 QY 202 -----F 202
 DB 291 KPREEQNSTYRVSVLTVLHODLNGKEYCKVKVSNKALPAIEKTIKAKGQPREPOVY 350
 QY 203 TLRISERVE-----AEDGVVYCMOG-----LQSPFTFGPGTK 234
 DB 351 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSK 410
 QY 235 VDIKRGSGSGGAL-----APTSSTTKTQLQLEHLLDQL 270
 DB 411 LTVDSRWQGNVFCVSWHEALHNYHTQKSLSPGKAPTSSSTTKTQLQLEHLLDQL 470
 QY 271 MTLNGINNYKNPKLTRMLTFKFMPPKATELKHLCLEELKPLEEVLNLAQSKNHLR 330
 DB 471 MTLNGINNYKNPKLTRMLTFKFMPPKATELKHLCLEELKPLEEVLNLAQSKNHLR 530
 QY 331 RLISINIVIVLELKGSETTFMCEYADETATIVFELNWRWTFCSIIISLT 381

Db	531	RDLISNINVLKSGSETTFCYADETATVEFLNRWITFCQSIISTLT	581
RESULT 12			
AAB83156			
ID	AAB83156	standard; protein; 583 AA.	
AC	AAB83156;		
XX			
XX			
DT	02-JUL-2001	(first entry)	
XX			
DE	Ganglioside GM2 antibody-related protein #1.		
XX			
KW	Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.		
XX			
OS	Unidentified.		
XX			
PN	WO200123431-A1.		
XX			
PD	05-APR-2001.		
XX			
PF	29-SEP-2000; 2000WO-JP06775.		
XX			
PR	30-SEP-1999; 99JP-0278292.		
XX			
PA	(KYOW) KYOWA HAKKO KOGYO KK.		
XX			
PI	Hanai N, Nakamura K, Niwa R;		
XX			
DR	WPI; 2001-266142/27.		
XX			
PT	Monoclonal antibodies against ganglioside GM2 combined with drugs,		
XX			
PT	radioisotopes or proteins for treatment and diagnosis of cancer -		
XX			
PS	Claim 43; Page 61-65; 80pp; Japanese.		
XX			
CC	The present invention relates to derivatives of an antibody against		
CC	ganglioside GM2. The antibody may be a monoclonal antibody or its		
CC	fragments. The antibody is combined with a radioactive isotope,		
CC	protein or small drug in the treatment and diagnosis of cancer.		
XX			
SQ	Sequence 583 AA;		
Query Match 47.4%; Score 943; DB 22; Length 583;			
Best Local Similarity 39.3%; Pred. No. 4.7e-58;			
Matches 233; Conservative 44; Mismatches 94; Indels 22; Gaps 12;			
QY	1	QVQLVQSGGGLVOPGSLRLSCAASGFTFRSNAMGVWROAPGKLEWVSGISGGSTYY	60
Db	1	EVOLVSGAEVKKPGASVKVSKASGYTFDYNMDWVKSPGQGLEWVGYYIPNNGGTGY	60
QY	61	ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAK--HTGGGVWDPIDYWGOGTLVT	118
Db	61	NQPKSKVTITVDTSTAYMELHLSRSEDVAVYYCATYGHYYGMF---AWGQGTLYT	117
QY	119	VSSGGGALEIVLQPSLSPVPTG-----EPASISCRSS-----	152
Db	118	VSSAS-----TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGV	170
QY	153	---QSLHNSGYTLQWYLOKPCQS--POLLIYSGSHRAS-----	187
Db	171	HTFPALQSSGLYSVTVTPSSSLGTQTYICNVNHPKSPNTKVDKVKPKSCDKTHTCP	230
QY	188	-----GVPD-----RFGSGVSGTGD---	201
Db	231	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNA	290
QY	202	-----	201
Db	291	KTKPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSKNALKALPAPIETKISKAKGP	350
QY	202	-FTLRTSRVE-----AEDVGYYCMQG-----LQSPFTFGPG	232

Db	351	VYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSFFLY	410
QY	233	TKVDIKRGGSGGAL-----APTSSTKTKTQLQLEHLLLD	268
Db	411	SKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGKAPTSSSTKTKTQLQLEHLLLD	470
QY	269	LQMLNGINNYKNPKLRLMFLTKFYMPKATKELKHLQCLEELKPLEEVNLQAQKNFHL	328
Db	471	LQMLNGINNYKNPKLRLMFLTKFYMPKATKELKHLQCLEELKPLEEVNLQAQKNFHL	530
QY	329	RPRLISNINVLKSGSETTFCYADETATVEFLNRWITFCQSIISTLT	381
Db	531	RPRLISNINVLKSGSETTFCYADETATVEFLNRWITFCQSIISTLT	583
RESULT 13			
ABP45980			
ID	ABP45980	standard; Protein; 244 AA.	
XX			
AC	ABP45980;		
XX			
DT	19-AUG-2002	(first entry)	
XX			
DE	Human BlyS binding scFv	SEQ ID 1991.	
XX			
KW	BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;		
KW	tumour necrosis factor; B cell proliferation; B cell differentiation;		
KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;		
KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;		
KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;		
KW	common variable immunodeficiency; acquired immunodeficiency syndrome.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200202641-A1.		
XX			
PD	10-JAN-2002.		
XX			
PF	15-JUN-2001; 2001WO-US19110.		
XX			
PR	16-JUN-2000; 2000US-212210P.		
PR	17-OCT-2000; 2000US-240816P.		
PR	16-MAR-2001; 2001US-276248P.		
PR	21-MAR-2001; 2001US-277379P.		
PR	25-MAY-2001; 2001US-293499P.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.		
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;		
XX			
DR	WPI; 2002-114799/15.		
XX			
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for		
XX	the diagnosis and treatment of cancers and immune disorders -		
PS	Claim 1; Page 2776-2777; 3148pp; English.		
XX			
CC	This invention describes novel antibodies that immunospecifically bind to		
CC	B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the		
CC	tumour necrosis factor (TNF) super family and induces B cell		
CC	proliferation and differentiation. The antibodies of the invention have		
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,		
CC	antirheumatic and antiAIDS activity and can be used in vaccines to		
CC	inhibit the expression and activity of BlyS. The antibodies bind to BlyS		
CC	and so may be used to detect and quantitate the presence of BlyS in		
CC	biological samples and may be used in this way to diagnose disease		
CC	associated with aberrant expression of BlyS. They may also be		
CC	administered to treat diseases associated with aberrant BlyS expression		
CC	and activity such as cancer, immune, and autoimmune disorders and		
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,		
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and		
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent		

CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX
SQ Sequence 244 AA;
Query Match 46.0%; Score 914.5; DB 23; Length 244;
Best Local Similarity 72.6%; Pred. No. 1.7e-56;
Matches 183; Conservative 22; Mismatches 26; Indels 21; Gaps 4;
QY 1 QVQLVQSGGGLVOPGGSURLSLCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGGSTYY 60
DB 1 EVQLVQSGGGLVPGGKURLSLCAASGFTFRSSYMMWVRQAPCKGLEWVSSISSSSHIYY 60
QY 61 ADSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYYCAK-HTGGGVWMDIDYWGQGLTVTV 119
DB 61 ADSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYYCARVHSSGS-----WGQGLTVTV 113
QY 120 SGGG-----ALEIVLTQSPSLPVTPEGPASISCRSSQSLHNSGYTLDMY 167
DB 114 SSGGGGGGGGGGGSALDVYMTQSPSLPVTGLGPASISCRSSQSLVHSDGNTYLNWF 173
QY 168 LQPGQSPOLLIVSGSHRASGVDPDRFSGVSGTDFTLRISRVEAEDVGYYICMQLQSPF 227
DB 174 QRPQSGSPRLIYKVSNRDFGVPDRFSGSGGTFTLKISRVEAEDVGYYICMQLQTHR-I 232
QY 228 TFGPGTKVDIKR 239
DB 233 TFGQGRLEIKR 244

RESULT 14
AAB20434
ID AAB20434 standard; Protein; 249 AA.

XX
AC AAB20434;
XX
DT 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 193/K2 scFv.

XX Factor IX: FIX; Factor IXa: FIXa; scFv: antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

XX Chimeric - Mus musculus.
OS Chimeric - Synthetic.

XX Key Location/Qualifiers
FH Protein 1..121
FT /label= VH
FT Region 98..110
FT Peptide 122..135
FT /label= Linker
FT Protein 136..249
FT /label= VL
FT Region 230..238
FT /label= CDR3

XX WO200119992-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-EP08936.

XX 14-SEP-1999; 99AT-0001576.

XX (BAXT) BAXTER AG.

XX Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;

XX WPI; 2001-290358/30.

DR N-PSDB; AAF30724.

XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
PS Claim 10; Fig 15; 138pp; English.

XX The present sequence is that of a single chain Fv (scFv) derivative
CC of antibody 193/K2, comprising the heavy (VH) and light (VL) chain
CC variable regions of 193/K2 joined by an artificial, flexible linker
CC peptide. The scFv was obtained by PCR amplification of cDNAs for
CC 193/K2 VH and VL regions and cloning in vector pDAP2. 193/K2 is
CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,
CC including scFv and CDR3 fragments, have factor VIIIa (FVIIIa) cofactor
CC activity or FIXa activating activity. Administration leads to an
CC increase in the procoagulant activity of FIXa, even in the presence
CC of FVIIIa inhibitors. This allows for rapid blood coagulation even
CC in the absence of FVIII or FVIIIa, and in the case of FVIII
CC inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis.

XX Sequence 249 AA;

Query Match 45.7%; Score 909; DB 22; Length 249;

Best Local Similarity 69.9%; Pred. No. 4.1e-56;

Matches 174; Conservative 28; Mismatches 37; Indels 10; Gaps 1;

QY 1 QVQLVQSGGGLVOPGGSURLSLCAASGFTFRSNAMGWVRQAPCKGLEWVSGISGGSTYY 60

DB 1 EVQLVESGGGLVPGGKURLSLCAASGFTFTYTHSWVRQTPKRLKLEWVATISSGGSTYY 60

QY 61 ADSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWMDIDYWGQGLTVTVS 120

DB 61 PDSVGRFTTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGHHGYSDFYWGQGLTVTVS 120

QY 121 -----SGGALIEIVLTQSPSLPVTPEGPASISCRSSQSLHNSGYTLDMYLOK 170

DB 121 SGGGSGGSGRASGGGGSQIVLTQSPSLPVLSDQASISCRSSQSLVHNSGYTLDMYLOK 180

QY 171 PQGSPOLLIVSGSHRASGVDPDRFSGVSGTDFTLRISRVEAEDVGYYICMQLQSPFTF 230

DB 181 PQGSPKLLIYKVSNRFGVDPKFSGSGSGIDFTLKISRVEAEDLGVIYCFQGSHPVPTFG 240

QY 231 PGTKVDIKR 239

DB 241 GGTKLEIKR 249

RESULT 15

AAM24101

ID AAM24101 standard; Protein; 384 AA.

XX AAM24101;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1626.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder;

XX biodiversity; gene therapy; nutrition.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

```
XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR N-PSDB: AAH98760.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX Claim 20; Page 1102-1103; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
XX Sequence 384 AA;
SQ
Query Match 44.4%; Score 883.5; DB 22; Length 384;
Best Local Similarity 66.3%; Pred. No. 4.2e-54;
Matches 185; Conservative 22; Mismatches 47; Indels 25; Gaps 5;
QY 1 QVQLVQSGGGLVPGGSLRLCAASGFTFSRNAMGWVRQAPGKLEWWSGISGGSTYY 60
DB :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 EVQLVESGGGLVPGGSLRLCAASGFTFSRYAMSWVRQAPGKLEWWSGISGGSTYY 79
QY 61 ADSVKGRTISRDNSKNTLYLQMNSLRAEDTAVYCAK-----HTGGGVWDP-----I 108
DB :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 ADSVKGRTISRDNSQNTLYLQMNSLRAEDTAVYCAKSHPAYYSGSYSHYYGYGM 139
QY 109 DWVGQGLTVTVSSG-----GGAL--EIVLTQSLPLVTPGEPASISCRSSQSLHSN 159
DB :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
140 DWVGQGLTVTVSSGSGSGGAGTGEIVLTQSPGTLSLSPGERATLSCRASQSVSS- 198
QY 160 GYTLDDWLYLQKPGQSPQLLYSGHRSRSGVPDRFSGVSGTDEFTLRISRVAEADVYYC 219
DB :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
199 ---YLAWYQKPKQAPRLCIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYC 255
QY 220 MQGLQSPFTFGPTKVDIKRGSGGGGALAPTSSSTKKT 258
DB :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
256 QQYGSPTTFGGQTKRVEIKRTVAAPSVFIFPPSDEQLKS 294
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Search completed: March 14, 2003, 11:47:36
Job time : 37.7681 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:34 ; Search time 11.9515 seconds
(without alignments)
937.967 Million cell updates/sec

Title: US-09-822-698A-5

Perfect score: 1990
Sequence: 1 QVQLVQSGGGLVPGGSLRL.....IVEFLNRWITFCQSIISTLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1052	52.9	281	4	US-09-025-769B-178
2	862	43.3	247	4	US-09-227-693-34
3	862	43.3	248	1	US-08-331-398A-34
4	862	43.3	248	2	US-08-331-397B-34
5	862	43.3	248	2	US-08-759-804A-34
6	798	40.1	245	4	US-08-918-148-75
7	797	40.1	289	3	US-09-184-658-63
8	790	39.7	366	3	US-08-875-811-55
9	781	39.2	282	2	US-08-860-174A-10
10	778	39.1	245	4	US-08-918-148-78
11	776.5	39.0	301	2	US-08-661-052-14
12	776.5	39.0	301	4	US-09-188-082-14
13	776.5	39.0	301	4	US-09-364-088-14
14	776.5	39.0	301	4	US-09-102-716-14
15	776.5	39.0	553	2	US-08-661-052-16
16	776.5	39.0	553	4	US-09-188-082-16
17	776.5	39.0	553	4	US-09-364-088-16
18	776.5	39.0	553	4	US-09-102-716-16
19	770.5	38.7	365	3	US-08-875-811-53
20	765.5	38.5	244	4	US-08-918-148-77
21	765	38.4	245	4	US-08-918-148-76
22	764	38.4	263	2	US-08-752-844-66
23	763	38.3	284	4	US-08-564-164A-2
24	758	38.1	277	2	US-08-256-790-2
25	750	37.7	228	5	PCT-US92-08257-9
26	731.5	36.8	248	2	US-08-887-352B-22
27	731.5	36.8	248	4	US-09-109-207C-22

28 731.5 36.8 248 4 US-09-296-005-22 Sequence 22, Appl
29 730.5 36.7 248 2 US-08-887-352B-23 Sequence 23, Appl
30 730.5 36.7 248 4 US-09-109-207C-23 Sequence 23, Appl
31 730.5 36.7 248 4 US-09-296-005-23 Sequence 23, Appl
32 730 36.7 252 1 US-08-133-804-4 Sequence 4, Appl
33 730 36.7 252 1 US-08-461-838-4 Sequence 4, Appl
34 730 36.7 252 2 US-08-461-886-4 Sequence 4, Appl
35 728.5 36.6 535 4 US-08-983-035A-38 Sequence 65, Appl
36 726.5 36.5 236 2 US-08-190-199A-65 Sequence 38, Appl
37 717 36.0 240 2 US-08-459-354-4 Sequence 4, Appl
38 717 36.0 240 2 US-08-077-253-4 Sequence 4, Appl
39 717 36.0 240 3 US-08-333-840-4 Sequence 4, Appl
40 713 35.8 223 2 US-08-190-199A-63 Sequence 63, Appl
41 713 35.8 240 1 US-08-488-113B-148 Sequence 148, Appl
42 713 35.8 240 1 US-08-477-484B-148 Sequence 148, App
43 713 35.8 240 2 US-08-646-360-148 Sequence 148, App
44 713 35.8 240 4 US-08-839-765-148 Sequence 148, App
45 713 35.8 240 4 US-09-136-389-148 Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/025,769B
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-178

Query Match 52.9%; Score 1052; DB 4; Length 281;
Best Local Similarity 81.5%; Pred. No. 1.le-81;
Matches 207; Conservative 11; Mismatches 20; Indels 16; Gaps 2;

```
QY 1 QVLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGISGGSTYY 60
Db 26 EQLVSGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLWVSAISGGSTYY 85
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVMDPIDYWGQGLTVTVS 120
Db 86 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCARWGGDGY-ANDYWGQGLTVTVS 144
QY 121 -----SGGGALEIVLTQSPSLPVTTPGEPASISCRSSQSLHLSNGYTYLD 165
Db 145 SAGGSGGGGSGGGGSDIVMTQSPSLPVTTPGEPASISCRSSQSLHLSNGYNYLD 204
QY 166 WYLQPGQSPQLLIYSGSHRASGVPDRFSGVSGTDFTLRLSRVEAEDVGVVYCMGGLQS 225
Db 205 WYLQPGQSPQLLIYLSNRASGVPDRFSGSGGTDFTLKLSRVEAEDVGVVYCOOHYTT 264
QY 226 PTFPGGTAKVDIKR 239
Db 265 PTFGGGTAVEIKR 278

RESULT 2
US-09-227-693-34
; Sequence 34, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Ital
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/331,396
; FILING DATE:
; APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-227-693-34
```

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Query Match 43.3%; Score 862; DB 4; Length 247;
Best Local Similarity 67.6%; Pred. No. 1.3e-65;
Matches 167; Conservative 28; Mismatches 40; Indels 12; Gaps 2;

QY 2 VQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLWVSGISGGSTYYA 61
Db 3 VKLVESGGGLVQPGGSLRLSCATSGFTSDYYMYWVROTPEKLEWVAYISNDSSAAYS 62
QY 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVMDPIDYWGQGLTVTVS- 120
Db 63 DTVKGRFTISRDNARNTLYLQMSRLKSEDFAIYSCARGLAAGW--FAYWGQGLTVTVSS 120
QY 121 -----SGGGALEIVLTQSPSLPVTTPGEPASISCRSSQSLHLSNGYTYLDWYLQKP 171
Db 121 GGGSGGGGSGGGGSDVMTQSPSLPVSIGDQASISCRSSQIIVHSNGNTYLEWYLQKP 180
QY 172 GQSPQLLIYSGSHRASGVPDRFSGVSGTDFTLRLSRVEAEDVGVVYCMGGLQSPETFGP 231
Db 181 GQSPKLLIYKVSNRFSRSGVPDRFSGSGGTDFTLKLSRVEAEDLGVIYCFQGGSHVPTFGS 240
QY 232 GTKVDIK 238
Db 241 GTKLEIK 247

RESULT 3
US-08-331-398A-34
; Sequence 34, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

```

;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein

```

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:	
; LENGTH: 248 amino acids	
; TYPE: amino acid	
; TOPOLOGY: linear	
; MOLECULE TYPE: protein	
US-08-759-804A-34	
Query Match 43.3%; Score 862; DB 2; Length 248;	
Best Local Similarity 67.6%; Pred. No. 1.3e-65;	
Matches 167; Conservative 28; Mismatches 40; Indels 12; Gaps 2;	
QY 2	VQLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWVSGISGGSTIYA 61
Db 3	VKLVESGGGLVQPGGSLKSCATSGFTSDYMYWVRQTPKRLLEWVAYISNDSSAAYS 62
QY 62	DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS- 120
Db 63	DTVKGRFTISRDNKNTLYLQMSRLKSEPTATYSCARGLAWAW--FAYWGQGLTVTVSS 120
QY 121	-----SGGALEIVLTQSPSLPVPTEPEPASISCRSSQSLHLSNGTYTLDWYLQRP 171
Db 121	GGGSGGGGGGGSDVIMTQSPSLPVSIGDQASISCRSSQIIVHSNGTYLLEWYLQRP 180
QY 172	GQSPQLIYSGSHRAGVDPDRFSGVSGDTFTLRISRVEAEDGVYYCMQGLQSPPTFGP 231
Db 181	GQSPKLLIYKVNRFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYYCFQGSHVPTFGS 240
QY 232	GTRVDIK 238
Db 241	GTKLEIK 247
RESULT 6	
US-08-918-148-75	
; Sequence 75, Application US/08918148A	
; Patent No. 6342220	
; GENERAL INFORMATION:	
; APPLICANT: Adams, Camellia	
; APPLICANT: W.	
; APPLICANT: Carter, Paul J.	
; APPLICANT: Fendly, Brian M.	
; APPLICANT: Gurney, Austin L.	
; TITLE OF INVENTION: Agonist Antibodies	
; FILE REFERENCE: P0979	
; CURRENT APPLICATION NUMBER: US/08/918,148A	
; CURRENT FILING DATE: 1997-08-25	
; NUMBER OF SEQ ID NOS: 79	
; SEQ ID NO 75	
; LENGTH: 245	
; TYPE: PRT	
; ORGANISM: artificial	
US-08-918-148-75	
Query Match 40.1%; Score 798; DB 4; Length 245;	
Best Local Similarity 63.1%; Pred. No. 3.4e-60;	
Matches 157; Conservative 27; Mismatches 47; Indels 18; Gaps 3;	
QY 1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWVSGISGGSTIY 60
Db 3	EVQLVQSGGGLVKPGGSLRLSCAASGFTFDYIMSWIRQAPGKLEWVSISSGSTIYY 62
QY 61	ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
Db 63	ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARWSE---DAFDIWGQGTWTVTS 119
QY 121	-----SGGALEIVLTQSPSLPVPTEPEPASISCRSSQSLHLSNGTYTLDWYLQK 170
Db 120	SGGGSGGGGGGGSDIVMTQSPSTLSASVGDRAVITCRASEGIYH----WLAVTQQK 174
QY 171	PQSPQLIYSGSHRAGVDPDRFSGVSGDTFTLRISRVEAEDGVYYCMQGLQSPPTFG 230
Db 175	PGKAPKLLIYKASSLASGAPSRFSGSGGADFTLTLSLQPDPTATYICQYSNYPLTFG 234

; SEQUENCE CHARACTERISTICS:	
; LENGTH: 248 amino acids	
; TYPE: amino acid	
; TOPOLOGY: linear	
; MOLECULE TYPE: protein	
US-09-184-658-63	
Query Match 40.1%; Score 797; DB 3; Length 289;	
Best Local Similarity 62.7%; Pred. No. 5.2e-60;	
Matches 156; Conservative 33; Mismatches 44; Indels 16; Gaps 2;	
QY 1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWVSGISGGSTIY 60
Db 23	EVQLVESGGGVQPGGSLKSCAASGFTNTYGMSSWVRQTPDKRLLEWATINSNGLTIFY 82
QY 61	ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
Db 83	ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 137
QY 121	S-----GGGALEIVLTQSPSLPVPTEPEPASISCRSSQSLHLSNGTYTLDWYLQ 169
Db 138	SGGGSGGGGGGGSDVMTQSPSTLTSLVTITGQASISCKSSQSLGSDGLTYLILWLQ 197

QY 170 KPGSPQLLIYSGSHRAGVDPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTF 229
 Db 198 RPOQPKRLIFLVELSDGVDPDRFTSGSGTDFTLKISRRAEDLGVYYCQGTFFHTF 257
 QY 230 PGTKVDIK 238
 Db 258 GAGTKLELK 266

RESULT 8
 US-08-875-811-55
 ; Sequence 55, Application US/08875811
 ; Patent No. 6045793
 ; GENERAL INFORMATION:
 ; APPLICANT: Rybak, Susanna M.
 ; APPLICANT: Newton, Dianne L.
 ; APPLICANT: Boque, Lluís
 ; APPLICANT: Wlodawer, Alexander
 ; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/875,811
 ; FILING DATE: 19-FEB-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US97/02588
 ; FILING DATE: 19-FEB-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/011,800
 ; FILING DATE: 21-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Faris, Susan K.
 ; REGISTRATION NUMBER: 41,739
 ; REFERENCE/DOCKET NUMBER: 015280-244100US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 55:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 366 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-875-811-55

Query Match 39.7%; Score 790; DB 3; Length 366;
 Best Local Similarity 46.4%; Pred. No. 2.8e-59;
 Matches 180; Conservative 50; Mismatches 110; Indels 48; Gaps 8;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
 Db 2 QVQLQSGGPELKPGETVTKISCKASGYTFNNGMNVKQAPGKGLKWMGINTYTGESTY 61
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVDPIDYWGQGLTVTVS 120
 Db 62 ADDPKGRFAFSLETSASAAQLQINLNKEDATYFCARFAIKG-----DYWGQGLTVTVS 116
 QY 121 -----SGGGALEIVLTQSPLSLPVTPGEPASISCRSSQSLHLSNGITYLDWYLOK 170
 Db 117 SGGGGGGGGGGGSDIVLTQSPFNPVTLGTSASISCRSTKSLHLSNGITYLDWYLOK 176

QY 171 PGOSPOLLIYSGSHRAGVDPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTF 230
 Db 177 PGOSPOLLIYQMSNLASGVDPDRFSSGSGTDFTLRISRVEAEDVGYYCAQNLPIRPTF 236
 QY 231 PGTKVDIKRGGSG--GGALAPTSSSTKKTQLQLEHLHLLDQLMILNGINNYKNPKLTRML 288
 Db 237 GGTKLEIKRAAAAKLNDQAQPKSDMDLTFQKKHITNTROVDCDNI-----MS 286
 QY 289 TFKYMPKATELKHLOCLEELKPLEEVL-NLAQSKNFHLRPRDLISINIVILELKS 347
 Db 287 TNLFHCKDKNT-----FIYSRPEPKAICKGIASKNVLTTSEFVLSDCNV----- 332
 QY 348 ETTFMEYADETATVEEFLNRWITFCQS 375
 Db 333 -FSRPCKYKLLKST-----NKFCVTCEN 354

RESULT 9
 US-08-860-174A-10
 ; Sequence 10, Application US/08860174A
 ; Patent No. 5989830
 ; GENERAL INFORMATION:
 ; APPLICANT: DAVIS, Paul James
 ; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
 ; APPLICANT: VERHOEIJEN, Martine Elisa
 ; APPLICANT: WILSON, Steve
 ; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
 ; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: WASHINGTON, D.C.
 ; STATE:
 ; COUNTRY: UNITED STATES
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
 ; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/860,174A
 ; FILING DATE: June 16, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95307332.7
 ; FILING DATE: October 16, 1995
 ; APPLICATION NUMBER: PCT/EP/96/03605
 ; FILING DATE: August 14, 1996
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 282 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-860-174A-10

Query Match 39.2%; Score 781; DB 2; Length 282;
 Best Local Similarity 63.5%; Pred. No. 1.2e-58;
 Matches 160; Conservative 23; Mismatches 53; Indels 16; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGGSTYY 60
 Db 23 QVQLQSGGDLVQPGSLTSCATSGFTSFVAFSWVRQTSKLSLEWATISSIDYTYTY 82
 QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKH--TGGGVWDPIDYWGQGLTVT 118
 Db 83 SDNVKGRFTISRDNKNTLYLQMSLSKSEDVAVYYCARHGYGKGYF--DYWGQGLTVT 139
 QY 119 VS-----SGGGALEIVLTQSPLSLPVTPGEPASISCRSSQSLHLS-NGITYLDWY 167
 Db 140 VSSGGGGGGGGGGGSDIELTQSPFLTVTAGEKVTMNCQSGSLNSYNQRNLTWY 199

Qy 168 LQKPGSPOLLIIYSGSHRASGVDPDRFSGSVSGTDFTLRISRVEADVGYYVCMQGLQSPF 227
| | | | | 1:1111 | | | | | 1:111111 | | | | | 1:1111 | | | | |
Db 200 QOKGQPKLLIYWASTRESGVDPDRFTASGSGTDFTLISSVQAEADLAVIYQNDYTYPF 259
| | | | | 1:1111 | | | | | 1:111111 | | | | | 1:1111 | | | | |
Qy 228 TFGPGTKVDIKR 239
| | | | | 1111111111
Db 260 TRFGGKLEIKR 271
| | | | | 1111111111

RESULT 10
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78

Query Match 39.1%; Score 778; DB 4; Length 245;
Best Local Similarity 62.2%; Pred. No. 1.7e-58;
Matches 155; Conservative 27; Mismatches 49; Indels 18; Gaps 3;
Qy 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWYSGISGGSTYV 60
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Db 3 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWYSSISSSSYIY 62
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVNDPDIYWGQGLTVTS 120
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Db 63 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGS---TGMVWGRGLTVTS 119
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Qy 121 -----SGGGALEIVLTQSPSLPTPGEPAISCRSSQSLHNSGYTLDWYLOK 170
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Db 120 SGGGSGGGSGGGGSKIQTSPSTLSASIGDRVTITCRASEGIYH-----WLAWYQOK 174
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Qy 171 PGQSPOLLIIYSGSHRASGVDPDRFSGSVSGTDFTLRISRVEADVGYYVCMQGLQSPFTFG 230
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Db 175 PGAKPLLYKASSLASGAPSRFSGSGSGTDFTXTISSLPQDDFATYYCOQSYNPLTFG 234
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Qy 231 PGTKVDIKR 239
| | | | | 1111111111
Db 235 GGTKLEIKR 243
| | | | | 1111111111

RESULT 11
US-08-661-052-14
; Sequence 14, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; STREET: 60 State Street, Suite 510
; CITY: Boston

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/661,052
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MX1-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-661-052-14

Query Match 39.0%; Score 776.5; DB 2; Length 301;
Best Local Similarity 61.5%; Pred. No. 3e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;
Qy 2 VOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWYSGISGGSTIYA 61
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Db 21 IQLVESGGVQVQGRSLRLSCSSGFIISDNYMTYVWRQAPGKLEWVATISDGGSTIYP 80
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Qy 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----KHTGGVNDPDIYWGQGLTV 117
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Db 81 DSVKGRFTISRDNKNTLYLQMNLSRPEDTGVYFCARGYYRGEA-----MDYWGQGLTV 135
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Qy 118 TVS-----SGGGALEIVLTQSPSLPTPGEPAISCRSSQSLH-SNGYTYLDW 166
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Db 136 TVSSGGGSGGGSGGGSDIQLTQSPSSLASVGRVTITCKSSQSVLYSSNQKNYLAW 195
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Qy 167 YLQKPGSPOLLIIYSGSHRASGVDPDRFSGSVSGTDFTLRISRVEADVGYYVCMQGLQSP 226
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Db 196 YQKREGKAPKLLIYWASTRESGVPSRFSGSGSGTDFTTISSLPQDDIATYYCHQYLSS- 254
| | | | | 1:1111111111 | | | | | 1:1111111111 | | | | | 1:1111111111 | | | | |
Qy 227 TFGPGTKVDIKRGGSGGG 246
| | | | | 1111111111
Db 255 WFGGQTKVEIKSSCGGG 274
| | | | | 1111111111

RESULT 12
US-09-188-082-14
; Sequence 14, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston

```
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-188-082-14

Query Match          39.0%; Score 776.5; DB 4; Length 301;
Best Local Similarity 61.5%; Pred. No. 3e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;

QY 2 VOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKGLVWVSGSGGTYVA 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 IQLVESGGVVQPGSLRLSCSSGGFISDNMYWVQAPGKGLVWVATISDGGSTYYP 80
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 DSVKGRFTISRDNSKNTLYIQMNSLRADETAVYCA----KHTGGGVWDPIDYWGQGLV 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 DSVKGRFTISRDNSKNTLYIQMNSLRPEDTGVYFCARGVYRGEA-----MDYWGQGLV 135
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 118 TVS-----SGGGALEIVLTQSPSLPVPVTPGEPASTSCRSSQSLH-SNGYTYLDW 166
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 136 TVSSGGGGGGGGGGGGSDIQLTQSPSSLSASVGDRTVITCKSSQSVLYSSNQKNYLAW 195
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QY 167 YLQPGQSPQLLIYSGHRSAGVDPDRFSGVSGTDFTLRLSRVEAEDVGYYICMQGLQSP 226
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Db 196 YQKPGKAPKLLIYWASTRESGVPSRFSGSGGTFTFTISSLPEDIAITYYCHQYLSS- 254
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QY 227 FTFGPGTKVDIKRGGSGG 246
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RESULT 13
US-09-364-088-14
; Sequence 14, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-364-088-14

Query Match          39.0%; Score 776.5; DB 4; Length 301;
Best Local Similarity 61.5%; Pred. No. 3e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;

QY 2 VOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKGLVWVSGSGGTYVA 61
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Db 21 IQLVESGGVVQPGSLRLSCSSGGFISDNMYWVQAPGKGLVWVATISDGGSTYYP 80
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QY 62 DSVKGRFTISRDNSKNTLYIQMNSLRADETAVYCA----KHTGGGVWDPIDYWGQGLV 117
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Db 81 DSVKGRFTISRDNSKNTLYIQMNSLRPEDTGVYFCARGVYRGEA-----MDYWGQGLV 135
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 118 TVS-----SGGGALEIVLTQSPSLPVPVTPGEPASTSCRSSQSLH-SNGYTYLDW 166
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QY 167 YLQPGQSPQLLIYSGHRSAGVDPDRFSGVSGTDFTLRLSRVEAEDVGYYICMQGLQSP 226
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Db 255 WTFGGGTKEIKSSCSGGG 274
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RESULT 14
US-09-102-716-14
; Sequence 14, Application US/09102716
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
;              Joel Goldstein
;              Robert Graziano
;              Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-102-716-14

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Query Match 39.0%; Score 776.5; DB 4; Length 301;
Best Local Similarity 61.5%; Pred. No. 3e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;

QY 2 VQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYYA 61
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QY 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----KHTGGVMDPIDYWGQGLV 117
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81 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----MDYWGQGLTPV 135
QY 118 TVS-----SGGGALEIVLTQSLPVTGPEPASISCRSSQSLH-SNGYTYLDW 166
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136 TVSSGGGGGGGGGGGGSDIQLTQSPSSLSASVGRVITCKSSQSVLYSSNQKNYLAW 195
QY 167 YLQKPGQSPQLLIYSGSHRASGVDPDRFSGSVSGTDFTLRISRVEADVGYYCMQGLQSP 226
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
196 YQKPGKAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCHQYLSS- 254
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255 WTFGGGTKEIKSSCSGGG 274

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RESULT 15
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-661-052-16

Query Match 39.0%; Score 776.5; DB 2; Length 553;
Best Local Similarity 61.5%; Pred. No. 7e-58;
Matches 160; Conservative 28; Mismatches 51; Indels 21; Gaps 5;

QY 2 VQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYYA 61
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
21 IQLVESGGGVQVQGRSLRLSCSSGFTFSDNYMYVRQAPGKLEWVATISDGGSTYYTP 80
QY 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----KHTGGVMDPIDYWGQGLV 117
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
81 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA----MDYWGQGLTPV 135
QY 118 TVS-----SGGGALEIVLTQSLPVTGPEPASISCRSSQSLH-SNGYTYLDW 166
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
136 TVSSGGGGGGGGGGGGSDIQLTQSPSSLSASVGRVITCKSSQSVLYSSNQKNYLAW 195
QY 167 YLQKPGQSPQLLIYSGSHRASGVDPDRFSGSVSGTDFTLRISRVEADVGYYCMQGLQSP 226
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
196 YQKPGKAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCHQYLSS- 254
QY 227 FTFGPGTKVDIKRGGSGGG 246
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255 WTFGGGTKEIKSSCSGGG 274

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Search completed: March 14, 2003, 11:50:16
Job time : 13.9515 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:47:44 : Search time 11.5894 Seconds
(without alignments)
1515.277 Million cell updates/sec

Title: US-09-822-698A-5
Perfect score: 1990
Sequence: 1 QVOLVSGGGLVQPGSLRL.....IVEFLNRWITFCQSIITLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PublishedApplications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	860.5	43.2	240	9	US-09-968-561A-2
3	860.5	43.2	240	10	US-09-192-854-2
4	842	42.3	288	10	US-09-818-247-22
5	777.5	39.1	241	1	US-08-779-457-50
6	767.5	38.6	268	10	US-09-976-118-1
7	757	38.0	249	12	US-10-039-785-53
8	746.5	37.5	269	12	US-10-027-770-5
9	745.5	37.5	269	12	US-10-027-770-2
10	742	37.3	255	10	US-09-811-737-15
11	731.5	36.8	248	10	US-09-920-171-22
12	730.5	36.7	248	10	US-09-920-171-23
13	730	36.7	252	9	US-09-887-853-4
14	728.5	36.6	535	9	US-09-968-851-38
15	717.5	36.1	262	10	US-09-811-737-19
16	717	36.0	240	9	US-09-782-504-4
17	698	35.1	310	12	US-10-052-798-11
18	680	34.2	133	10	US-09-766-543-8
19	680	34.2	153	10	US-09-149-721-3

20	680	34.2	153	10	US-09-923-246-111	Sequence 111, Appl
21	678.5	34.1	245	9	US-09-991-470-27	Sequence 27, Appl
22	676.5	34.0	309	12	US-10-052-798-9	Sequence 9, Appl
23	674	33.9	133	9	US-10-051-657A-1	Sequence 1, Appl
24	669	33.6	331	10	US-09-033-525-2	Sequence 2, Appl
25	667	33.5	451	10	US-09-822-698A-26	Sequence 26, Appl
26	666	33.5	133	10	US-09-766-543-14	Sequence 14, Appl
27	663.5	33.3	260	10	US-09-811-737-16	Sequence 16, Appl
28	663	33.3	312	12	US-10-052-798-10	Sequence 10, Appl
29	662	33.3	260	9	US-09-782-672-2	Sequence 2, Appl
30	660	33.2	129	9	US-10-172-399-12	Sequence 12, Appl
31	644	32.4	121	10	US-09-822-698A-3	Sequence 3, Appl
32	644	32.4	250	9	US-09-887-853-2	Sequence 2, Appl
33	637.5	32.0	260	10	US-09-811-737-17	Sequence 17, Appl
34	635.5	31.9	276	10	US-09-786-543-12	Sequence 12, Appl
35	628.5	31.6	267	10	US-09-766-543-10	Sequence 10, Appl
36	618	31.1	240	10	US-09-976-787-28	Sequence 28, Appl
37	618	31.1	240	10	US-09-865-198-27	Sequence 27, Appl
38	617.5	31.0	269	9	US-09-749-873-109	Sequence 109, Appl
39	613	30.8	238	10	US-09-976-787-29	Sequence 29, Appl
40	613	30.8	238	10	US-09-865-198-28	Sequence 28, Appl
41	605	30.4	256	9	US-10-247-488-2	Sequence 2, Appl
42	605	30.4	258	9	US-10-247-488-4	Sequence 4, Appl
43	604	30.4	249	9	US-10-237-667-18	Sequence 18, Appl
44	604	30.4	249	9	US-10-237-708-18	Sequence 18, Appl
45	604	30.4	249	9	US-10-237-866-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPHI-IL-2
US-09-822-698A-5

Query Match	100.0%;	Score	1990;	DB	10;	Length	381;
Best Local Similarity	100.0%;	Pred. No.	6.1e-111;				
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Gaps	0;						
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Db	121	SGGGALEIVLQSPSLPVTPEGPASISCRSSQSLLSNGYTYLDWYLOKPGSQPLLII	180				
Qy	181	SGSHRASCVPRFSGSVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGPTKVDIKRG	240				
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DB 301 LKHLOCLEELPLEVLNLAQSKNFHLPRDLISNINVLKGSSETTCEYADETA 360
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DB 361 TIVEFLNRWITFCQSIISTLT 381
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RESULT 2
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US200201642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match 43.2%; Score 860.5; DB 9; Length 240;
Best Local Similarity 68.4%; Pred. No. 2.4e-44;
Matches 171; Conservative 22; Mismatches 36; Indels 21; Gaps 3;

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DB 116 SGGGGSGGGGGGGGTDIQTQSPSSLSASVGDRTVITCRASQSI-----SSYLNWYQQ 170
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DB 231 GQGTKVEIKR 240
| |||||

RESULT 4
US-09-818-247-22
; Sequence 22, Application US/09818247
; Patent No. US20020102657A1
; GENERAL INFORMATION:
; APPLICANT: Mostov, Keith E.
; APPLICANT: Chapin, Steven J.
; APPLICANT: Richman-Eisenstat, Janice
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Stalk Region of p19R and Methods of Use T
; FILE REFERENCE: 18062B-0009100S
; CURRENT APPLICATION NUMBER: US/09/818,247
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: WO PCT/US01/09699
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,197
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,198
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Pelb/4AF/myc/6HIS
US-09-818-247-22

Query Match 42.3%; Score 842; DB 10; Length 288;
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; APPLICANT: KIRCHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10 with site directed mutagenesis
US-10-027-770-5

Query Match 37.5%; Score 746.5; DB 12; Length 269;
Best Local Similarity 55.9%; Pred. No. 1.5e-37;
Matches 151; Conservative 40; Mismatches 56; Indels 23; Gaps 4;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 6 EVKLVEGGDLVQPGGSLKLSCAASGFTSHYGMVWVQTPDKRLVWVATIGSRGTTHY 65
Qy 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT-----GGGVNDPIDYWGQ 114
Db 66 PDSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT-----GGGVNDPIDYWGQ 125
Qy 115 TLTVSS-----SGGGALEIVLTQSPLSPLPTPEGPASISCRSSQSLHNSGYTL 164
Db 126 ASVTVSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 184
Qy 165 DWYLPKQSPQLLIYSGSHRASGVPDRFSGSVSGTDFTLRISRVEADGVVYCMQGLQ 224
Db 185 NWFOKPGQPEKLLIYAIISNRGSGVPARFSGSGGTDFSLNIHPVEDDPAMVFCQOTKE 244
Qy 225 SPFTFGPGTKVDIKRGGGGGGGALAPTSSS 254
Db 245 VPTFEGGTTKLEIKRADA-----APIVSA 268

RESULT 9
US-10-027-770-2
; Sequence 2, Application US/10027770
; Patent No. US20020151684A1
; GENERAL INFORMATION:
; APPLICANT: MAYER, BRUCE
; APPLICANT: SAKSELA, KALLE
; APPLICANT: KIRCHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10
US-10-027-770-2
```

```

; APPLICANT: KIRCHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10 with site directed mutagenesis
US-10-027-770-5

Query Match 37.5%; Score 746.5; DB 12; Length 269;
Best Local Similarity 55.9%; Pred. No. 1.5e-37;
Matches 151; Conservative 40; Mismatches 56; Indels 23; Gaps 4;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 6 EVKLVEGGDLVQPGGSLKLSCAASGFTSHYGMVWVQTPDKRLVWVATIGSRGTTHY 65
Qy 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT-----GGGVNDPIDYWGQ 114
Db 66 PDSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHT-----GGGVNDPIDYWGQ 125
Qy 115 TLTVSS-----SGGGALEIVLTQSPLSPLPTPEGPASISCRSSQSLHNSGYTL 164
Db 126 ASVTVSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 184
Qy 165 DWYLPKQSPQLLIYSGSHRASGVPDRFSGSVSGTDFTLRISRVEADGVVYCMQGLQ 224
Db 185 NWFOKPGQPEKLLIYAIISNRGSGVPARFSGSGGTDFSLNIHPVEDDPAMVFCQOTKE 244
Qy 225 SPFTFGPGTKVDIKRGGGGGGGALAPTSSS 254
Db 245 VPTFEGGTTKLEIKRADA-----APIVSA 268

RESULT 9
US-10-027-770-2
; Sequence 2, Application US/10027770
; Patent No. US20020151684A1
; GENERAL INFORMATION:
; APPLICANT: MAYER, BRUCE
; APPLICANT: SAKSELA, KALLE
; APPLICANT: KIRCHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10
US-10-027-770-2
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; Query Match 37.5%; Score 745.5; DB 12; Length 269;
; Best Local Similarity 55.9%; Pred. No. 1.7e-37;
; Matches 151; Conservative 38; Mismatches 58; Indels 23; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKGLEWVSGISGGSTYY 60
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 EVKLVSGLDLVQPGGSLRLSCAASGFTSHYGMWSVRQTPDKRLWVATIGSRGTYY 65
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAK-----HTGGGVWDPIDYWGQ 114
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 PDSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCVRKSEFYNYGNTYYISAMDYWGQ 125
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 115 TLTVTS-----SGGGALEIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTL 164
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 ASVTVSGGGSGGGSDIVLTQSPASLAIVSLGQRATISCRASES-VDNYGFSFM 184
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 165 DWYLOKPGQSPQLLIYSGSHRASGVDPDRFGSGVSGTDFTLRISRVEADGVYYCMQGLQ 224
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 NWFOOKPGQPPKLLIYATSNRSGVGPAPRFGSGSGTDFSLNIHPVERDDSAMVFCQQTKE 244
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 225 SPFTFGPTKVDIKRKGSGGSGALAPTSSS 254
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 VPWTFGGGTLKLEIKRADA-----APTUSA 268
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-09-811-737-15
; Sequence 15, Application US/09811737
; Patent No. US20020099180A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Human PAP-alpha-specific antibodies
; FILE REFERENCE: 1-1129
; CURRENT APPLICATION NUMBER: US/09/811,737
; CURRENT FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-737-15

Query Match 37.3%; Score 742; DB 10; Length 255;
Best Local Similarity 60.3%; Pred. No. 2.6e-37;
Matches 152; Conservative 27; Mismatches 53; Indels 20; Gaps 3;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKGLEWVSGISGGSTYY 60
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVESGGTLVQPGGSLRLSCAASGFTFSYAMSWIRQAPGKLEWVSGISASGGYID 60
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRVTISRDNKNTLYLQMSLRAEDTAVYYCAK--GGYQMLDHWGGQGLTVTS 118
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 SGG-----GALIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWY 167
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 SASLTKGPKLEEGEFSEARVDIQMTQSPSSLSASTGDRVTITCRASQDI-----SSYLA 173
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 168 LOKPGQSPQLLIYSGSHRASGVDPDRFGSGVSGTDFTLRISRVEADGVYYCMQGLQSPF 227
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 174 QQAPGKAPHLMLMGATTLQTVSPFRSGSGSGTDFTLTITSLQSEDFAITYYCOQYIYPP 233
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 228 TFGPTKVDIKR 239
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 234 TFGGTRVEIKR 245
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-920-171-22
; Sequence 22, Application US/09920171
; Patent No. US20020054878A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sfv sequence derived from MAEL1
US-09-920-171-22

Query Match 36.8%; Score 731.5; DB 10; Length 248;
Best Local Similarity 60.6%; Pred. No. 1.1e-36;
Matches 152; Conservative 30; Mismatches 54; Indels 15; Gaps 6;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGVWRQAPGKGLEWVSGISGGSTY 59
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNWIRQAPGKLEWVASIT-YDGS 59
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGLTV 118
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 YNPVKGRVTISRDNKNTLYLQMSLRAEDTAVYYCARGSHYFGWH-FAVWGQGLTV 118
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 VSSGGGALE-----IVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYL 168
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 VSSEGGSGEGGSGGSDIQLTQSPSSLSASVGRVTITCRASKP-VDGEGDLYNNYQ 177
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 169 OKPGQSPQLLIYSGSHRASGVDPDRFGSGVSGTDFTLRISRVEADGVYYCMQGLQSPFT 228
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 QRPGRAPKLLIYAASYLESFSGVPSFRSGSGGTDFTLTITSLQPEDFAITYYCOQSHEDPYT 237
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 229 FGGPTKVDIKR 239
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FGGGTRVEIKR 248
; :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-920-171-23
; Sequence 23, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 23
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sfv sequence derived from MAEL1
US-09-920-171-23
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Query Match 36.7%; Score 730.5; DB 10; Length 248;
Best Local Similarity 60.6%; Pred. No. 1.2e-36;
Matches 152; Conservative 29; Mismatches 55; Indels 15; Gaps 6;
QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFSR-N-AMGWVQAPGKLEWVSGISGGSTY 59
DB 1 EYQLVESGGGLVPGGSLRLSCAVSGYITSGYSNNWIRQAPGKLEWVASIKYS-GETK 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-GGVWDPIDYWGQGLTVT 118
DB 60 YNPSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTG-HYFGHH-FAVWGGGLTVT 118
QY 119 VSSGGGALE-----IVLTQSPSLPVTPGPASISCRSSQSLHNSGNYTLDMYLQKPG 172
DB 119 VSSEGGSGGSEGGGDIQLTQSPSSLSASVGRVITTCRAKP-VDEGDSYLNWYQ 177
QY 169 QKPGSQPLLISGHRASGVPDRFSGVSGTDFTLRLSRVEAEDVGVYCMQGLQSPFT 228
DB 178 QKPGKAPKLLIYAASYLESGVPSRFSGSGGTDFTLTISSLPQDFATYYCQSHEDPYT 237
QY 229 FGPQTKVDIKR 239
DB 238 FGGQTKVEIKR 248

RESULT 13
US-09-887-853-4
; Sequence 4, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; Oppermann, Hermann
; Houston, L. L.
; Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-887-853-4

Query Match 36.7%; Score 730; DB 9; Length 252;

Best Local Similarity 57.5%; Pred. No. 1.3e-36;
Matches 145; Conservative 38; Mismatches 59; Indels 10; Gaps 3;
QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFSR-NAMGWVQAPGKLEWVSGISGGSTY 60
DB 2 EVQLQSGPELVRPGASVRMSCKSSGYITDFYMNVRQSHGKSLDYIGVISPSGVTCY 61
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHTGGGVWDPIDYWGQGLTVTVS 120
DB 62 NQKPKGKATLTVDKSSSTAYMELSLTSEDSAVVYCA-GSSGNK-AMDYHGHCASVTVS 119
QY 121 SGGA-----LEIVLTQSPSLPVTPGPASISCRSSQSLHNSGNYTLDMYLQKPG 172
DB 120 SSGSSSSGSSSSSDVVMVTQPLSLPVSLGDQASISCRSSQSLVHNSGNTYLNWYLOKAG 179
QY 173 QSPOLLISGHRASGVPDRFSGVSGTDFTLRLSRVEAEDVGVYCMQGLQSPFTFGPG 232
DB 180 QSPKLLIYKYSNRFSGVDPDRFSGSGGTDFTLRLSRVEAEDLGIYFCSTQTHVPPTFGGG 239
QY 233 TKVDIKRGGSG 244
DB 240 TKLEIKRGGGG 251

RESULT 14
US-09-968-851-38
; Sequence 38, Application US/09968851
; Publication No. US20020193561A1
; GENERAL INFORMATION:
; APPLICANT: CONSELLER, EMMANUEL
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,851
; FILING DATE: 03-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,035
; FILING DATE: 20-Feb-1998
; APPLICATION NUMBER: PCT/FR96/01111
; FILING DATE: 17-JUL-1996
; APPLICATION NUMBER: FR 95/08729
; FILING DATE: 19-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Strauss, William L.
; REGISTRATION NUMBER: 47,114
; REFERENCE/DOCKET NUMBER: 03804.0142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-968-851-38

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:54 ; Search time 15.5732 Seconds
(without alignments)
2351.940 Million cell updates/sec

Title: US-09-822-698A-5
Perfect score: 1990
Sequence: 1 QVOLVQSGGLVQPGSGURL.....IVEFLNRWITFCQSIISTLT 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734	36.9	249	2 S41374	single chain Fv an
2	680	34.2	153	1 ICHU2	interleukin-2 prec
3	680	34.2	153	1 ICGI2	interleukin-2 prec
4	583.5	29.3	268	2 A56446	Ig heavy chain v r
5	543	27.3	119	2 S31107	Ig heavy chain - h
6	542	27.2	119	2 C36005	Ig heavy chain v r
7	541	27.2	233	2 JC5322	p53 specific singl
8	537	27.0	136	2 S40357	Ig kappa chain v-j
9	535.5	26.9	120	2 S48798	Ig heavy chain v r
10	534	26.8	140	2 S31686	Ig heavy chain v r
11	533	26.8	135	2 S40342	Ig kappa chain - h
12	531	26.7	119	2 S31108	Ig heavy chain - h
13	530.5	26.7	154	2 JN0698	interleukin 2 prec
14	530	26.6	117	1 K2HUGM	Ig kappa chain pre
15	529	26.6	160	2 S05271	Ig heavy chain pre
16	528	26.5	112	2 S58207	Ig light chain v r
17	528	26.5	119	2 D36005	Ig heavy chain v r
18	528	26.5	121	2 I55673	Ig heavy chain - h
19	528	26.5	132	2 S26882	Ig kappa chain v r
20	527	26.5	127	2 S38489	Ig heavy chain - h
21	527	26.5	140	2 S31588	Ig heavy chain v r
22	526	26.4	125	2 S40356	Ig kappa chain - h
23	526	26.4	134	2 S31699	Ig heavy chain v r
24	522	26.2	112	2 S58206	Ig light chain v r
25	522	26.2	123	2 S31114	Ig heavy chain - h
26	522	26.2	138	2 S31666	Ig heavy chain v r
27	518.5	26.1	124	2 S20782	Ig heavy chain v r
28	518	26.0	120	2 S26278	Ig heavy chain v r
29	511.5	25.7	126	2 S40339	Ig kappa chain - h

30 509.5 25.6 112 2 PH1647 Ig heavy chain v r
31 508.5 25.6 116 2 S31110 Ig heavy chain - h
32 505 25.4 121 2 S40371 Ig kappa chain - h
33 503 25.3 109 2 PH1649 Ig heavy chain v r
34 503 25.3 143 2 S23624 Ig heavy chain v r
35 501 25.2 121 2 S19666 Ig heavy chain pre
36 501 25.2 140 2 A30532 Ig heavy chain v r
37 500 25.1 113 1 K2HUTW Ig kappa chain v-i
38 498 25.0 121 2 G36005 Ig heavy chain v r
39 498 25.0 131 2 S40372 Ig kappa chain v-j
40 496.5 24.9 151 2 A60943 Ig heavy chain pre
41 495.5 24.9 108 2 PH1648 Ig heavy chain v r
42 494.5 24.8 140 2 S70442 Ig heavy chain pre
43 494 24.8 134 2 S31679 Ig heavy chain v r
44 492.5 24.7 122 2 S20772 Ig heavy chain v r
45 492 24.7 121 2 S31113 Ig heavy chain - h

ALIGNMENTS

RESULT 1
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti
A:Reference number: S41374
A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:229480

Query Match 36.9%; Score 734; DB 2; Length 249;
Best Local Similarity 58.6%; Pred. No. 1.8e-45;
Matches 146; Conservative 36; Mismatches 55; Indels 12; Gaps 2;
Qy 1 QVOLVQSGGLVQPGSGSLRSCASGFTFRSNAMGVWRQAPGKLEWVGSGSGSTYY 60
Db 1 QVOLVQSGGLVQPGSGSLRSCASGFTFRSNAMGVWRQAPGKLEWVGSGSGSTYY 60
Qy 61 ADSVKGRFTISRDNSKNTLYLQMSLRADTVAVYCAKHTGGGVWDPIDYWGQGLTVTVS 120
Db 61 VPRQDKRATITADTSSNTAYLLLSLTSETAVYICARR--DTLYTSLGVWGGSTVTVS 118
Qy 121 -----SGGALIEIVTQSPSLPVTTPGEPASISCRSSQSLHNSGYTYLDWYLOK 170
Db 119 SRGGSGGGSGGGGGSDIELTQSPSPVWVTPGESVSISSCRSSKSLYSDGDSYLFWFLQR 178
Qy 171 PQGSPQLLYSGSHRASGVDPDRFSGSVSGVDFTLRISRVAEADVGVVYCMQGLQSPFTFG 230
Db 179 PQGSPQLLYRMSNLASGVDPDRFSGSGSTFSLRISRVAEADVGVVYCMQHREYPLTFG 238
Qy 231 PGTKVDIKR 239
Db 239 AGTKLELKR 247

RESULT 2
ICHU2
interleukin-2 precursor [validated] - human
N:Alternate names: IL-2; T-cell growth factor
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 08-Dec-2000
C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;
R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.
Nucleic Acids Res. 12, 5005-5013, 1984
A:Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo
A:Reference number: A93524; MUID:84247353; PMID:6330695

A:Accession: A01849
A:Molecule type: DNA
A:Residues: 1-153 <HOL>
A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2529
R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniiguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983
A:Title: Structure of the human interleukin 2 gene.
A:Reference number: A21192; MUID:84170243; PMID:6324170
A:Accession: A21192
A:Molecule type: DNA
A:Residues: 1-153 <FU>
A:Cross-references: GB:J00264; NID:g186294; PIDN:AA48509.1; PID:g5729676
R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabtree
Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984
A:Title: T-cell growth factor: complete nucleotide sequence and organization of the gene
A:Reference number: A20961; MUID:84170356; PMID:6608729
A:Accession: A20961
A:Molecule type: DNA
A:Residues: 1-153 <HO2>
A:Cross-references: GB:K02056; NID:g186302; PIDN:AA98792.1; PID:g386819
R:Laabli, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis,
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31209
A:Molecule type: mRNA
A:Residues: 11-117 <LAA>
A:Cross-references: EMBL:214955
A:Note: this sequence is shown from the beginning of the fragment to the chromosomal bre
R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Hamuro
Nature 302, 305-310, 1983
A:Title: Structure and expression of a cloned cDNA for human interleukin-2.
A:Reference number: A93297; MUID:83167472; PMID:6403867
A:Accession: A93297
A:Molecule type: mRNA
A:Residues: 1-153 <TAN>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCRC
R:Nagata, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K.;
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
A:Title: Cloning of interleukin 2 mRNAs from human tonsils.
A:Reference number: A90113; MUID:84023840; PMID:6312994
A:Accession: A90113
A:Molecule type: mRNA
A:Residues: 1-153 <MAE>
A:Cross-references: GB:J00264; NID:g186294; PIDN:AA48509.1; PID:g5729676
A:Experimental source: tonsillar mononuclear cells
R:Devos, R.; Platinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau
Nucleic Acids Res. 11, 4307-4323, 1983
A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia
A:Reference number: A93478; MUID:83246551; PMID:6306584
A:Accession: A93478
A:Molecule type: mRNA
A:Residues: 1-153 <DEV>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: splenocytes
R:Eizenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.
J. Neurochem. 64, 1928-1936, 1995
A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as
A:Reference number: I56518; MUID:95239150; PMID:7722480
A:Accession: I56518
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-152 <EIZ>
A:Cross-references: GB:S77834; NID:g999000
A:Accession: I73624
A:Molecule type: mRNA
A:Residues: 5-7, 'F', 9-17, 'P', 19-32, 'X', 34-45, 'X', 47-143 <RES>
A:Cross-references: GB:S77835; NID:g999001; PIDN:AA414264.1; PID:g4261964
R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.

A:Reference number: I52528
A:Accession: I52528
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <RE2>
A:Cross-references: GB:M33199; NID:g186296; PIDN:AA59139.1; PID:g553508
R:Siebnlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M
Mol. Cell. Biol. 6, 3042-3049, 1986
A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes
A:Reference number: I57603; MUID:87064618; PMID:3491296
A:Accession: I57603
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <RE3>
A:Cross-references: GB:M13879; NID:g186305; PIDN:AA59141.1; PID:g553509
R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6883-6892, 1988
A:Title: Structure-activity relationships of recombinant human interleukin 2.
A:Reference number: I52401; MUID:89062420; PMID:3264184
A:Contents: recombinant IL-2 and mutants expressed in E. coli
A:Accession: I52401
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'M', 21-153 <RE4>
A:Cross-references: GB:M22005; NID:g186300; PIDN:AA59140.1; PID:g386818
A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold with
R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
A:Title: Amino acid sequence and post-translational modification of human interleukin
A:Reference number: A94009; MUID:85038540; PMID:6333684
A:Accession: A94009
A:Molecule type: protein
A:Residues: 21-153 <ROB>
A:Note: disulfide bonds and carbohydrate binding site were determined
n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)
R:Conradt, H.S.; Nimitz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.
J. Biol. Chem. 264, 17368-17373, 1989
A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-
de.
A:Reference number: A34463; MUID:90008901; PMID:2793860
A:Accession: A34463
A:Molecule type: protein
A:Residues: 21-35 <CON>
A:Note: the O-linked glycosylation site in recombinant material matched that from hum
R:Grabenhorst, E.; Hofer, B.; Nimitz, M.; Jaeger, V.; Conradt, H.S.
Eur. J. Biochem. 215, 189-197, 1993
A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro
A:Reference number: S34052; MUID:93345493; PMID:8344280
A:Contents: annotation; glycosylation of variant forms expressed in insect cells
C:Genetics:
A:Gene: GDB:IL2
A:Cross-references: GDB:119344; OMIM:147680
A:Map position: 4q26-4q27
A:Introns: 49/3; 69/3; 117/3
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status experimental <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:78-125/Disulfide bonds: #status experimental
Query Match 34.2% Score 680; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 7.2e-42;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 APTSSSTKKTQLQLEHLLDLQMLINGNNYKNPKLTRMLTKFYMPKATLKHLCLE 308
DB 21 APTSSSTKKTQLQLEHLLDLQMLINGNNYKNPKLTRMLTKFYMPKATLKHLCLE 80
QY 309 ELKLPLEEVNLQAQKNFHLPRDLISNINVLKLGSETTMCCEYADETATVEFLNR 368
DB 81 ELKLPLEEVNLQAQKNFHLPRDLISNINVLKLGSETTMCCEYADETATVEFLNR 140

Qy 369 WITFCQSIISTLT 381

Db 141 WITFCQSIISTLT 153

RESULT 3

ICG12

Ig heavy chain - common gibbon
N:Alternate names: IL-2; T-cell growth factor
C:Species: Hylotates lar (common gibbon, white-banded gibbon)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C:Accession: A94067; A01849
R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtree, Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985
A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that contains interleukin-2 precursor
A:Reference number: A94067; MUID:86042650; PMID:3877307
A:Accession: A94067
A:Molecule type: mRNA
A:Residues: 1-153 <CH>
A:CROSS-references: GB:M11144; NID:g177014; PID:AAA35454.1; PID:g177015
A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201
A:Note: The integration of a retrovirus sequence containing a 5' LTR into the 3' noncoding region of the interleukin-2 gene
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status predicted <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:78-125/Disulfide bonds: #status predicted

Query Match 34.2%; Score 680; DB 1; Length 153;

Best Local Similarity 100.0%; Pred. No. 7.2e-42;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 APTSSSTKTKQLQLEHLLDQMLNGINNYKNPKLTRLTFFKPYMPKKATLKHQCLE 308

Db 21 APTSSSTKTKQLQLEHLLDQMLNGINNYKNPKLTRLTFFKPYMPKKATLKHQCLE 80

Qy 309 EEKPLEEVLNLAQSKNPHLRDLISNIVIVLELKGSETTFMCEYADETATVEFLNR 368

Db 81 EEKPLEEVLNLAQSKNPHLRDLISNIVIVLELKGSETTFMCEYADETATVEFLNR 140

Qy 369 WITFCQSIISTLT 381

Db 141 WITFCQSIISTLT 153

RESULT 4

AS6446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/c)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A. J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the heavy chain V region of the anti-digoxin antibody
A:Reference number: A56446; MUID:95229583; PMID:7713873
A:Accession: A56446
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:CROSS-references: GB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.3%; Score 583.5; DB 2; Length 268;

Best Local Similarity 47.8%; Pred. No. 1.2e-34;

Matches 119; Conservative 36; Mismatches 75; Indels 19; Gaps 3;

Qy 1 QVOLVSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGSTYY 60

Db 3 QVKLQSGGAEKVPKASVKLSCTTSFNKIDTYMHVVKRPEQGLEWIGRTAPANGITKY 62

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTLTVTS 120

Db 63 DPKFQGRATIAADSSNTAYLQLSLTSEDVAVYYCASY--LTRYENWGQGLTLTVTS 119

Qy 121 -----SGGALEIVLTQSPSLSPVTPGEPASISCRSSOSLLHSNGYTYLDWYLOK 170

Db 120 SGGGSGGGSGGGGSDIELTQSPAIMSASLGKVTMSCRASSV-----NFIYWYQOK 173

Qy 171 PGQSPQLLIYSGSHRAGVDPDRFSGVSGYGTDTFLRISRVEAEADVGVYCMQGLQSPFTFG 230

Db 174 SDASPKLWVYVYTHLPQVPAFSGSGSGNSYSLTISSEGEADAATYYCQQTSSPFTFG 233

Qy 231 PGTKVDIKR 239

Db 234 SGTLEIKR 242

RESULT 5

S31107

Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kanter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:CROSS-references: EMBL:X62955
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 27.3%; Score 543; DB 2; Length 119;

Best Local Similarity 87.6%; Pred. No. 3.5e-32;

Matches 106; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

Qy 1 QVOLVSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGSTYY 60

Db 1 EVOLVESGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGTSGSGSTYY 60

Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTLTVTS 120

Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDPGASY--FDYWGQGLTLTVTS 118

Qy 121 S 121

Db 119 S 119

RESULT 6

C36005

Ig heavy chain V region (30pl) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C:Accession: C36005
R:Schroeder Jr., H.W.; Wang, J.Y. Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: C36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:CROSS-references: GB:M18513
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 27.2%; Score 542; DB 2; Length 119;

Best Local Similarity 87.6%; Pred. No. 4.2e-32;
Matches 106; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVGISGGSTYY 60
Db 1 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVOLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGSTYY 60
QY 61 ADSVKGRFTISRDN SKNTLYLQMNSLRADPTAVYYCAKHTGGGVDPIDYWGGTLLVTWS 120
Db 1 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 ADSVKGRFTISRDN SKNTLYLQMNSLRADPTAVYYCAKDAGWG--SGFDYWGQTLLVTWS 118

QY 121 S 121
Db 119 S 119

RESULT 7
JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JN>
A:Experimental source: hybridoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. I

Query Match 27.2%; Score 541; DB 2; Length 233;
Best Local Similarity 48.8%; Pred. No. 1.2e-31;
Matches 118; Conservative 33; Mismatches 71; Indels 20; Gaps 5

QY 6 QSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVGISGGSTYYADSVK 65
Db 2 ESGAEIVRGASVKLSCTTSGFNIIDYMHVKKRPQGLEGICRIDPENGADMTRSSG 61

QY 66 GRFTISRDN SKNTLYLQMNSLRADPTAVYYCAKHTGGGVDPIDYWGGTLLVTWS ---- 120
Db 62 VKATMTADTSSNTAYLQLSLSLTSEDTAVYYC--NAG-----MDYWGQGTITVTVS GGKG 113

QY 121 -----SGGALETVLQTSPSLPVTPGPASPISCSSQLSHNGTYLDWLQKPGQSP 175
Db 114 SGPRASGGGSDELITQSPLASLVIGQRATISCRASK-VSTSGSYMHWNQKPKQPP 172

QY 176 QLIIYSGHRSAPVDPRFGSGVSGDFTDLIRSRVAEDVGYIYCMQGLSPFFTEGPGTKV 235
Db 173 RLIIYLVSNEESGVPARFSGSGSDFTDLIHIPVEEDAATYYC-QHIRELTRSEGSKTL 231

QY 236 DI 237
Db 232 EI 233

RESULT 8
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40357
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: EMBL:X72467
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 27.0%; Score 537; DB 2; Length 136;
Best Local Similarity 83.9%; Pred. No. 1.1e-31;
Matches 104; Conservative 9; Mismatches 9; Indels 2; Gaps

Qy 116 LVTYVSGGALFIVLTQSPLSLPVTGPGEPASTICSRSSOSLLHSNGTYLWDYLOKPGOSP 175
::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 12 MLWVS--GV--DIVTQSPSLSPVTGPGEPASTICSRSSOSLLHSNGTYLWDYLOKPGOSP 69
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 176 QLLIYSGSHRASGVPRDFSGVSGTGDTFLIRISRVEADVGVIYCMOGLQSPFTFGPTKV 235
|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 70 QLLIYLSGNRASGVPRDFSGSGTGDTFLIKISRVEADVGVIYCMOALQTPTTFQGQTKV 129
|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 236 DIKR 239
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 130 EIKR 133
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9

S48798
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S48798
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies
A:Reference number: S48797
A:Accession: S48798
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MAH>
A:Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 26.9%; Score 535.5; DB 2; Length 120;
Best Local Similarity 86.9%; Pred. No. 1.2e-31;
Matches 106; Conservative 3; Mismatches 10; Indels 3; Gaps

Qy 1 QVLIVQSGGLVPQGGSLRLSCAASGTTFRSNAMGWVRQAPKGLEWWVSGISGSGSTYY 60
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 EVQLLESQGLVPQGGSLRLSCAASGTTFSYAMSWVRQAPKGLEWVAISGSGSTYY 60
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 61 ADSVKGRFTISRDNSKNTLYQMNSLRRAEDTAVYCYCAKHTGGGVMDPI-DYWGGQGLTVTV 119
|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 ADSVKGRFTISRDNSKNTLYQMNSLRRAEDTAVYCYCAKDR-GFWSGYKDYWGQGLTVTV 118
|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 120 SS 121
||
Db 119 SS 120
||

RESULT 10

S31686
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31686
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operons
A:Reference number: S31585
A:Accession: S31686
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUIT>
A:Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 26.8%; Score 534; DB 2; Length 140;
Best Local Similarity 86.0%; Pred. No. 1.9e-31;
Matches 104; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGSGGSGTYY 60
:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGSGSTYY 79
:

QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAKH---TGGGVWDPIDYWGGQGLTV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 SDSVKGRTISRDNKNTLYLQMSLRADTAIVYCAKCPFAGGSPFDYWGGQGLTVTS 139
:

QY 121 S 121
+
Db 140 S 140

RESULT 11

S40342
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40342
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40342
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <KLE>
A:Cross-references: EMBL:X72452; NID:g441372; PID:g441373
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 26.8%; Score 533; DB 2; Length 135;
Best Local Similarity 83.9%; Pred. No. 2.2e-31;
Matches 104; Conservative 8; Mismatches 10; Indels 2; Gaps 1;

QY 116 LVTYSSGGGALVIVLTQSLPLVTPGEPASISCRSSQLLHNSGYTYLDWYLQKPGQSP 175
::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 MLAWVSGSG--DIVMTQSPSLPLVTPGEPASISCRSSQLLHNSGYNYLDWYLQKPGQSP 62
:

QY 176 QLLIYSGSHRASGVPDRFGSGSGTDFTLKISRVEAEDGVIYCYCMQGLQSPFTFGPGTKV 235
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 QLLIYSGSHRASGVPDRFGSGSGTDFTLKISRVEAEDGVIYCYCMQALQTPRTFGGQTKV 122
:

QY 236 DIKR 239
+
Db 123 EIKR 126

RESULT 12

S31108
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31108
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31108
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62956
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 26.7%; Score 531; DB 2; Length 119;
Best Local Similarity 85.5%; Pred. No. 2.6e-31;
Matches 106; Conservative 3; Mismatches 7; Indels 8; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGSGGSGTYY 60
:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSAISGSGGSGTYY 60
:

QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAKH---TGGGVWDPIDYWGGQGLTV 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAKDRRLTG----TFDIWGGQGLTV 115
:

QY 118 TVSS 121
+
Db 116 TVSS 119

RESULT 13

JN0698
interleukin 2 precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C:Accession: JN0698
R:Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993
A:Title: Sequence and functional characterization of feline interleukin 2.
A:Reference number: JN0698; MUID:93356765; PMID:8352761
A:Accession: JN0698
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-154 <COZ>
A:Cross-references: GB:LJ9402; NID:g304313; PIDN:AAA02865.1; PID:g304314
C:Superfamily: interleukin-2
C:Keywords: growth factor

Query Match 26.7%; Score 530.5; DB 2; Length 154;
Best Local Similarity 78.4%; Pred. No. 3.9e-31;
Matches 105; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 249 APTSSSTKKTKQLQLHLQLDLQMLNGINNYKNPKLTRLMTFKFYMPKKATELKHQCLE 308
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 APASSTKETVTKQLQLDLRLLLNGVNNPENPKLSRLMTFKFYVPKKATELHQLCLV 80
:

QY 309 EELKPLEEVNLAQSKNFHLRP-ROLISINIVIVLELKGSETTFMCEYADATATVEFLN 367
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 EELKPLEEVNLAQSKNFHLNHIKELMSINIVTVLKGSETFTTCNYDDETATVEFLN 140
:

QY 368 RWITFCQSIISFLT 381
+
Db 141 KWITFCQSIISFLT 154

RESULT 14

K2HUGM
Ig kappa chain precursor V-II region (GM607) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A01889; B24452
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.
A:Reference number: A01889; MUID:84191506; PMID:6325927
A:Accession: A01889
A:Molecule type: mRNA
A:Residues: 1-117 <KLO>
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:I36265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1d
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
 F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>
 F:20-99/Domain: immunoglobulin homology <IMM>
 F:27-97/Disulfide bonds: #status predicted

Query Match 26.6%; Score 530; DB 1; Length 117;
 Best Local Similarity 87.2%; Pred. No. 3e-31;
 Matches 102; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 123 GGALEIVLTQSPVLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLRQPGSPQLLIYSG 182

Db 1 GSSGDIVMTQSPVLPVTPGEPASISCRSSQSLHLSNGYNYLDWYLRQPGSPQLLIYLG 60

QY 183 SHRAGVDPDRFSGSGVTDFTLRISRVAEADVGVYCMQGLQSPETFGGTVKDIKR 239

Db 61 SNRAGVDPDRFSGSGVTDFTLRISRVAEADVGVYCMQGLQSPETFGGTVKDIKR 117

RESULT 15

S05271

Ig heavy chain precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996

C:Accession: S05271; S04602

R:Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A:Reference number: S05270

A:Accession: S05271

A:Molecule type: mRNA

A:Residues: 1-160 <KIS1>

A:Cross-references: EMBL:X14584

R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A:Reference number: S04601; MUID:89296497; PMID:2500644

A:Accession: S04602

A:Molecule type: mRNA

A:Residues: 1-144 <KIS2>

A:Cross-references: EMBL:X14584

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 529; DB 2; Length 160;

Best Local Similarity 69.7%; Pred. No. 5.2e-31;

Matches 108; Conservative 11; Mismatches 18; Indels 18; Gaps 3;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPKGLEWVSGISGSGSTYY 60

Db 20 EVQLLEGGGGLVQPGGSLRLSCAASGFTFTSTAMSWVROAPKGLEWVAISGSGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGV----WDPIDYWGQGT 116

Db 80 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKAVRVGVISYYYGMVWGQGT 139

QY 117 VTVSSGGGALVLTQSPVLPVTPGEPASISCRS 151

Db 140 VTVSSGSAS-----APTLFPL-----VSCEN 160

Search completed: March 14, 2003, 11:51:07

Job time : 16.5732 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:44:44 ; Search time 8.69202 Seconds
(without alignments)
1818.046 Million cell updates/sec

Title: US-09-822-698A-5

Perfect score: 1990

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....IVEFLNRWITFCQSIITLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	680	34.2	153	1 IL2_HUMAN	P01585 homo sapien
2	652.5	32.8	154	1 IL2_MACMU	P51498 macaca mula
3	647.5	32.5	154	1 IL2_CERTO	P46649 cercopithecus
4	644.5	32.4	154	1 IL2_MACFA	Q29615 macaca fasc
5	534.5	26.9	154	1 IL2_MIRAN	O62641 mirounga an
6	530.5	26.7	154	1 IL2_FELCA	Q07885 felis silve
7	530	26.6	117	1 KV2E_HUMAN	P06309 homo sapien
8	513.5	25.8	153	1 IL2_RABIT	O77620 oryctolagus
9	502	25.2	155	1 IL2_CANFA	Q29416 canis famil
10	500	25.1	113	1 KV2D_HUMAN	P01617 homo sapien
11	478.5	24.0	112	1 KV2C_HUMAN	P01616 homo sapien
12	478.5	24.0	155	1 IL2_MERUN	Q08081 meriones un
13	472.5	23.7	154	1 IL2_PIG	P26891 sus scrofa
14	471	23.7	117	1 KV3C_HUMAN	P01764 homo sapien
15	467.5	23.5	115	1 KV2A_HUMAN	P01614 homo sapien
16	466.5	23.4	114	1 KV3B_HUMAN	P01763 homo sapien
17	461	23.2	149	1 IL2_HORSE	P37997 equus cabal
18	460.5	23.1	152	1 IL2_ORCOR	O97513 orcinus orc
19	456.5	22.9	122	1 KV3G_HUMAN	P01768 homo sapien
20	455	22.9	113	1 KV2B_HUMAN	P01615 homo sapien
21	450.5	22.6	122	1 KV3A_HUMAN	P01762 homo sapien
22	449.5	22.6	116	1 KV3T_HUMAN	P01781 homo sapien
23	447	22.5	121	1 KV3J_HUMAN	P01771 homo sapien
24	447	22.5	133	1 KV2F_HUMAN	P06310 homo sapien
25	445.5	22.4	155	1 IL2_RAT	P17108 rattus norv
26	438.5	22.0	116	1 HV05_CARAU	P19181 carassius a
27	437.5	22.0	122	1 HV3H_HUMAN	P01769 homo sapien
28	437.5	22.0	126	1 HV3K_HUMAN	P01772 homo sapien
29	435.5	21.9	136	1 HV16_MOUSE	P01783 mus musculu
30	435	21.9	115	1 HV3D_HUMAN	P01765 homo sapien
31	432	21.7	113	1 KV2E_MOUSE	P03976 mus musculu
32	432	21.7	117	1 HV02_CANFA	P01785 canis famil
33	429	21.6	113	1 KV2G_MOUSE	P01631 mus musculu

34	428	21.5	119	1 HV3L_HUMAN	P01770 homo sapien
35	427	21.5	115	1 HV3F_HUMAN	P01767 homo sapien
36	423	21.3	113	1 KV2F_MOUSE	P01630 mus musculu
37	422.5	21.2	120	1 HV3U_HUMAN	P01782 homo sapien
38	419.5	21.1	119	1 HV3M_HUMAN	P01774 homo sapien
39	419	21.1	120	1 HV3E_HUMAN	P01766 homo sapien
40	417.5	21.0	119	1 HV3N_HUMAN	P01775 homo sapien
41	414	20.8	119	1 HV3L_HUMAN	P01773 homo sapien
42	408.5	20.5	169	1 IL2_MOUSE	P04351 mus musculu
43	405	20.4	155	1 IL2_SHEEP	P19114 ovis aries
44	404	20.4	166	1 IL2_MUSSP	Q08867 mus spretus
45	404	20.3	155	1 IL2_BOVIN	P05016 bos taurus

ALIGNMENTS

RESULT 1					
IL2_HUMAN					
ID	IL2_HUMAN	STANDARD;	PRT;	153 AA.	
AC	P01585;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)				
DE	(Alfaesleukin).				
GN	IL2.				
OS	Homo sapiens (Human), and				
OS	Hylobates lar (Common gibbon).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606, 9580;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human;				
RX	MEDLINE=84247353; PubMed=6330695;				
RA	Holbrook N.J., Lieber M., Crabtree G.R.;				
RT	"DNA sequence of the 5' flanking region of the human interleukin 2				
RT	gene: homologues with adult T-cell leukemia virus.;"				
RL	Nucleic Acids Res. 12:5005-5013(1984).				
[2]					
RN					
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human;				
RX	MEDLINE=83167472; PubMed=6403867;				
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,				
RA	Yoshimoto R., Hamuro J.;				
RT	"Structure and expression of a cloned cDNA for human interleukin-2.;"				
RL	Nature 302:305-310(1983).				
[3]					
RN					
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human;				
RX	MEDLINE=84023840; PubMed=6312994;				
RA	Maeda S., Nishino N., Obaru K., Mita S., Nomiya H., Shimada K.,				
RA	Fujimoto K., Teranishi T., Hirano T., Onoue K.;				
RT	"Cloning of interleukin 2 mRNAs from human tonsils.;"				
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).				
[4]					
RN					
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human;				
RX	MEDLINE=83246551; PubMed=6306584;				
RA	Devos R., Plaetinck G., Cheroutre H., Simons G., Degraeve W.,				
RA	Tavernier J., Remaut E., Fiers W.;				
RT	"Molecular cloning of human interleukin 2 cDNA and its expression in				
RT	E. coli.;"				
RL	Nucleic Acids Res. 11:4307-4323(1983).				
[5]					
RN					
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human;				
RX	MEDLINE=84170356; PubMed=6608729;				
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,				
RA	Wiskocil R.L., Crabtree G.R.;				
RT	"T-cell growth factor: complete nucleotide sequence and organization				
RT	of the gene in normal and malignant cells.;"				

RL Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=84170243; PubMed=6324170;
RA Fujita T., Takaoka C., Matsui H., Taniguchi T.;
RT "Structure of the human interleukin 2 gene."
RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=95239150; PubMed=7722480;
RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
expression by astrocytes."
RL J. Neurochem. 64:1928-1936(1995).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=96422299; PubMed=8824916;
RA Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;
RT "Sequence of interleukin-2 isolated from human placental poly A+ RNA:
possible role in maintenance of fetal allograft."
RL Mol. Reprod. Dev. 43:180-186(1996).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=92335891; PubMed=1631562;
RA Bazan J.F.;
RT "Unravelling the structure of IL-2."
RL Science 257:410-412(1992).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RC SPECIES=Human;
RX MEDLINE=86042650; PubMed=3877307;
RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,
RGreengard J.S., Crabtree G.R., Lin Y.;
RT "A viral long terminal repeat in the interleukin 2 gene of a cell
line that constitutively produces interleukin 2."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).
RN [15]
RP SEQUENCE FROM N.A.
RC SPECIES=H.lar;
RX MEDLINE=86042650; PubMed=3877307;
RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,
RGreengard J.S., Crabtree G.R., Lin Y.;
RT "A viral long terminal repeat in the interleukin 2 gene of a cell
line that constitutively produces interleukin 2."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RC SPECIES=Human;
RX MEDLINE=86042650; PubMed=3877307;
RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,
RGreengard J.S., Crabtree G.R., Lin Y.;
RT "A viral long terminal repeat in the interleukin 2 gene of a cell
line that constitutively produces interleukin 2."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).
RN [17]
RP X-RAY CRYSTALLOGRAPHY.
RC SPECIES=Human;
RX MEDLINE=92335891; PubMed=1631562;
RA Bazan J.F.;
RT "Unravelling the structure of IL-2."
RL Science 257:410-412(1992).
RN [18]
RP RESPONSE TO ABOVE LETTER.
RA McKay D.B.;
RL Science 257:412-413(1992).
RN [19]
RP STRUCTURE BY NMR.
RX MEDLINE=92335891; PubMed=1510960;
RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,
RCampbell I.D.;
RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR
experiments."
RL Biochemistry 31:7741-7744(1992).
RN [20]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95111955; PubMed=7529123;
RA Bamorough P., Hedgecock C.J., Richards W.G.;
RT "The interleukin-2 and interleukin-4 receptors studied by molecular
modelling."
RL Structure 2:839-851(1994).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
WHICH INVOLVES IL2 AND BCNA.
CC -!- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used
in patients with renal cell carcinoma or metastatic melanoma.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -!- DATABASE: NAME=R&D Systems' cytokine source book: IL2;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=206".
CC -----
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CC -----
CC EMBL: J00264; AAD48509.1; -
DR EMBL: X01586; CAA25742.1; -
DR EMBL: V00564; CAA23827.1; -
DR EMBL: X00695; CAA25292.1; -
DR EMBL: K02056; AAA98792.1; -
DR EMBL: M13879; AAA59141.1; -
DR EMBL: K03174; AAA35453.1; -
DR EMBL: S77834; AAD14263.2; -
DR EMBL: S82692; AAB46883.1; -
DR


```
Query Match          34.2%; Score 680; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 2e-47;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 APTSSSTKKTQLEHLLLDLQMLINGINNNKPKLTRLMTFKFYMPKKATELKHLCLE 308
      |||
DB 21 APTSSSTKKTQLEHLLLDLQMLINGINNNKPKLTRLMTFKFYMPKKATELKHLCLE 80
      |||

QY 309 ELKPLEEVNLAKSKNFHLRPRDLISNINVLKSGSETTFMCEYADETATIVFELNR 368
      |||
DB 81 ELKPLEEVNLAKSKNFHLRPRDLISNINVLKSGSETTFMCEYADETATIVFELNR 140
      |||

QY 369 WITFCQSIISTLT 381
      |||
DB 141 WITFCQSIISTLT 153
      |||

RESULT 2
IL2_MACMU
ID IL2_MACMU STANDARD; PRT; 154 AA.
AC PS1498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca mulatta (Rhesus macaque), and
OS Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U19847; AAB60400.1; -
DR EMBL; U19852; AAB6714.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; Interleukin-2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126
FT VARIANT 78 126 BY SIMILARITY.
```

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SQ SEQUENCE 154 AA; 17685 MW; 6AEBA480F204BA49 CRC64;
Query Match          32.8%; Score 652.5; DB 1; Length 154;
Best Local Similarity 97.0%; Pred. No. 3.2e-45;
Matches 130; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 249 APTSSSTKKTQLEHLLLDLQMLINGINNNKPKLTRLMTFKFYMPKKATELKHLCLE 308
      |||
DB 21 APTSSSTKKTQLEHLLLDLQMLINGINNNKPKLTRLMTFKFYMPKKATELKHLCLE 80
      |||

QY 309 ELKPLEEVNLAKSKNFHLRPRDLISNINVLKSGSETTFMCEYADETATIVFELNR 367
      |||
DB 81 ELKPLEEVNLAKSKNFHLRPRDLISNINVLKSGSETTFMCEYADETATIVFELNR 140
      |||

QY 368 WITFCQSIISTLT 381
      |||
DB 141 WITFCQSIISTLT 154
      |||

RESULT 3
IL2_CERTO
ID IL2_CERTO STANDARD; PRT; 154 AA.
AC P46649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OS Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecidae.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U19846; AAB60399.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; Interleukin-2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT VARIANT 25 25 R -> S.
FT VARIANT 74 74 K -> E.
```

[illegible]

QY 183 SHRASGVDRFSGSVSGTDTLRISRVEADVGVYCMQGLQSPFTFGGKVDIKR 239
 Db 61 SNRASGVDRFSGSVSGTDTLRISRVEADVGVYCMQGLQSPFTFGGKVDIKR 117

RESULT 8

IL2_RABIT
 ID IL2_RABIT STANDARD; PRT; 153 AA.
 AC Q77620;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN IL2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=20304414; PubMed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the
 RT European rabbit (Oryctolagus cuniculus).";
 RL Cytokine 12:535-565(2000).
 CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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 CC -----

DR EMBL; AF068057; AAC23838.1; -;
 DR HSP; P01585; 31NK.
 DR InterPro: IPR000779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PR00265; INTERLEUKIN2.
 DR ProDom; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 153 INTERLEUKIN-2.
 FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 111 111 N-LINKED (GLCNA. . .) (POTENTIAL).
 FT DISULFID 78 125 BY SIMILARITY.
 SQ SEQUENCE 153 AA; 17256 MW; 81735362DDDB86 CRC64;

Query Match 25.8%; Score 513.5; DB 1; Length 153;
 Best Local Similarity 80.9%; Pred. No. 3.9e-34;
 Matches 106; Conservative 9; Mismatches 13; Indels 3; Gaps 3;

QY 249 APTSSSTKTKQLQLEHLLDQLMILGNNYKPKLRLTKFKYMPKPKATELKHLCIE 308
 Db 21 APTSSSTKTKQLQLEHLLDQLMILGNNYKPKLRLTKFKYMPKPKATELKHLCIE 80
 QY 309 EELKPLEEVNLQAQKNFH-LRPDLISINIVIVLELKGSETTFMCEYADETATVEFLN 367
 Db 81 EELKPLEEVNLQAQKNHGGNTRESINIVTLKLGSE-TFMCEY-DETATVEFLN 138
 QY 368 RWITFCQSIIIS 378
 Db 368 RWITFCQSIIIS 149

RESULT 9

IL2_CANFA
 ID IL2_CANFA STANDARD; PRT; 155 AA.
 AC Q29416; Q28249;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN IL2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=XBRED21/12/93; TISSUE=Lymph node;
 RX MEDLINE=95337423; PubMed=7612930;
 RA Dunham S.P., Argyle D.J., Onions D.E.;
 RT "The isolation and sequence of canine interleukin-2.";
 RL DNA Seq. 5:177-180(1995).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=96016696; PubMed=8571541;
 CC Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J.,
 CC Henthorn P.S.;
 CC "A single nucleotide insertion in the canine interleukin-2 receptor
 CC gamma chain results in X-linked severe combined immunodeficiency
 CC disease.";
 CC Vet. Immunol. Immunopathol. 47:203-213(1995).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Beagle; TISSUE=Spleen;
 CC MEDLINE=95347614; PubMed=7622066;
 CC Knapp D.W., Williams J.S., Andrisani O.M.;
 CC "Cloning of the canine interleukin-2-encoding cDNA.";
 CC Gene 159:281-282(1995).
 CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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DR EMBL; D30710; BAA06378.1; -;
 DR EMBL; U28141; AAA68969.1; -;
 DR EMBL; U11689; AAA75360.1; -;
 DR HSP; P01585; 31NK.
 DR InterPro: IPR000779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PR00265; INTERLEUKIN2.
 DR ProDom; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 155 INTERLEUKIN-2.
 FT CARBOHYD 24 24 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 112 112 N-LINKED (GLCNA. . .) (POTENTIAL).
 FT DISULFID 79 127 BY SIMILARITY.
 FT CONFLICT 4 4 M -> I (IN REF. 3).

```

FT CONFLICT 37 37 Q -> R (IN REF. 3).
FT CONFLICT 151 151 F -> Y (IN REF. 3).
FT CONFLICT 154 154 L -> M (IN REF. 3).
SQ SEQUENCE 155 AA; 17668 MW; D123E486B7F4AC1D CRC64;

Query Match 25.2%; Score 502; DB 1; Length 155;
Best Local Similarity 73.3%; Pred. No. 3.2e-33;
Matches 99; Conservative 17; Mismatches 17; Indels 2; Gaps 2;

QY 249 AP-TSSSKTKQLOLEHLLDQMLNLCINNYKNPKLTRMLTFKFPKPKATELKHLOCL 307
DB 21 APTSSSTKETEQMEQLLDQLLGVNNYENPQLSRMLTFKFPKPKATEFTHLOCL 80

QY 308 EELKPLEEVLNLAQSKNHLR-PRDLISININVLKLGSETfMFCYADETATIVFEL 366
DB 81 AEELKNLEVLGLPQSKNVHLTDTKELISNNVTLKLGSETSYNCEYDEETATITEFL 140

QY 367 NRWTFQCSIISTLT 381
DB 141 NKWTFQCSIFSTLT 155

RESULT 10
KV2D_HUMAN STANDARD; PRT; 113 AA.
ID KV2D_HUMAN
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01887; K2HUML.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 113 AA; 12316 MW; 0C3C8F81F1843CA CRC64;

PRT; A01888; K2HUTW.
DR HSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Anyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C8F81F1843CA CRC64;

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Query Match 25.1%; Score 500; DB 1; Length 113;
Best Local Similarity 82.3%; Pred. No. 3.1e-33;
Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 127 EIVLTQSPLSPLPVTGPEPASISCRSSQSLHSHNGVITYLDWYLKQKQSPQLLIYSGSHRA 186
DB 1 DIVLTQSPLSPLPVTGPEPASISCRSSQSLHSHNGVITYLDWYLKQKQSPQLLIYALS NRA 60

QY 187 SGVPDRFSGSVSGTDTFLIRISVEAEADVGVYCMQGLQSPFTFGPGTKVDIKR 239
DB 61 SGVPDRFSGSGTDTFLIRISVEAEADVGVYCMZALQAPITFGGTRLEIKR 113

RESULT 11
KV2C_HUMAN STANDARD; PRT; 112 AA.
ID KV2C_HUMAN
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01887; K2HUML.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 24.0%; Score 478.5; DB 1; Length 112;
Best Local Similarity 78.8%; Pred. No. 1.6e-31;
Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

QY 127 EIVLTQSPLSPLPVTGPEPASISCRSSQSLHSHNGVITYLDWYLKQKQSPQLLIYSGSHRA 186
DB 1 DIVLTQSPLSPLPVTGPEPASISCRSSQSLHSHNGVITYLDWYLKQKQSPQLLIYALS NRA 59

QY 187 SGVPDRFSGSVSGTDTFLIRISVEAEADVGVYCMQGLQSPFTFGPGTKVDIKR 239
DB 60 SGVPDRFSGSGTDTFLIRISVZABZBVGYYCMQALQTLPLTFGGGTNVEIKR 112

RESULT 12
IL2_MERON STANDARD; PRT; 155 AA.
ID IL2_MERON
AC Q08081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.

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OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RC MEDLINE=94174702; PubMed=8128610;
RA Mai Z., Kousoulas K.G., Horohov D.W., Klei T.R.;
RT "Cross-species PCR cloning of gerbil (Meriones unguiculatus)
interleukin-2 cDNA and its expression in COS-7 cells.";
RL Vet. Immunol. Immunopathol. 40:63-71(1994).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC -----
DR EMBL; X68779; CAA48679.1; -.
DR PIR; S33509; S33509.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
SQ SEQUENCE 155 AA; 17602 MW; D0F74AA1A381CDDA CRC64;

Query Match 24.0%; Score 478.5; DB 1; Length 155;
Best Local Similarity 70.1%; Pred. No. 2.4e-31;
Matches 94; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

QY 249 APTSSSTKKTQLQLEHLLDLQMLNGINNYKNPKLTRLMTFKFYMPPKATELKHLCLE 308
DB 21 APTSSPAKEAQVYQLQLLDLQQLGGINNYKNPKLPMLTFKFYMPPKATELKHLCLE 80

QY 309 EELKPLEEVLNLAQSKNFHRLPR-DLISINIVIVLELKGSETTFMCFYADETATVEFLN 367
DB 81 EELGPLHVLNVLQSKNLYLEDAGNFISNIRVTVMKLGSENTLNCDFDDETVTVEFLS 140

QY 368 RWITFCQSIISTLT 381
DB 141 RWITFCQSAISTWT 154

RESULT 13
IL2_PIG
ID IL2_PIG STANDARD; PRT; 154 AA.
AC P26891;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Sus scrofa (Pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE="T-cell;
RC MEDLINE=91274360; PubMed=2054386;
RA Goodall J.C., Emery D.C., Bailey M., English L.S., Hall L.;
RT "cDNA cloning of porcine interleukin 2 by polymerase chain reaction.";
RL Biochim. Biophys. Acta 1089:257-258(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RA Lefevre F.;
RN Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Iwata H., Hasegawa A., Yamamoto M., Oida T., Endo Y., Inoue T.;
RT "Structure of the porcine chromosomal interleukin-2 gene.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; X56750; CAA40071.1; -.
DR EMBL; X58428; CAA41330.1; -.
DR EMBL; AB041935; BAB16110.1; -.
DR PIR; S15473; S15473.
DR PIR; S16241; S16241.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17401 MW; F3B95E43D4A3D3E1 CRC64;

Query Match 23.7%; Score 472.5; DB 1; Length 154;
Best Local Similarity 71.6%; Pred. No. 7.2e-31;
Matches 96; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

QY 249 APTSSSTKKTQLQLEHLLDLQMLNGINNYKNPKLTRLMTFKFYMPPKATELKHLCLE 308
DB 21 APTSSSTKTKRKLQLEPLLDLQQLLEKVENYENADLSRMLTFKFYMPPKATELKHLCLE 80

QY 309 BELKPLEEVLNLAQSKNF-HLRPRDLISINIVIVLELKGSETTFMCFYADETATVEFLN 367
DB 81 EELKALEGLVNLGSKNSDSANIKESMNNINVTVLELKGSETSPKCYDDDETATVEFLN 140

QY 368 RWITFCQSIISTLT 381
DB 141 RWITFCQSIYSTLT 154

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RESULT 14
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
DR EMBL; J00236; AAA53516.1; -;
DR EMBL; M35415; AAA58735.1; -;
DR HSR; A02047; H3H026.
DR PIR; P01772; 2FB4.
DR Genew; HGNC:5545; IGHV.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 23.7%; Score 471; DB 1; Length 117;
Best Local Similarity 91.8%; Pred. No. 6.6e-31;
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNAMGWYRQAPGKLEWVSIGSGGSTYY 60
Db :||||:|||||
20 EQVLESGGGLVQPGGSLRLSCAASGFTFSRYAMSWYRQAPGKLEWVSIGSGGSTYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK 98
Db :|||||
80 GDSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK 117

RESULT 15
KV2A_HUMAN
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
```

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type)".
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -|- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01885; K2HUCM.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 23.5%; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.8%; Pred. No. 1.2e-30;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 127 EIVLTQSLPLSVTPGEPASISCRSSQSLHS-NGVTYLDWYLOKPGSQPLLIVSGSHR 185
Db :||||:|||||
2 DIVMTQPLSLPVTGEPASISCRSSQSLDGDGNTYLNWYLOKAGQSPQLLIYTLSTYR 61

QY 186 ASGVPPDRFSGSVSGTDTLIRSRVEADGVYVCMQGLQSPFTFGPTKVDIKR 239
Db :|||||
62 ASGVPPDRFSGSVSGTDTLIRSRVQAEDEVYVCMQRLPIPTFGQTKLEIRR 115

Search completed: March 14, 2003, 11:48:07
Job time : 9.69202 secs
```


GenCore version 5.1.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 11:45:09 ; Search time 28.2491 Seconds
(without alignments)
2778.994 Million cell updates/sec

Title: US-09-822-698A-5
Perfect score: 1990
Sequence: 1 QVQLVQSGGGLVPGGSLRL.....IVEFLNRWITFCQSIISTLT 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rviro.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678.5	34.1	298	11 Q9QYF0	Q9QYF0 mus musculus
2	666	33.5	150	4 Q9C001	Q9C001 homo sapien
3	660.5	33.2	156	4 Q13169	Q13169 homo sapien
4	632.5	31.8	154	6 Q9XS38	Q9XS38 papio hamad
5	617	31.0	139	4 Q16334	Q16334 homo sapien
6	544.5	27.4	241	11 Q921A6	Q921A6 mus musculus
7	541	27.2	597	4 Q96BB9	Q96BB9 homo sapien
8	517	26.0	218	11 Q925S1	Q925S1 mus musculus
9	509	25.6	155	6 Q9XT83	Q9XT83 halichoerus
10	507	25.5	121	4 Q9UL71	Q9UL71 homo sapien
11	503.5	25.3	573	4 Q8WU38	Q8WU38 homo sapien
12	503.5	25.3	613	4 Q8WU1	Q8WU1 homo sapien
13	489.5	24.6	471	4 Q8TC77	Q8TC77 homo sapien
14	483	24.3	113	4 Q9UL90	Q9UL90 homo sapien
15	481	24.2	487	11 Q99KA4	Q99KA4 mus musculus
16	480	24.1	116	4 Q9UL93	Q9UL93 homo sapien

17	479.5	24.1	118	4 Q9UL72	Q9UL72 homo sapien
18	471.5	23.7	112	4 Q9HCC1	Q9HCC1 homo sapien
19	470.5	23.6	118	4 Q9UL91	Q9UL91 homo sapien
20	470	23.6	147	4 Q9Y509	Q9Y509 homo sapien
21	466.5	23.4	138	11 Q70329	Q70329 mesocricetu
22	465	23.4	238	11 Q99M37	Q99M37 mus musculus
23	461.5	23.2	154	6 Q9XT84	Q9XT84 delphinapter
24	460	23.1	494	4 Q96K68	Q96K68 homo sapien
25	457	23.0	239	11 Q8VC55	Q8VC55 mus musculus
26	452.5	22.7	122	4 Q9UL84	Q9UL84 homo sapien
27	452.5	22.7	155	11 Q923T2	Q923T2 sigmodon hi
28	446	22.4	238	11 Q8VC16	Q8VC16 mus musculus
29	446	22.4	473	11 Q91Z05	Q91Z05 mus musculus
30	445	22.4	479	11 Q91WP5	Q91WP5 mus musculus
31	444	22.3	119	11 Q920E7	Q920E7 mus musculus
32	441	22.2	239	4 Q8TCD0	Q8TCD0 homo sapien
33	438.5	21.5	114	4 Q9UL80	Q9UL80 homo sapien
34	426.5	21.4	486	11 Q91Z07	Q91Z07 mus musculus
35	423.5	21.3	105	6 Q62773	Q62773 felis silve
36	423	21.3	131	4 Q9UL88	Q9UL88 homo sapien
37	423	21.3	480	11 Q91XEL	Q91XEL mus musculus
38	416.5	20.9	469	11 Q8R3V9	Q8R3V9 mus musculus
39	413.5	20.8	150	11 P70291	P70291 mus musculus
40	413.5	20.8	169	11 Q9QUS8	Q9QUS8 mus musculus
41	411.5	20.7	150	11 P70294	P70294 mus musculus
42	408.5	20.5	437	11 Q9R1A4	Q9R1A4 mus musculus
43	408	20.5	95	4 Q9ULB6	Q9ULB6 homo sapien
44	407.5	20.5	116	6 Q29138	Q29138 trichechus
45	407	20.5	155	6 Q9GL83	Q9GL83 capra hircu

ALIGNMENTS

RESULT 1

Q9QYF0 PRELIMINARY; PRT; 298 AA.
 AC Q9QYF0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CN 8 scfv.
 GN CN 8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=SPLEEN;
 RX MEDLINE=20183931; PubMed=10706631;
 RA Shinohara N., Demura T., Fukuda H.;
 RT "Isolation of a vascular cell wall-specific monoclonal antibody
 RT recognizing a cell polarity by using a phase display subtraction
 RT method.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
 DR EMBL; AB036341; BAA88633.1; -.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00406; IGV; 2.
 SQ SEQUENCE 298 AA; 31867 MW; EOF96B8A17004317 CRC64;

Query Match 34.1%; Score 678.5; DB 11; Length 298;
 Best Local Similarity 53.1%; Pred.No. 1e-47;
 Matches 138; Conservative 35; Mismatches 66; Indels 21; Gaps 4;

QY 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAWGVRQAPEGKLEWVSGISGGSTYY 60
 Db 40 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAWGVRQAPEGKLEWVSGISGGSTYY 99
 QY 61 ADSVGRFTISDMSKNTLYLQMNSLRAEDTAVYCAKHTGGVMDPDIWYQGQTLTVS 120

DR	PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ	SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;
	Query Match 31.8%; Score 632.5; DB 6; Length 154;
	Best Local Similarity 92.5%; Pred. No. 2.3e-44;
	Matches 124; Conservative 5; Mismatches 4; Indels 1; Gaps 1;
QY	249 APTSSSTKTKQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKLHQCLE 308
Db	21 APTSSSTKTKQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKLHQCLE 80
QY	309 EELKPLEEVNLQAQSKNPHLR-PRDLSININVIVLELKGSSETTFMCEYADETATIVEFLN 367
Db	81 EELKPLEEVNLQAQSKNPHLR-PRDLSININVIVLELKGSSETTFMCEYDDDTATIEFLN 140
QY	368 RWITFCSIISTLT 381
Db	141 GWITFCSIISTLT 154
RESULT 5	
Q16334	PRELIMINARY; PRT; 139 AA.
ID	Q16334 AC
AC	Q16334:
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE	IL-2 protein (Fragment).
GN	IL-2
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	[1]
RX	SEQUENCE FROM N.A.
RP	MEDLINE=95239150; PubMed=7722480;
RA	Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT	"Interleukin-2 transcripts in human and rodent brains: possible
RT	expression by astrocytes."
RL	J. Neurochem. 64:1928-1936(1995).
DR	EMBL: S77835; AAD14264.1; -.
DR	HSP; P01585; 3INK.
DR	InterPro: IPR000779; Interleukin-2.
DR	Pfam: PF00715; IL2; 1.
DR	PRINTS; PR00265; INTERLEUKIN2.
DR	ProDom: PD003649; Interleukin-2; 1.
DR	SMART: SM00189; IL2; 1.
DR	PROSITE; PS00424; INTERLEUKIN_2; 1.
FT	NON_TER 1
SQ	SEQUENCE 139 AA; 15986 MW; 731FBA406DC63C5 CRC64;
	Query Match 31.0%; Score 617; DB 4; Length 139;
	Best Local Similarity 98.4%; Pred. No. 3.8e-43;
	Matches 121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	249 APTSSSTKTKQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKLHQCLE 308
Db	17 APTSSSTKTKQLQLEHLLDLQMILGXINNYKNPKLTRMLTFKFYMPKKATELKLHQCLE 76
QY	309 EELKPLEEVNLQAQSKNPHLR-PRDLSININVIVLELKGSSETTFMCEYADETATIVEFLN 368
Db	77 EELKPLEEVNLQAQSKNPHLR-PRDLSININVIVLELKGSSETTFMCEYADETATIVEFLN 136
QY	369 WIT 371
Db	137 WIT 139
RESULT 6	
Q921A6	PRELIMINARY; PRT; 241 AA.
ID	Q921A6 AC
AC	Q921A6:
DT	01-DEC-2001 (TREMBLrel. 19, Created)

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Best Local Similarity 69.0%; Pred. No. 5.8e-36;
Matches 109; Conservative 14; Mismatches 17; Indels 18; Gaps 3;

QY 1 QVOLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSGSTYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSAISGGSGSTYY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAK-----HTGGGVMDPIDYWGQGT 116
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKDPGYSASGNTREDYWGQGT 139
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 VTVSSGGGALVLTQSPSLSPVTPGEPASISCRSSQS 154
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 140 VTVSSGSAS-----APTLPFL-----VSCSNSPS 163

RESULT 8
Q925S1
ID AC Q925S1 PRELIMINARY; PRT; 218 AA.
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2
DR NON_TER 218 218
FT SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 26.0%; Score 517; DB 11; Length 218;
Best Local Similarity 48.0%; Pred. No. 1.2e-34;
Matches 107; Conservative 39; Mismatches 57; Indels 20; Gaps 4;

QY 1 QVOLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSGSTYY 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||||
Db 3 QVKLQSGPELKKPGETVRISCKASGYTTTAGMQVQKMPGKGLKWTGWINTHSGVPEY 62
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||||

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKHTGGGVMD---PIDYWGQGTLY 117
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||||
Db 63 AEEFKGRFAFSLTSSASTAYLQISLNKEDTATYFCMR-----WDYDGGFAYWGQGTTV 116
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||||

QY 118 TVSSGG-----GALEIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWY 167
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 117 TVSSGGGGGGGGGGSDIVLTQSPASLAVSLQQRATISCRASES-VDNIGISFMNWF 175
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 168 LQKPGSPOLLVYSGSHRASGVDPFRFSGVSGTDTFLIRSRVE 210
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 176 QQKPGPPKLLIYAASKQSGVPGAGILLASGSGTDFSLNIYPME 218
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9

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Q9XT83
ID AC Q9XT83 PRELIMINARY; PRT; 155 AA.
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99221046; PubMed=10206205;
RA St-Laurent G., Bellevue C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) Interleukin
RT 2.";
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072871; AAD40848.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 155 AA; 17860 MW; F18F49AC672241A CRC64;

Query Match 25.6%; Score 509; DB 6; Length 155;
Best Local Similarity 75.8%; Pred. No. 3.4e-34;
Matches 102; Conservative 15; Mismatches 16; Indels 2; Gaps 2;

QY 249 AP-TSSSTKTKTQLEHLLDQLMILNGINNYKNPKLTRMLTFKFPMPKKATELKLQCL 307
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 APTSSSTKETQOQLLELLDRLLLGVNYPQLSRMLTFKFTPKKATELTHLQCL 80
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 308 EEELKPLEEVNLAAQSNFHLRP-RDLISNIVNVLKGSFTFPCYEADETATIFEFL 366
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 PEELKLEEVLYLAPNKNFHLTDIKELMSNINVTLLKLGSETRFKCEYDDTATITEFL 140
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 367 NRWITFCQSIITSLT 381
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 141 NKWITFCQSIIFSLT 155
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
Q9UL71
ID AC Q9UL71 PRELIMINARY; PRT; 121 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2Fb4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

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FT NON_TER 1 1
SQ NON_TER 121 121
SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 25.5%; Score 507; DB 4; Length 121;
Best Local Similarity 81.0%; Pred. No. 3.5e-34;
Matches 98; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLVQSGGVLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGVVPGGSLRLSCAASGFTFDGYAMHWVRQAPGKGLVWVSLISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVMDPIDYWGQGLTVTVS 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTALYYCAKGVTTIYDRFDIWGQGTWTVS 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 121 S 121
Db 121 S 121

RESULT 11
Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 63.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 25.3%; Score 503.5; DB 4; Length 573;
Best Local Similarity 59.1%; Pred. No. 6.7e-33;
Matches 110; Conservative 16; Mismatches 39; Indels 21; Gaps 6;

QY 1 QVQLVQSGGVLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 EVQLVESGGVLVPGGSLRLSCAASGFTFDYAMHWVRQAPGKGLVWVSGISNWSIGY 79
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGG-----GVMDPIDYWGQGLTV 117
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTALYYCAKHSIGSYIGYYGMDVWGQGTTV 139
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 118 TVSSGGGALVLTQSPSLSPVTPG-----EPASISCRSSQSLHSNHTYTLDWYLQK 170
|||||
Db 140 TVSSAP-----TKAPDVFIISGCRHPKDNPSVVLACLITG--YHPTSVT-VTWYMTG 189
|||||

QY 171 PQSPQ 176
|
Db 190 QSQ-PQ 194

RESULT 12
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Q8WUK1 PRELIMINARY; PRT; 613 AA.
ID Q8WUK1;
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 25.3%; Score 503.5; DB 4; Length 613;
Best Local Similarity 67.5%; Pred. No. 7.4e-33;
Matches 104; Conservative 11; Mismatches 24; Indels 15; Gaps 3;

QY 1 QVQLVQSGGVLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 QVQLVESGGGVVPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLVWVAIVYDGSNKY 79
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVMDPIDYWGQGLTVTVS 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKDWSEGV-ETFDIWGQGTWTVS 138
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 121 SGGGALVLTQSPSLSPVTPGEPASISCRSSQS 154
|||
Db 139 SGSAS-----APTLFPL-----VSCNSPS 158
|||

RESULT 13
Q8TC77 PRELIMINARY; PRT; 471 AA.
ID Q8TC77;
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 24.6%; Score 489.5; DB 4; Length 471;
Best Local Similarity 50.5%; Pred. No. 7.1e-32;
Matches 111; Conservative 20; Mismatches 48; Indels 41; Gaps 6;

QY 1 QVQLVQSGGVLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
|||
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Db 20 EVLVESGGGLVPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSMSSSSSYIYY 79
Qy 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTG--GGVNDPIDYWGQGLTIV 118
Db 80 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCARDLRQLTSYW-YFDLWGRGLTIV 138
Qy 119 VSSGGGALIVLTQSPFLSLPTVTPG-----EPASISCRSS----- 152
Db 139 VSSAS-----TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 191
Qy 153 ---QSLLHSNGYTYLDWLQKPGQS--PQLLIYSGSHRAS 187
Db 192 HTFPAVLQSSGLYSUSSVTVTPSSSLGTQTYICNVNHRKPS 231

RESULT 14
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD36260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 24.3%; Score 483; DB 4; Length 113;
Best Local Similarity 78.5%; Pred. No. 3e-32;
Matches 95; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

Qy 1 QVLVQSGGGLVPGGSLRLSCAASGFTFSRNAMGWVRQAPGKGLWVSGISGGSGSYIY 60
Db 1 EVLVESGGVVPQGGSLRLSCAASGFTFSYGMHVRQAPGKGLWVAFIRYDGSNKYY 60
Qy 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVNDPIDYWGQGLTIVTS 120
Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAK-----DLNWYWGQGLTIVTS 112
Qy 121 S 121
Db 113 S 113

RESULT 15
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AA04786.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DDB333077B CRC64;

Query Match 24.2%; Score 481; DB 11; Length 487;
Best Local Similarity 41.5%; Pred. No. 3.7e-31;
Matches 134; Conservative 33; Mismatches 102; Indels 54; Gaps 15;

Qy 1 QVLVQSGGGLVPGGSLRLSCAASGFTFSRNAMGWVRQAPGKGLWVSGISGGSGSYIY 60
Db 20 EVLVESGGGLVPGGSLRLSCAASGFTFSYAMSVVROTPEKRLWVATISDGGSYIY 79
Qy 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGG---GVNDPIDYWGQGLTIV 117
Db 80 PDNVKGRFTISRDNKNTLYLQMSHLKSEDTAMYYCARDMGSGSPYGGYSRFDYWGQGTI 139
Qy 118 TVSSGGGALIVLTQSPSLP-VTPGEPASISCRSSQSLHS---NGYTYLDWLQKPGQ 173
Db 140 TVSSESARNPTIY---PLTLPRALSDPVIIGC-----LIHDFPSGTWNVTW--GKSGK 189
Qy 174 S-----PQLLIYSGSHRASGVPDRFSVSGVSGTDFTL-RISRVEADV--GVVYCMOGLQ 224
Db 190 DITVNFPPAL-----ASG-----GGYTMSSQLTLPAVECPGESVKCSVQHDNSAVQ 237
Qy 225 SPFTFGGTVKDIKRGSGGGGALAPTS--SSTKKTQLOLEHLL-----DLQMLNGINN 278
Db 238 -----ELDVKCSGPPPPCPPCPSPCHPSLSLQRPALDILLGSDASLTCTLNGLRN 288
Qy 279 YKNPKLT-RMLTFKFPMPKATE 300
Db 289 PEGAVFTWEPSTGKDAVQKKAQV 311

Search completed: March 14, 2003, 11:49:35
Job time : 31.2491 secs
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